

STIC-Biotech/ChemLib

172534

me

From: CR
Sent: Sunday, November 27, 2005 12:15 PM
To: STIC-Biotech/ChemLib
Subject: FE
Sequence search of Application No. 10/600,645

Please do a standard search on:

- (i). SEQ ID NO: 2 against both commercial and interference amino acid databases;
(ii). SEQ ID NO: 1 and 2 against both commercial and interference nucleic acid databases.

Thank you very much!

Ruixiang Li
GAU 1646
REM 4D75
Mail Box 4C70
(571) 272-0875

2 aa 532

1 na 1813

me

STIC-BIOTECH/ChemLib

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

Date completed: _____
Searcher: Beverly e 2523
Terminal time: _____
Elapsed time: _____
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site
____ STIC
____ CM-1
____ Pre-S
Type of Search
____ N.A. Sequence
____ A.A. Sequence
____ Structure
____ Bibliographic

Vendors
____ IG
____ STN
____ Dialog
____ APS
____ Geninfo
____ SDC
____ DARC/Questel
____ Other ☒ GEN

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STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 172534

TO: Ruixiang Li
Art Unit: 1646
Location: rem/4D75/4C70
Serial Number: 10/600645

Monday, December 12, 2005

From: Beverly Shears
Location: Biotech-Chem Library
REM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Search Notes

Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

Published Applications Database - November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).



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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 12:46:28 / Search time 6240 Seconds
(without alignments)
16515.573 Million cell updates/sec

Title: US-10-600-645-1

Perfect score: 1813
Sequence: 1 CTAGTGGATCCCGGGCTG.....TTCCAGGACTGTGCAGAAATGC 1813

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1813	100.0	1813	6	AR169902 Sequence
2	1813	100.0	1813	6	AR382508 Sequence
3	1750.4	96.5	3003	6	CQ986812 Sequence
4	1750.4	96.5	3003	6	CS027157 Sequence
5	1750.4	96.5	3003	9	RATRALK3
6	1750.4	96.5	3167	6	CQ986810 Sequence
7	1750.4	96.5	3167	6	CQ986811 Sequence
8	1750.4	96.5	3167	6	CS027155 Sequence
9	1750.4	96.5	3167	6	CS027156 Sequence
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11	1595.8	88.0	1599	9	D17667 Rat mRNA fo
12	1584.6	87.4	2292	9	MUSBMPRC
13	1584.6	87.4	5288	9	BC042611 Mus muscu
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15	1581.4	87.2	2070	6	AR140650 Sequence
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17	1581.4	87.2	2070	6	AR264352 Sequence
18	1581.4	87.2	2070	6	AR475173 Sequence

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20	1574.2	86.8	2402	6	AR174013 Sequence
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22	1574.2	86.8	2402	9	MMU04672 Sequence
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24	1488.6	82.1	1599	9	MMALK3A
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28	1387	76.5	2932	6	AR164270 Sequence
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ALIGNMENTS

RESULT 1	AR169902	Sequence 1 from patent US 6291206.	1813 bp	DNA	linear	PAT 17-DEC-2001
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DEFINITION	AR169902	Sequence 1 from patent US 6291206.	1813 bp	DNA	linear	PAT 17-DEC-2001
ACCESSION	AR169902	Sequence 1 from patent US 6291206.	1813 bp	DNA	linear	PAT 17-DEC-2001
VERSION	AR169902.1	GI:17907859	1813 bp	DNA	linear	PAT 17-DEC-2001
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ORGANISM	Unknown.	Unknown.	1813 bp	DNA	linear	PAT 17-DEC-2001
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AUTHORS	Wozney, J.M., Celeste, A.J., Thies, R.Scott. and Yamaji, N.	Wozney, J.M., Celeste, A.J., Thies, R.Scott. and Yamaji, N.	1813 bp	DNA	linear	PAT 17-DEC-2001
TITLE	BMP receptor proteins	BMP receptor proteins	1813 bp	DNA	linear	PAT 17-DEC-2001
JOURNAL	Patent: US 6291206-A 1 18-SEP-2001;	Patent: US 6291206-A 1 18-SEP-2001;	1813 bp	DNA	linear	PAT 17-DEC-2001
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QY	61	ATGACTCAGCTATACACTTACATCAGATTACTCGGAGCCCTGTCTGTTTCATCTTCAT	120	
Db	61	ATGACTCAGCTATACACTTACATCAGATTACTCGGAGCCCTGTCTGTTTCATCTTCAT	120	
QY	121	GTTCAAGGGCAGAACTTAGATAGTATGCTCCATGGTACTGCTGATGAAATCAGACGTGGAC	180	
Db	121	GTTCAAGGGCAGAACTTAGATAGTATGCTCCATGGTACTGCTGATGAAATCAGACGTGGAC	180	
QY	181	CAGAGAAGCCGAAAATGGAGTGGAGTGTAGCACCAGGACACCTTACCTTTCTTAAAA	240	
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QY	241	TGCTATTGCTCAGGACATGCCCGCAGATGACGCTATTAAATAACATGCATTAATGGC	300	

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QY 1801 CTCTCGAAGATGC 1813
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RESULT 2
AR382508
LOCUS AR382508 1813 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6610513.
ACCESSION AR382508
VERSION AR382508.1 GI:40091231
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1813)
AUTHORS Wozney,J.M., Celeste,A.J., Thies,R.S. and Yamaji,N.
TITLE Receptor proteins
JOURNAL Patent: US 6610513-A 1 26-AUG-2003;
Genetics Institute, LLC.; Cambridge, MA
FEATURES
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
LOCUS CQ986812 3003 bp DNA linear PAT 25-JAN-2005
DEFINITION Sequence 121 from Patent WO2005003158.
ACCESSION CQ986812
VERSION CQ986812.1 GI:58194651
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1
AUTHORS Brunkow,M.E., Galas,D.J., Kovacevich,B., Mulligan,J.T.,
Paepke,B.W., van Ness,J., and Winkler,D.G.
TITILE Compositions and methods for increasing bone mineralization
JOURNAL Patent: WO 2005003158-A 121 13-JAN-2005;
Celltech R & D, Inc. (US)
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Best Local Similarity 99.6%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 6; Indels 2; Gaps 2;
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QY 90 ACTGGGAGCCTGCTCTGTTTCATCTTCATGTTTCAAGGCGAGAAATCTAGATGATGCT 149

[illegible]

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Qy	1770	TCACAGGCTGCTAACAGTAAACCTTTTCAGGACTCTCGCAAGATGC	1813
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DEFINITION	Sequence 90 from Patent WO2005014650.		linear
ACCESSION	CS027157		PAT 03-MAR-2005
VERSION	CS027157.1		
KEYWORDS	GI:60496971		
SOURCE	Rattus norvegicus (Norway rat)		
ORGANISM	Rattus norvegicus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
AUTHORS	Winkler,D.G., Shi,J. and Latham,J.		
TITLE	Antibodies specific for sclerostin and methods for increasing bone mineralization		
JOURNAL	Patent: WO 2005014650-A 90 17-FEB-2005; Celltech R & D, Inc. (US)		
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Qy	1290	AGAAGTCTGGACGAGCGCTGAGTAAACACCAATTTCCAGCCCTACATCATGCTGCATCAT	1349
Db	1312	AGAAGTCTGGACGAGCGCTGAGTAAACACCAATTTCCAGCCCTACATCATGCTGCATCAT	1371
Qy	1350	CTACAGCTTTGGTTTGGATCATTTGGGAGATGGCGCGCTCGCTGTATTTACAGAGGAATCGT	1409
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Qy	1410	GGAGGAATATCAATATACCATAATTACAAATGCTGCTGACCCATCTTTATGAAGACAT	1469
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Qy	1590	CAGACTCACAGCTTTTCAGAAATCAAGAGACGCTCGCAAAAGATGGTTGAAATCCAGGATGT	1649
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LOCUS			
DEFINITION			
ACCESSION			
VERSION			
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SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
AUTHORS			
TITLE			

JOURNAL	Submitted (26-AUG-1994) Shinichiro Oida, Faculty of Dent., Tokyo Medical and Dental University, Department of Biochemistry; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113, Japan (Tel:03-3813-6111(ex.5126), Fax:03-5684-8047)		
COMMENT	On Jun 29, 1996 this sequence version replaced gi:599585.		
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Best Local Similarity	99.6%;	Pred. No. 0;	
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QY	90	ACTGGAGCGCTCTGTTCATCATTTCTCATGTTCAAGGGCAGAAATCTAGATAGTATGCT	149
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QY	210	AGCACAGAGGACCTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCAGATGA	269
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QY	390	CAAGGATTACACAAAGCCACCTACGCGAGCAATAGAAATGTTCTCGGACCAATTTGTG	449

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QY	1590	CAGACTCACAGCTTTTGAGAAATCAAGAGACGCTCGCAAAGATGTTGAAATCCCAAGGATGT	1649
Db	1612	CAGACTCACAGCTTTTGAGAAATCAAGAGACGCTCGCAAAGATGTTGAAATCCCAAGGATGT	1671
QY	1650	AAAGATTGACAAACAGTTTTTGAGAAAGAAATTTAGACTGCGAAGAAATTCACCCGAGGAAG	1709
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QY	1710	GGTCGAGTTAGCATGGACTAGGATGTCGGCTTGGTTTTCCAGACTCTCTCTTACCATCT	1769
Db	1732	GGTCGAGTTAGCATGGACTAGGATGTCGGCTTGGTTTTCCAGACTCTCTCTTACCATCT	1790
QY	1770	TCACAGGCTGCTAACAGATAAACCTTTTCAGGACTCTGCAGAAATGC	1813
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DEFINITION	Sequence 119 from Patent WO2005003158.	linear	PAT 25-JAN-2005
ACCESSION	CQ986810		
VERSION	CQ986810.1	GI:58194649	
KEYWORDS			
SOURCE	Rattus sp.		
ORGANISM	Rattus sp.		
REFERENCE	1		
AUTHORS	Brunkow, M.E., Galas, D.J., Kovacevich, B., Mulligan, J.T.,		
TITLE	Preper, B.W., van Ness, J. and Winkler, D.G.		
JOURNAL	Compositions and methods for increasing bone mineralization		
FEATURES	Patent: WO 2005003158-A 119 13-JAN-2005;		
source	Celltech R & D, Inc. (US)		
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Db	255	ACTGGGAGCCTGTCTGTTCATCATTTCTCATGTTCAAGGGCAGAAATCTAGATAGTATGCT	314
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DEFINITION      Sequence 120 from Patent WO2005003158.
ACCESSION      CQ986811
VERSION        CQ986811.1  GI:58194650
KEYWORDS
SOURCE
ORGANISM      Rattus norvegicus (Norway rat)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
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REFERENCE
AUTHORS      Brunkow,M.E., Galas,D.J., Kovacevich,B., Mulligan,J.T.,
Paepker,B.W., van Ness,J. and Winkler,D.G.
TITLE      Compositions and methods for increasing bone mineralization
JOURNAL      Patent: WO 2005003158-A 120 13-JAN-2005;
Celltech R & D, Inc. (US)
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Best Local Similarity 99.6%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

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QY	1650	AAAGATTGACAAACAGTTTTCAGAAAGAAATTTAGACTGCAAGAAATTCACCCGAGGAAG	1709	Db	615	CAACCAATTTTGCAGCCTACACTGCCCCCTGTGCTTATAGGCCCATTTCTTTGATGGCAG	674
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AUTHORS		Antibodies specific for sclerostin and methods for increasing bone mineralization		QY	930	TTTTATAGCTGCAGACATTTAAAGGCACCGGTTCTTGGACTCAGCTGTATTTGATTACTGA	989
TITLE		Patent: WO 2005014650-A 89 17-FEB-2005; Celltech R & D, Inc. (US)		Db	1095	TTTTATAGCTGCAGACATTTAAAGGCACCGGTTCTTGGACTCAGCTGTATTTGATTACTGA	1154
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LOCUS 3167 bp mRNA linear ROD 27-MAY-1995
DEFINITION bone morphogenetic protein type IA receptor [rats, mRNA, 3167 nt].
ACCESSION S75359
VERSION S75359.1 GI:834007
KEYWORDS
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 3167)
Takeda,K.
REFERENCE Expression of serine/threonine kinase receptors during ectopic bone
formation induced by bone morphogenetic protein (BMP)
Kokubyo Gakkai Zasshi 61 (4), 512-526 (1994)
7897267
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 160455] from the original journal article.
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ORIGIN

Query Match 96.5%; Score 1750.4; DB 9; Length 3167;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 6; Indels 2; Gaps 2;
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RESULT 11
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LOCUS RATRB4R1 1599 bp mRNA linear ROD 04-FEB-1999
DEFINITION Rat mRNA for bone morphogenetic protein 4 receptor, complete cds.
ACCESSION D17667
VERSION D17667.1 GI:684975
KEYWORDS bone morphogenetic protein 4 receptor.
SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE
AUTHORS Ikeda T. and Takahashi H.
TITLE Expression pattern of bone morphogenetic protein 4 receptor in embryo and adult rat
JOURNAL unpublished
REFERENCE 2 (bases 1 to 1599)
AUTHORS Takahashi H.
TITLE Direct Submission
JOURNAL Submitted (16-SEP-1993) Hiroshi Takahashi, Tokyo Metropolitan
Institute of Gerontology, Department of Pathology; 35-2 Sakaecho,,
Itabashi-Ku, Tokyo 173, Japan (Tel:03-3964-3241(ex.3034),
Fax:03-3579-4776)
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Db 1260 TGGAAATTGCTGTTATTTGCTGACCTGGGCTAGCTGTTAAATTTCAACAGTGATACAAATGA 1319
QY 1239 AGTTGACATATACCTTTGAACACACAGGGTGGGCAACAGGGGGTACATGGCTCCAGAAATGCT 1298
Db 1320 AGTTGACATATACCTTTGAATACACAGGGTGGGCAACAGGGGTACATGGCTCCAGAAATGCT 1379
QY 1299 GGACAGAGCGCTGAGTAAACCAATTTCCAGCCCTACATCATGGCTGACATCTACAGCTT 1358
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QY 1359 TGGTTTGTATCATTTGGGAGATGGCCCGCTGCTGTATTACAGAGGAAATCGTGGAGGAATA 1418
Db 1440 TGGTTTGTATCATTTGGGAAATGGCTCGTGTATTACAGAGGAAATCGTGGAGGAATA 1499
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Db 1500 TCAATTTACATATTAACAATGCTGCTAGTGACCCATCTCTATGAGGACATCGTGGAGGT 1559
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Db 1560 TGTGTGTGTGAACCGCTTGGGCCCAATCGTGTCTAACCGCTGGAACAGTGATGATGCTT 1619
QY 1539 TCGACCGCTTTTGAAGCTGATGTCAGAAATGCTGGGCCCAATAATCCAGCATCCAGACTCAC 1598
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QY 1599 AGCTTTGAGAAATCAAGAAGACGCTCGCAAAAGATGTTGAATCCAGGATGTAAGAATTTG 1658
Db 1680 AGCTTTGAGAAATCAAGAAGACACTTGCAGAAATGTTGAATCCAGGATGTAAGAATTTG 1739
QY 1659 AC----AAACAGTTTTGAGAAAGATTTAGACTGCAAGAAATTC----ACCCGAGGAAG 1710
Db 1740 ACAATTAACAATTTTGGAGGGAATTTAGACTGCAAGAACTTTCTTACCAAGGAATGG 1799
QY 1711 GTGGAGTTAGCATGACTAGGATGTCGGCTGTTTCCAGACTCTCTCTCTTACCATCTT 1770
Db 1800 GTGGAGTTAGCATGGAATAGGATGTTGACTTGGTTTCCAGACTCTCTCTCTTA-CATCTT 1858
QY 1771 CACAGGCTGTAAACAGTAAACCTTTCCAGACTCTCAGAAATGC 1813
Db 1859 CACAGGCTGTAAACAGTAAACCTTACCCTACTCTACAGAATAC 1901

RESULT 13
BC042611
LOCUS
DEFINITION
Mus musculus bone morphogenetic protein receptor, type 1A, mRNA
(cDNA clone MGC:36094 IMAGE:5364272), complete cds.
ACCESSION
BC042611
VERSION
BC042611.1
KEYWORDS
MGC.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 5288)
AUTHORS
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E.,
Schnier, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16999-16903 (2002)
1247932
2 (bases 1 to 5288)
Direct Submission
Submitted (02-JAN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbe-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 53 Row: 9 Column: 18
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.

FEATURES

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ORIGIN

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Best Local Similarity 94.2%; Pred. No. 0;
Matches 1680; Conservative 0; Mismatches 94; Indels 9; Gaps 3;

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235 CTGCTCTGTTTCATCATTTCTCATGTTTCAAGGGCAGAAATCTAGATAGTAGTATGCTTCCATGTCAC 294
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295 TGGTATGAATCAGAGCTGGACCCAGAGAGCGGAAATGAGTACGCTGATGAGTACGAGCAGCAGCAG 354
219 GGACACCTTACCTTCTTAAATGCTATTGCTCAGGACACTGCCAGAGTACGCTGATGAGTACGAGCAG 278
355 GGATACCTTGCCTTCTTAAAGTCTATTGCTCAGGACACTGCCAGAGTACGCTGATGAGTACGAGCAG 414
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415 TAAACATGATTAATTAATGGCCATTGCTTTGCCATTATAGAAAGAGATGATCAGGAGAG 474
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475 AACCACATTAACCTTCTGGGCTGATGAAGTATGAAGCTCTGATTTTCAATGCAAGGATTC 534
399 ACCAAAGCCAGCTACGACGAGACAAATAGAAATGCTCGGACCAATTTGTGCAACCAATA 458
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699 ACAAGCTCTGCTAGTGGATCTGGATACCTTTATTTGTTTACGCGAAGTATGCGGTAAGTC 758
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[illegible]

RESULT 15
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DEFINITION	Sequence 13 from patent US 6207814.				
ACCESSION	AR140650				
VERSION	AR140650.1	GI:14463146			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 2070)				
AUTHORS	Miyazono,K., ten Dijke,P., Franzen,P., Yamashita,H. and Heldin,C.-H.				
TITLE	Activin receptor-like kinases, ALK-3 and ALK-6, and nucleic acids encoding them				
JOURNAL	Patent: US 6207814-A 13 27-MAR-2001;				
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	Best Local Similarity 94.1%; Pred. No. 0;				
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Job time : 6247 secs

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Qy	1599	AGCTTTGAGAAATCAAGAAAGCGCTCGCAAGATGTTGAAATCCAGAGATGTAAGATTTG	1658
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 05:59:38 ; Search time 767 Seconds
(without alignments)
15753.700 Million cell updates/sec

Title: US-10-600-645-1
Perfect score: 1813
Sequence: 1 CTAGTGGATCCCCGGGCTG.....TTCAGGACTCTGCAGATGC 1813

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	1750.4	96.5	3167	14	Adw28816 Rat bone
5	1750.4	96.5	3167	14	Adw28815 Rat bone
6	1750.4	96.5	3167	14	Adw28815 Rat bone
7	1750.4	96.5	3167	14	Adx97428 Rat bone
8	1581.4	87.2	2070	2	AAZ09847 Rat bone
9	1581.4	87.2	2070	14	AAZ09847 Rat bone
10	1579.8	87.1	2070	2	Ady51875 Murine AL
11	1574.2	86.8	2402	2	AAQ66640 Mouse Act
12	1574.2	86.8	2402	2	AAQ90184 Rat bone
13	1574.2	86.8	2402	2	Aat27228 Bone morp
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				10	ACF05952 Human bon

20	1387	76.5	2932	14	Adw28812 Human bon
21	1387	76.5	2932	14	Adx07490 Cyclin-de
22	1387	76.5	2932	14	Adx97425 Human bon
23	1387	76.5	2932	14	Ady51867 Human ALK
24	1387	76.5	2932	14	Aec02077 Nucleotid
25	1385.4	76.4	2932	2	AAQ66636 Human Act
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33	978.2	54.0	1185	12	ACH87174 Human gen
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40	716	39.5	1952	14	Ady51879 Murine AL
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ALIGNMENTS

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XX
25-MAR-2003 (revised)
DT 28-SEP-1995 (first entry)
XX
DE Sequence encoding bone morphogenic protein receptor CFK1-23a.
XX Bone morphogenic protein; receptor; serine/threonine kinase; BMP; bone;
KW cartilage; injury; treatment; inhibition; ss.
XX Rattus rattus.
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FT /product= "Bone morphogenic protein receptor."
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PN W09507982-A1.
XX
23-MAR-1995.
XX
07-SEP-1994; 94WO-US010080.
PR 17-SEP-1993; 93US-00123934.
XX (GEMY) GENETICS INST INC.
XX
PI Wozney JM, Celeste AJ, Thies RS, Yamaji N;
XX WPI; 1995-131350/17.
DR P-PSDB; AAR70237.
XX
PT Truncated BMP and serine/threonine kinase receptor proteins - used to
XX inhibit the effects of BMP-2 and/or BMP-4.
PS Claim 2; Page 48-50; 83pp; English.
XX
CC Truncated bone morphogenic protein (BMP) receptors and serine/threonine

kinase receptors may be used in compositions to inhibit the effects of BMP's such as BMP 2 and BMP-4. The truncated receptors comprise the ligand binding domain, but not the serine/threonine kinase and CC transmembrane domains. The truncated proteins are soluble and will be excreted into supernatant by recombinant mammalian cells expressing them. CC Such cells can be delivered in a medium or matrix which partially impedes CC their mobility, thereby localising the cells to a site of bone or CC cartilage injury. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 1813 BP; 506 A; 397 C; 439 G; 471 T; 0 U; 0 Other;

Query Match 100.0%; Score 1813; DB 2; Length 1813;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CTAGTGGATCCCCCGGCTGCAGAAATCTCGCGCGCCAGGACACGTCGGAATTGGACA	60
DB	1	CTAGTGGATCCCCCGGCTGCAGAAATCTCGCGCGCCAGGACACGTCGGAATTGGACA	60
QY	61	ATGACTCAGCTATACACTTACATCAGATTACTGGGAGCCCTGCTGTTTCATCTTCAT	120
DB	61	ATGACTCAGCTATACACTTACATCAGATTACTGGGAGCCCTGCTGTTTCATCTTCAT	120
QY	121	GTTCAAGGCGAGAACTCTAGATAGTATGCTCCATGGTACTGGTATGAATCAGACGTTGGAC	180
DB	121	GTTCAAGGCGAGAACTCTAGATAGTATGCTCCATGGTACTGGTATGAATCAGACGTTGGAC	180
QY	181	CAGAAGAAGCCGGAATGGAGTACGTTAGCACACGAGGACACCTTACCTTTCTTAAAA	240
DB	181	CAGAAGAAGCCGGAATGGAGTACGTTAGCACACGAGGACACCTTACCTTTCTTAAAA	240
QY	241	TGCTATTGCTCAGGACACTGCCCCAGATGACGCTATTAAACACATGCAATTAATGGC	300
DB	241	TGCTATTGCTCAGGACACTGCCCCAGATGACGCTATTAAACACATGCAATTAATGGC	300
QY	301	CATTGCTTTGCCATTATAGAAGATGATCAGGAGAAACACCGTTAACTCTCGGGTCT	360
DB	301	CATTGCTTTGCCATTATAGAAGATGATCAGGAGAAACACCGTTAACTCTCGGGTCT	360
QY	361	ATGAAGTATGAAGCTCTGATTTTCAATGCAAGATTCACCAAAAGCCAGCTACGCAGG	420
DB	361	ATGAAGTATGAAGCTCTGATTTTCAATGCAAGATTCACCAAAAGCCAGCTACGCAGG	420
QY	421	ACAATAGATGTTGTCGACCAATTTGTGCAACCAATATTTGCAAGCTTACCTGCCCCCT	480
DB	421	ACAATAGATGTTGTCGACCAATTTGTGCAACCAATATTTGCAAGCTTACCTGCCCCCT	480
QY	481	GTGTTTATAGGCCATTTCTTTGATGCGAGCGTCCGATGCTGCTGCTCTCTATG	540
DB	481	GTGTTTATAGGCCATTTCTTTGATGCGAGCGTCCGATGCTGCTGCTCTCTATG	540
QY	541	GCTGCTGTTATGTCGCCATGATCGCTTCTCCAGCTGCTTCTGTTACAAACATTACTGT	600
DB	541	GCTGCTGTTATGTCGCCATGATCGCTTCTCCAGCTGCTTCTGTTACAAACATTACTGT	600
QY	601	AGAGTATCTCAAGCAGAGGTGTTTCAACCGTGAATTTGGAAACAGGATGAAGCATTTAT	660
DB	601	AGAGTATCTCAAGCAGAGGTGTTTCAACCGTGAATTTGGAAACAGGATGAAGCATTTAT	660
QY	661	CCAGTAGGAGATCACTGAAAGACCTGATTGACAGCTCAAAAGCTCTGGTAGTGATCT	720
DB	661	CCAGTAGGAGATCACTGAAAGACCTGATTGACAGCTCAAAAGCTCTGGTAGTGATCT	720
QY	721	GGATTACCTTTATTTGTTTTCAGCGAACTATTGGCAAAACAGATTCAGATGTTTCGGCAGGTT	780
DB	721	GGATTACCTTTATTTGTTTTCAGCGAACTATTGGCAAAACAGATTCAGATGTTTCGGCAGGTT	780
QY	781	GGTAAGGCGCGGTATCGAGAGATGATGGATGGGTAAATGGCGGTGGAATAAGTGGCTGTC	840
DB	781	GGTAAGGCGCGGTATCGAGAGATGATGGATGGGTAAATGGCGGTGGAATAAGTGGCTGTC	840
QY	841	AAAGTATTTTTTACCCTCAAGAGCTAGCTGTTTATAGAGAAACAGAAATCTTACCAGCG	900

DB	841	AAAGTATTTTTTACCCTCAAGAGCTAGCTGTTTATAGAGAAACAGAAATCTTACCAGCG	900
QY	901	GTGTTAATGCGTCATGAAATAATATCTTGTTTATAGTGCAGACATTTAAAGCACCCGGT	960
DB	901	GTGTTAATGCGTCATGAAATAATATCTTGTTTATAGTGCAGACATTTAAAGCACCCGGT	960
QY	961	TCCTGGACTCAGCTGTTTGAATTTACTGATTAACCATGAGAAATGGGCTCTCTATGACTTC	1020
DB	961	TCCTGGACTCAGCTGTTTGAATTTACTGATTAACCATGAGAAATGGGCTCTCTATGACTTC	1020
QY	1021	CTGAAATGTGCCACCTTGGACACCGAGCCCTACTCAAGTTAGCTTATTTCTGCTGCTGT	1080
DB	1021	CTGAAATGTGCCACCTTGGACACCGAGCCCTACTCAAGTTAGCTTATTTCTGCTGCTGT	1080
QY	1081	GCTCTGTGCCACCTCCACACAGAAATTTATGGCACGCAAGCAAGCCTGCAATTTGCTCAT	1140
DB	1081	GCTCTGTGCCACCTCCACACAGAAATTTATGGCACGCAAGCAAGCCTGCAATTTGCTCAT	1140
QY	1141	CGAGACCTGAAGAGCAAAAACATCTTATTAGAAAATGGTATGCTGTTATTCGTGAC	1200
DB	1141	CGAGACCTGAAGAGCAAAAACATCTTATTAGAAAATGGTATGCTGTTATTCGTGAC	1200
QY	1201	CTGGGCTTAGCTGTTTAAATTTCAACAGTGACACAAAATGAAGTTGACATACCTTTGAACACC	1260
DB	1201	CTGGGCTTAGCTGTTTAAATTTCAACAGTGACACAAAATGAAGTTGACATACCTTTGAACACC	1260
QY	1261	AGGTTGGGCACACGCGGTACATGCTCCAGAAAGTCTGGACGAGAGCCTGAGTAAAAAC	1320
DB	1261	AGGTTGGGCACACGCGGTACATGCTCCAGAAAGTCTGGACGAGAGCCTGAGTAAAAAC	1320
QY	1321	CATTTCACGCTTACATCATGCTGACATCTACAGCTTTGGTTGATCAATTTGGGAGATG	1380
DB	1321	CATTTCACGCTTACATCATGCTGACATCTACAGCTTTGGTTGATCAATTTGGGAGATG	1380
QY	1381	GCCCGTCTGCTGTTTACAGGAGAAATCGTGGAGGAATATCAATTTACCATATTACAACATG	1440
DB	1381	GCCCGTCTGCTGTTTACAGGAGAAATCGTGGAGGAATATCAATTTACCATATTACAACATG	1440
QY	1441	GTGCTTAGTGACCCATCTTATGAAGACATGCTGAGGTCGTGTTGTGAAACGCTTTGCCG	1500
DB	1441	GTGCTTAGTGACCCATCTTATGAAGACATGCTGAGGTCGTGTTGTGAAACGCTTTGCCG	1500
QY	1501	CCAAATCGTCTTAAACGCTGGAACAGTGAATGCTCTCGAGCCGTTTGAAGCTGATG	1560
DB	1501	CCAAATCGTCTTAAACGCTGGAACAGTGAATGCTCTCGAGCCGTTTGAAGCTGATG	1560
QY	1561	TCAGAAATGCTGGGCCCATTAATCCAGATCCAGACTCCAGCTTTGAGAAATCAAGAAGACG	1620
DB	1561	TCAGAAATGCTGGGCCCATTAATCCAGATCCAGACTCCAGCTTTGAGAAATCAAGAAGACG	1620
QY	1621	CTCGCAAAAGATGGTTGAATCCAGGATGTAAAGATTTGAACAAAGTTTGAAGAAAGAT	1680
DB	1621	CTCGCAAAAGATGGTTGAATCCAGGATGTAAAGATTTGAACAAAGTTTGAAGAAAGAT	1680
QY	1681	TTAGACTGCAAGAAATTCACCCGAGGAGGGTGGAGTTAGCATGCACTAGGATGTCGGCT	1740
DB	1681	TTAGACTGCAAGAAATTCACCCGAGGAGGGTGGAGTTAGCATGCACTAGGATGTCGGCT	1740
QY	1741	TGGTTTTTCAGACTCTCTCTCTACCATCTTTCAGAGCTGCTAACAGTAAACCTTTTCAGGA	1800
DB	1741	TGGTTTTTCAGACTCTCTCTCTACCATCTTTCAGAGCTGCTAACAGTAAACCTTTTCAGGA	1800
QY	1801	CTCTCGAGAAATGC 1813	
DB	1801	CTCTCGAGAAATGC 1813	

RESULT 2
ADW28817
ID ADW28817 standard; DNA; 3003 BP.
XX
AC
XX ADW28817;

DT	07-APR-2005	(first entry)
XX	Rat bone morphogenetic protein (BMP) receptor type I DNA Seq 121.	
XX	receptor; bone morphogenetic protein; bone injury; antibody production;	
KW	TGF beta antagonist; BMP-antagonist; osteopathic; osteopenias;	
KW	osteoporosis; gene; ds.	
XX	Rattus norvegicus.	
OS		
XX		
FH	Key Location/Qualifiers	
DE	CDS 83..1681	
FT	/tag= a	
FT	/product= "BMP receptor type I protein"	
FT		
PN	WO2005003158-A2.	
XX		
XX	13-JAN-2005.	
PD		
XX		
Pf	15-JUN-2004; 2004WO-US018910.	
PR		
XX	16-JUN-2003; 2003US-00463190.	
PA	(CLLT) CELLTECH R & D INC.	
XX		
XX	Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepier BW;	
PI	Van Ness J, Winkler DG;	
DR	WPI; 2005-081936/09.	
DR	P-PSDB; ADW28803.	
XX		
PT	New antibody or antigen-binding fragment that binds specifically to	
PT	sclerostin polypeptide and which inhibits binding of sclerostin	
PT	polypeptide to a bone morphogenic protein, useful for increasing bone	
PT	mineral content or density.	
XX		
PS	Disclosure; SEQ ID NO 121; 205pp; English.	
XX		
CC	This invention relates to a novel antibody or antigen-binding fragment	
CC	that binds specifically to a sclerostin (SOST) polypeptide and impairs	
CC	formation of a sclerostin homodimer. Specifically, it refers to an	
CC	antibody that competitively inhibits binding of the sclerostin	
CC	polypeptide to a bone morphogenic protein (BMP) Type I receptor binding	
CC	site or a BMP Type II receptor binding site. The present invention	
CC	describes a hybridoma cell capable of producing the antibody and a host	
CC	cell for antibody expression. Furthermore, it provides a nucleic acid	
CC	molecule encoding a transforming growth factor-beta (TGF-beta) binding	
CC	protein known as SOST (and also BEER) and methods for detection thereof.	
CC	Accordingly, such antibodies and osteopathic compositions of the	
CC	invention can be used for treating osteopenia, osteoporosis, fractures	
CC	and other disorders related to low bone mineral content and density. As	
CC	such, these compositions improve bone mineralization and can be described	
CC	as TGF-beta antagonists and/or BMP-antagonists. This polynucleotide is a	
CC	bone morphogenetic protein receptor type I DNA sequence given in an	
CC	exemplification of the invention.	
XX		
SQ	Sequence 3003 BP; 840 A; 626 C; 654 G; 883 T; 0 U; 0 Other;	
Query Match 96.5%; Score 1750.4; DB 14; Length 3003;		
Best Local Similarity 99.6%; Pred. No. 0;		
Matches 1776; Conservative 0; Mismatches 6; Indels 2; Gaps 2		
Qy	30 TGC GGCGCCGACAGGACAGCTGGCAATTTGGACAATGACTCAGCTATACATTACATCAGATT 89	
Dd	52 TGGCCCCGACAGGACAGCTGGCAATTTGGACAATGACTCAGCTATACATTACATCAGATT 111	
Qy	90 ACTGGGAGCCTGTCTGTTTCATCTTTCTCATGTTTCAAGGGCAGAATCTAGATAGTAGTGCT 149	
Dd	112 ACTGGGAGCCTGTCTGTTTCATCTTTCTCATGTTTCAAGGGCAGAATCTAGATAGTAGTGCT 171	
Qy	150 CCATGGTACTGGTATGAATCAGACGTGGACAGAAAGCCGGAATAATGGAGTGACGTT 209	
Dd	172 CCATGGTACTGGTATGAATCAGACGTGGACAGAAAGCCGGAATAATGGAGTGACGTT 231	

Db 532 CGTCCGATGGCTGGCTGCTCATCTCTATGGCTGTCTGTATTGTGCCATGATCGTCTT 591
QY 570 CTCAGAGCTGCTCTGTTTACAAACATTAATCTAGAGTATCTCAAGCAGAGGTGGTTACAA 629
Db 592 CTCAGAGCTGCTCTGTTTACAAACATTAATCTAGAGTATCTCAAGCAGAGGTGGTTACAA 651
QY 630 CCGTGACTTGGAAACAGGATGAAGCATTTATTCAGTAGGAGATCACTGAAAGACCTGAT 689
Db 652 CCGTGACTTGGAAACAGGATGAAGCATTTATTCAGTAGGAGATCACTGAAAGACCTGAT 711
QY 690 TGACCACTCAAAAGCTCTGGTAGTGGATCTGGAATACCTTTATTTGGTTTCAAGCAACTAT 749
Db 712 TGACCACTCAAAAGCTCTGGTAGTGGATCTGGAATACCTTTATTTGGTTTCAAGCAACTAT 771
QY 750 TGCCAAACAGATTCAAGATGTTGGCAGAGTTGGTAAGGCGCGGTATGGAGAGATGATGGAT 809
Db 772 TGCCAAACAGATTCAAGATGTTGGCAGAGTTGGTAAGGCGCGGTATGGAGAGATGATGGAT 831
QY 810 GGGTAAATGGCGTGGTGAAGAAAGTGGCTGTCAAAGTATTTTACCACCTGAAGAGCTAG 869
Db 832 GGGTAAATGGCGTGGTGAAGAAAGTGGCTGTCAAAGTATTTTACCACCTGAAGAGCTAG 891
QY 870 CTGGTTTAGAAGAAACAGAAATCTACAGACGGTGTAAATCGCTCATGAAATATATCTGG 929
Db 892 CTGGTTTAGAAGAAACAGAAATCTACAGACGGTGTAAATCGCTCATGAAATATATCTGG 951
QY 930 TTTTATAGCTGCAGACATTAAGGACCGGTTCTCGGACTCAGCTGTATTTGATTTACTGA 989
Db 952 TTTTATAGCTGCAGACATTAAGGACCGGTTCTCGGACTCAGCTGTATTTGATTTACTGA 1011
QY 990 TTACCATGAGAAATGGGTCTCTATGACTTCCTGAAATGTGCCACCTGGACACACAGAGC 1049
Db 1012 TTACCATGAGAAATGGGTCTCTATGACTTCCTGAAATGTGCCACCTGGACACACAGAGC 1071
QY 1050 CTTACTCAAGTTAGCTTATTTCTGCTGCTGTGTGTGCTGCTTCAACAGTGA 1109
Db 1072 CTTACTCAAGTTAGCTTATTTCTGCTGCTGTGTGTGCTGCTTCAACAGTGA 1131
QY 1110 TGCCAGCAGGCAAGCCTGCAATGCTCATCAGACCTGAAGAGCAAAACATCTTAT 1169
Db 1132 TGCCAGCAGGCAAGCCTGCAATGCTCATCAGACCTGAAGAGCAAAACATCTTAT 1191
QY 1170 TAAGAAATAGTGTAGTTGCTGTATTTGCTGACCTGGGCTAGCTGTTAAATTTCAACAGTGA 1229
Db 1192 TAAGAAATAGTGTAGTTGCTGTATTTGCTGACCTGGGCTAGCTGTTAAATTTCAACAGTGA 1251
QY 1230 CACAAATGAAGTTGACATACCTTTGAACACACCGGTGGGCAACCGGCTGACATGCTCC 1289
Db 1252 CACAAATGAAGTTGACATACCTTTGAACACACCGGTGGGCAACCGGCTGACATGCTCC 1311
QY 1290 AGAAGTGGCGAGAGCCTGAGTAAGAAACCAATTTCCAGCCCTACATCATGCTGACAT 1349
Db 1312 AGAAGTGGCGAGAGCCTGAGTAAGAAACCAATTTCCAGCCCTACATCATGCTGACAT 1371
QY 1350 CTACAGCTTTGGTTTGCATCATTTGGGAGATGGCGGCTGCTGTATTACAGAGGAATCGT 1409
Db 1372 CTACAGCTTTGGTTTGCATCATTTGGGAGATGGCGGCTGCTGTATTACAGAGGAATCGT 1431
QY 1410 GGAGGAATATCAATTAACCATATTACAACTATGTTGCTGCTAGTGACCCCATCTTATGAAGACAT 1469
Db 1432 GGAGGAATATCAATTAACCATATTACAACTATGTTGCTGCTAGTGACCCCATCTTATGAAGACAT 1491
QY 1470 GCGTAGGTCGTGTGTGTAAGCGCTTGGGCAATCGTCTTAACCGCTGGAAACAGTGA 1529
Db 1492 GCGTAGGTCGTGTGTGTAAGCGCTTGGGCAATCGTCTTAACCGCTGGAAACAGTGA 1551
QY 1530 TGAATGCTTCGAGCCGCTTTTGAAGCTGTATGAGATGCTGGGCCCAATATCCAGCATC 1589
Db 1552 TGAATGCTTCGAGCCGCTTTTGAAGCTGTATGAGATGCTGGGCCCAATATCCAGCATC 1611
QY 1590 CAGACTCACAGCTTTGAGAAATCAAGAGAGCGCTCGCAAGATGGTTGAATCCAGGATGT 1649

Db 1612 CAGACTCACAGCTTTGAGAAATCAAGAAGACGCTCGCAAGATGGTTGAATCCAGGATGT 1671
QY 1650 AAGATTTCGAAACAGGTTTGGAGAAAGATTTAGACTGCAAGAAATTCACCCGAGGAG 1709
Db 1672 AAGATTTCGAAACAGGTTTGGAGAAAGATTTAGACTGCAAGAAATTCACCCGAGGAG 1731
QY 1710 GGTGGAGTTAGCATGGACTAGGATGTGGCTTGGTTTCCAGACTCTCTCTTACCATCT 1769
Db 1732 GGTGGAGTTAGCATGGACTAGGATGTGGCTTGGTTTCCAGACTCTCTCTTCTA-CATCT 1790
QY 1770 TCACAGGCTGCTAACAGTAAACCTTTCCAGACTCTTCAGAAATGC 1813
Db 1791 TCACAGGCTGCTAACAGTAAACCTTTCCAGACTCTTCAGAAATGC 1833
RESULT 4
ADW28816
ID ADW28816 standard; DNA; 3167 BP.
XX
AC ADW28816;
XX
DT 07-APR-2005 (first entry)
XX
DE Rat bone morphogenetic protein (BMP) receptor type 1 DNA Seq 120.
XX
KW receptor; bone morphogenetic protein; bone injury; antibody production;
KW TGF beta antagonist; BMP-antagonist; osteopathic; osteopenias;
KW osteoporosis; gene; db.
XX
OS Rattus norvegicus.
XX
FH Key Location/Qualifiers
FT CDS 226..1824
FT /tag= a
FT /product= "BMP receptor type 1 protein"
XX
PN WO2005003158-A2.
XX
PD 13-JAN-2005.
XX
PF 15-JUN-2004; 2004WO-US018910.
XX
PR 16-JUN-2003; 2003US-00463190.
XX
PA (CLLT) CELLTech R & D INC.
XX
PI Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepers BW;
PI Van Ness J, Winkler DG;
XX
DR WPI; 2005-081936/09.
DR P-PSDB; ADW28802.
XX
XX New antibody or antigen-binding fragment that binds specifically to
PT sclerostin polypeptide and which inhibits binding of sclerostin
PT polypeptide to a bone morphogenic protein, useful for increasing bone
PT mineral content or density.
XX
PS Disclosure; SEQ ID NO 120; 205pp; English.
XX
CC This invention relates to a novel antibody or antigen-binding fragment
CC that binds specifically to a sclerostin (SOST) polypeptide and impairs
CC formation of a sclerostin homodimer. Specifically, it refers to an
CC antibody that competitively inhibits binding of the sclerostin
CC polypeptide to a bone morphogenic protein (BMP) Type I receptor binding
CC site or a BMP Type II receptor binding site. The present invention
CC describes a hybridoma cell capable of producing the antibody and a host
CC cell for antibody expression. Furthermore, it provides a nucleic acid
CC molecule encoding a transforming growth factor-beta (TGF-beta) binding
CC protein known as SOST (and also BBR) and methods for detection thereof.
CC Accordingly, such antibodies and osteopathic compositions of the
CC invention can be used for treating osteopenia, osteoporosis, fractures
CC and other disorders related to low bone mineral content and density. As
CC such, these compositions improve bone mineralization and can be described

CC as TGF-beta antagonists and/ or BMP-antagonists. This polynucleotide is a
CC bone morphogenetic protein receptor type 1 DNA sequence given in an
CC exemplification of the invention.

XX	Sequence	3167 BP; 908 A; 647 C; 688 G; 924 T; 0 U; 0 Other;
SQ	Query Match	96.5%; Score 1750.4; DB 14; Length 3167;
	Best Local Similarity	99.6%; Pred. No. 0;
	Matches	1776; Conservative 0; Mismatches 6; Indels 2; Gaps 2;
QY	30	TGCGGCGGACGACGTCGCAATTTGGCAATGACTCAGCTATACATCAGATT 89
DB	195	TGCGCGGACGACGTCGCAATTTGGCAATGACTCAGCTATACATCAGATT 254
QY	90	ACTGGAGCCTGTCTGTTTCATCATTTCTCATGTTTCAAGGCGAGATCTAGATGCT 149
DB	255	ACTGGAGCCTGTCTGTTTCATCATTTCTCATGTTTCAAGGCGAGATCTAGATGCT 314
QY	150	CCATGCTACTGTTGTAATCAGCTGGACGACGAGAGCGGAAATGGAGTACGTT 209
DB	315	CCATGCTACTGTTGTAATCAGCTGGACGAGAGAGCGGAAATGGAGTACGTT 374
QY	210	AGCACGAGGACACCTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCAGATGA 269
DB	375	AGCACGAGGACACCTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCAGATGA 434
QY	270	CGCTATTATAACACATGATCAATTAATGGCCATTGCTTTGCCATTATAGAAAGATGA 329
DB	435	CGCTATTATAACACATGATCAATTAATGGCCATTGCTTTGCCATTATAGAAAGATGA 494
QY	330	TCAGGAGAGAAACACGTTAACTTCTGGGTGATAGATGATGAAGCTCTGATTTCAATG 389
DB	495	TCAGGAGAGAAACACGTTAACTTCTGGGTGATAGATGATGAAGCTCTGATTTCAATG 554
QY	390	CAAGGATTCAACAAAGCCAGCTACGAGGACAAATAGAAATGTTGCGGACCAATTTGTG 449
DB	555	CAAGGATTCAACAAAGCCAGCTACGAGGACAAATAGAAATGTTGCGGACCAATTTGTG 514
QY	450	CAACCAATATTGCGAGCTACACTGCCCCCTGTGTTATAGGCCCATTTCTTTGATGGCAG 509
DB	615	CAACCAATATTGCGAGCTACACTGCCCCCTGTGTTATAGGCCCATTTCTTTGATGGCAG 674
QY	510	CGTCCGATGGCTGTGCTCATCTCTATGCTGTCTGTTATGTCGCATGATCGTCTT 569
DB	675	CGTCCGATGGCTGTGCTCATCTCTATGCTGTCTGTTATGTCGCATGATCGTCTT 734
QY	570	CTCCAGCTCTCTCTGTTACAAACATTTACTGTAAGAGTATCTCAAGCAGAGGTCTGTACAA 629
DB	735	CTCCAGCTCTCTCTGTTACAAACATTTACTGTAAGAGTATCTCAAGCAGAGGTCTGTACAA 794
QY	630	CGGTGACTTTGGAACAGGATGAAGCAATTTATTCAGTAGAGAAATCACTGAAGACCTGAT 689
DB	795	CGGTGACTTTGGAACAGGATGAAGCAATTTATTCAGTAGAGAAATCACTGAAGACCTGAT 854
QY	690	TGACAGGTCACAAAGCTCTGGTAGGATCTGGATACCTTTATTTGGTTCAGCGAACTAT 749
DB	855	TGACAGGTCACAAAGCTCTGGTAGGATCTGGATACCTTTATTTGGTTCAGCGAACTAT 914
QY	750	TGCCAAAACAGATTTCAGATGGTTTCGGCAGGTTGGTAAGGCGCGTATGAGAGATGATGAT 809
DB	915	TGCCAAAACAGATTTCAGATGGTTTCGGCAGGTTGGTAAGGCGCGTATGAGAGATGATGAT 974
QY	810	GGGTAAATGGCTGTGTGAAAAAGTGGCTGTCAAAGTATTTTTTACCCTGAAGAAAGCTAG 869
DB	975	GGGTAAATGGCTGTGTGAAAAAGTGGCTGTCAAAGTATTTTTTACCCTGAAGAAAGCTAG 1034
QY	870	CTGGTTTATAGAGAAACAGAAATCTACAGACGCTGTTAATGCTGATGAATATATCTGG 929
DB	1035	CTGGTTTATAGAGAAACAGAAATCTACAGACGCTGTTAATGCTGATGAATATATCTGG 1094
QY	930	TTTTATAGCTGACAGCATTTAAAGGACCCGGTTCTCGGACTCAGCTGTTATTTGATTACTGA 989
DB	1095	TTTTATAGCTGACAGCATTTAAAGGACCCGGTTCTCGGACTCAGCTGTTATTTGATTACTGA 1154

RESULT 5

ADM28815

ID ADM28815 standard; DNA; 3167 BP.

XX AC ADM28815;

XX DT 07-APR-2005 (first entry)

XX DE Rat bone morphogenetic protein (BMP) receptor type 1 DNA Seq 119.

XX KW receptor; bone morphogenetic protein; bone injury; antibody production;
XX TGF beta antagonist; BMP-antagonist; osteopathic; osteopenias;
XX KW osteoporosis; gene; ds.

OS Rattus sp.

QY	990	TTACCATGAGAAATGGGTCTCTCTATGACTTCTCTGAAATGTGCCACCCCTGGACACACAGAC 1049
DB	1155	TTACCATGAGAAATGGGTCTCTCTATGACTTCTCTGAAATGTGCCACCCCTGGACACACAGAC 1214
QY	1050	CCTACTCAAGTTAGCTTATTTCTGCTGCTGTGCTGTGCCACCTCCACACAGAAATTTA 1109
DB	1215	CCTACTCAAGTTAGCTTATTTCTGCTGCTGTGCTGTGCCACCTCCACACAGAAATTTA 1274
QY	1110	TGGCAGCAAGGCAAGCCTGCAATTTGCTCATCGAGACCTGAAGCAAAAAATCATCTTAT 1169
DB	1275	TGGCAGCAAGGCAAGCCTGCAATTTGCTCATCGAGACCTGAAGCAAAAAATCATCTTAT 1334
QY	1170	TAAAGAAATGGTAGTTGCTGTATTTGCTGACCTGGGCCCTAGCTGTAAATTTCAACAGTGA 1229
DB	1335	TAAAGAAATGGTAGTTGCTGTATTTGCTGACCTGGGCCCTAGCTGTAAATTTCAACAGTGA 1394
QY	1230	CACAAATGAAGTTGACATACCTTTGAACACAGAGGTGGGACCCAGCGGTATCATGGCTCC 1289
DB	1395	CACAAATGAAGTTGACATACCTTTGAACACAGAGGTGGGACCCAGCGGTATCATGGCTCC 1454
QY	1290	AGAAAGTGTGGAAGGAGCCTGAGTAAAAAACCATTTCAGGCCCTACATCATGGCTGACAT 1349
DB	1455	AGAAAGTGTGGAAGGAGCCTGAGTAAAAAACCATTTCAGGCCCTACATCATGGCTGACAT 1514
QY	1350	CTACAGCTTTGGTTGATCATTTGGGAGATGGCCGCTCGCTGTATTTACAGAGGAATCGT 1409
DB	1515	CTACAGCTTTGGTTGATCATTTGGGAGATGGCCGCTCGCTGTATTTACAGAGGAATCGT 1574
QY	1410	GGAGAAATCAATTTACCATATTACACATAGTGTGCTAGTGACCCCTCTTATGAAGACAT 1469
DB	1575	GGAGAAATCAATTTACCATATTACACATAGTGTGCTAGTGACCCCTCTTATGAAGACAT 1634
QY	1470	GCGTGAGTCTGTGTGTGAAACCGTTTCGGGCCAATCGTCTCTAAACCGCTGGAAACAGTGA 1529
DB	1635	GCGTGAGTCTGTGTGTGAAACCGTTTCGGGCCAATCGTCTCTAAACCGCTGGAAACAGTGA 1694
QY	1530	TGAATGCTTCGAGCCGTTTGAAGCTGATGTGAGAAATGCTGGGCCCAATTAATCCAGCATC 1589
DB	1695	TGAATGCTTCGAGCCGTTTGAAGCTGATGTGAGAAATGCTGGGCCCAATTAATCCAGCATC 1754
QY	1590	CAGACTCACGCTTTGAGAAATCAAGAGACGCTCGCAAGATGGTTGAATCCACGATGT 1649
DB	1755	CAGACTCACGCTTTGAGAAATCAAGAGACGCTCGCAAGATGGTTGAATCCACGATGT 1814
QY	1650	AAAGATTTGACAAACAGTTTGGAGAAAGAAATTTAGACTGCAAGAAATTCACCCGAGGAAG 1709
DB	1815	AAAGATTTGACAAACAGTTTGGAGAAAGAAATTTAGACTGCAAGAAATTCACCCGAGGAAG 1874
QY	1710	GGTGGATTAGCATGGACTAGGATGTGGGCTTGGTTTCCAGACTCTCTCTCTACATCT 1769
DB	1875	GGTGGATTAGCATGGACTAGGATGTGGGCTTGGTTTCCAGACTCTCTCTCTCTCTCTCTCT 1933
QY	1770	TCACAGGCTGCTAAACAGTAAACCTTTTCAGGACTCTGCAGAAATGC 1813
DB	1934	TCACAGGCTGCTAAACAGTAAACCTTTTCAGGACTCTGCAGAAATGC 1976

XX Key Location/Qualifiers
FH 226..1824
FT /*tag= a
FT /product= "BMP receptor type 1 protein"
XX
PN W02005003158-A2.
XX
XX 13-JAN-2005.
XX
XX 15-JUN-2004; 2004WO-US018910.
XX
XX 16-JUN-2003; 2003US-00463190.
XX
XX (CLLT) CELLTECH R & D INC.
XX
PI Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepers BW;
PI Van Ness J, Winkler DG;
XX
XX WPI; 2005-081936/09.
XX
XX P-PSDB; ADW28801.
XX
XX New antibody or antigen-binding fragment that binds specifically to
PT sclerostin polypeptide and which inhibits binding of sclerostin
PT polypeptide to a bone morphogenic protein, useful for increasing bone
PT mineral content or density.
XX
XX Disclosure; SEQ ID NO 119; 205pp; English.
XX
XX This invention relates to a novel antibody or antigen-binding fragment
CC that binds specifically to a sclerostin (SOST) polypeptide and impairs
CC formation of a sclerostin homodimer. Specifically, it refers to an
CC antibody that competitively inhibits binding of the sclerostin
CC polypeptide to a bone morphogenic protein (BMP) Type I receptor binding
CC site or a BMP type II receptor binding site. The present invention
CC describes a hybridoma cell capable of producing the antibody and a host
CC cell for antibody expression. Furthermore, it provides a nucleic acid
CC molecule encoding a transforming growth factor-beta (TGF-beta) binding
CC protein known as SOST (and also BEER) and methods for detection thereof.
CC Accordingly, such antibodies and osteopathic compositions of the
CC invention can be used for treating osteopenia, osteoporosis, fractures
CC and other disorders related to low bone mineral content and density. As
CC such, these compositions improve bone mineralization and can be described
CC as TGF-beta antagonists and/or BMP-antagonists. This polynucleotide is a
CC bone morphogenetic protein receptor type 1 DNA sequence given in an
CC exemplification of the invention.
XX
XX Sequence 3167 BP; 908 A; 647 C; 688 G; 924 T; 0 U; 0 Other;

Query Match 96.5%; Score 1750.4; DB 14; Length 3167;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

QY 30 TGGCGCGCCGACGACGTCGCAATGGACAATGACTCAGCTATACACTTACATCAGATT 89
DB 195 TGGCCCGGACGACGACGTCGCAATGGACAATGACTCAGCTATACACTTACATCAGATT 254
QY 90 ACTGGGAGCCTGCTGTTTCATCATTTCTCATGTTCAAGGCGACAATCTAGATAGTATGCT 149
DB 255 ACTGGGAGCCTGCTGTTTCATCATTTCTCATGTTCAAGGCGACAATCTAGATAGTATGCT 314
QY 150 CCATGGTACTGGTATGAATCAGACGTGGACACGAGAGAGCCGGAATGGAGTGACGTT 209
DB 315 CCATGGTACTGGTATGAATCAGACGTGGACACGAGAGAGCCGGAATGGAGTGACGTT 374
QY 210 AGCACCAGAGGACACCTTACCTTTCTTTAAATGCTATTGCTCAGGACACTGCCCCAGATGA 269
DB 375 AGCACCAGAGGACACCTTACCTTTCTTTAAATGCTATTGCTCAGGACACTGCCCCAGATGA 434
QY 270 CGCTATTATAACACATGCACTAATATGCGCCATTCGTTTGCCATTATAGAAGAGATGA 329
DB 435 CGCTATTATAACACATGCACTAATATGCGCCATTCGTTTGCCATTATAGAAGAGATGA 494

QY 330 TCAGGAGAAACCAACGTTAACTTTCTGGTGTATGAAGTATGAAGGCTCTGATTTTCAATG 389
DB 495 TCAGGAGAAACCAACGTTAACTTTCTGGTGTATGAAGTATGAAGGCTCTGATTTTCAATG 554
QY 390 CAAGGATTACCAAAAAGCCAGCTACGCGAGCAATAGAAATGTTGTGCGGACCAATTTGTG 449
DB 555 CAAGGATTACCAAAAAGCCAGCTACGCGAGCAATAGAAATGTTGTGCGGACCAATTTGTG 614
QY 450 CAACCAATATTGCGAGCCTACACTGCCCTGCTGTTATAGGCCCATCTCTTGTATGTCAG 509
DB 615 CAACCAATATTGCGAGCCTACACTGCCCTGCTGTTATAGGCCCATCTCTTGTATGTCAG 674
QY 510 CGTCCGATGGCTGGCTGCTCATCTATGCGCTGCTGTTATGTCGCCCATGATGCTCTT 569
DB 675 CGTCCGATGGCTGGCTGCTCATCTATGCGCTGCTGTTATGTCGCCCATGATGCTCTT 734
QY 570 CTCACAGCTGCTTCTGTTTACAAACATTTACTGTAAAGATATCTCAAGCAGAGAGTGTGTTACAA 629
DB 735 CTCACAGCTGCTTCTGTTTACAAACATTTACTGTAAAGATATCTCAAGCAGAGAGTGTGTTACAA 794
QY 630 CGTGACTTTGGAACAGGATGAAGCATTTATTCAGTAGGAGAAATCACTGAAGACCTGAT 689
DB 795 CGTGACTTTGGAACAGGATGAAGCATTTATTCAGTAGGAGAAATCACTGAAGACCTGAT 854
QY 690 TGACCAAGTACAAAGCTCTGGTAGTGGATCTGATTTACCTTTATTTGTTTTCAGGCAACTAT 749
DB 855 TGACCAAGTACAAAGCTCTGGTAGTGGATCTGATTTACCTTTATTTGTTTTCAGGCAACTAT 914
QY 750 TGCACCAAGATTCAGATGGTTTCGCGAGGTTGGTAAGGCCGGTATGGAGAAGTATGGAT 809
DB 915 TGCACCAAGATTCAGATGGTTTCGCGAGGTTGGTAAGGCCGGTATGGAGAAGTATGGAT 974
QY 810 GGGTAATGGCTGGTGAAGAAAGTGGCTGCTCAAGATATTTTTCACCACTGAAGAGCTAG 869
DB 975 GGGTAATGGCTGGTGAAGAAAGTGGCTGCTCAAGATATTTTTCACCACTGAAGAGCTAG 1034
QY 870 CTGGTTTACAGAAACAGAAATCTTACCAGACGGTGTAAATGCGTCATGAAATATACTTGG 929
DB 1035 CTGGTTTACAGAAACAGAAATCTTACCAGACGGTGTAAATGCGTCATGAAATATACTTGG 1094
QY 930 TTTTATAGCTGCAGACATTTAAAGGACCGGTTCTCGGACTCAGCTGTATTTGATTACTGA 989
DB 1095 TTTTATAGCTGCAGACATTTAAAGGACCGGTTCTCGGACTCAGCTGTATTTGATTACTGA 1154
QY 990 TTACCATGAGATGGTCTCTCTATGACTTCTTGAATATGTCACCTGACACCCAGAGAGC 1049
DB 1155 TTACCATGAGATGGGCTCTCTATGACTTCTTGAATATGTCACCTGACACCCAGAGAGC 1214
QY 1050 CCTACTCAAGTTAGCTTTATTTCTGCTGCTGTGCTGTGTCACCTCCACACAGAAATTTA 1109
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QY 1110 TGGCAGCGAAGCAAGCCTGCAATTTGCTCATCGAGACCTGAAAGAGCAAAAACATCTCTTAT 1169
DB 1275 TGGCAGCGAAGCAAGCCTGCAATTTGCTCATCGAGACCTGAAAGAGCAAAAACATCTCTTAT 1334
QY 1170 TAAAGAAAATGGTAGTTGCTGTATTTGCTGACCTGGGCGCTAGCTGTTTAAATTTCAACAGTGA 1229
DB 1335 TAAAGAAAATGGTAGTTGCTGTATTTGCTGACCTGGGCGCTAGCTGTTTAAATTTCAACAGTGA 1394
QY 1230 CACAAATGAAGTTGACATACCTTTGAACACAGGGTGGGCGACCCAGGCGGTACATGCTGCTC 1289
DB 1395 CACAAATGAAGTTGACATACCTTTGAACACAGGGTGGGCGACCCAGGCGGTACATGCTGCTC 1454
QY 1290 AGAAGTGTGCGAGAGCCTCAGTAAAAACATTTTCCAGCCCTACATCATGGCTGACAT 1349
DB 1455 AGAAGTGTGCGAGAGCCTCAGTAAAAACATTTTCCAGCCCTACATCATGGCTGACAT 1514
QY 1350 CTACAGCTTTGGTTTGTATCATTTGGAGATGGCCCGTCTGCTGTATTTACAGGAGGAATCGT 1409
DB 1515 CTACAGCTTTGGTTTGTATCATTTGGAGATGGCCCGTCTGCTGTATTTACAGGAGGAATCGT 1574
QY 1410 GGAGGAATATCAATTACCATAATTACAAATGCTGCTAGTGACCCCATCTTATGAAGACAT 1469

Db 795 CCGTGACTTGGAAACAGGATGAAGCATTTATTTCCAGTAGGAGAAATCACTGAAAGACCTGAT 854
Qy 690 TGACCAGTACAAAGCTCTGGTAGTGGATCTGGATTACCTTTATTTGGTTTCAGCGACTAT 749
Db 855 TGACCAGTACAAAGCTCTGGTAGTGGATCTGGATTACCTTTATTTGGTTTCAGCGACTAT 914
Qy 750 TGCCAAAACAGATTACAGATTGGTTTCGGCAGGTTGGTAAGGCGCGGTATGGAGAAGTATGGAT 809
Db 915 TGCCAAAACAGATTACAGATTGGTTTCGGCAGGTTGGTAAGGCGCGGTATGGAGAAGTATGGAT 974
Qy 810 GGGTAAATGGCGTGGTGAAGAGTGGCTGTCAAAGTATTTTTTACCCTGAAGAGCTAG 869
Db 975 GGGTAAATGGCGTGGTGAAGAGTGGCTGTCAAAGTATTTTTTACCCTGAAGAGCTAG 1034
Qy 870 CTGGTTTAGAGAAACAGAAATCTACACAGCGTGTAAATGCGTCTATGAATATATCTTGG 929
Db 1035 CTGGTTTAGAGAAACAGAAATCTACACAGCGTGTAAATGCGTCTATGAATATATCTTGG 1094
Qy 930 TTTTATAGCTGCAGACATTAAAGGCACCGGTTCTCGGACTCAGCTGTATTTGATTACTGA 989
Db 1095 TTTTATAGCTGCAGACATTAAAGGCACCGGTTCTCGGACTCAGCTGTATTTGATTACTGA 1154
Qy 990 TTACCATGAGAAATGGTCTCTATGACTTCTGAAATGTGCCACCTCGGACACAGAGC 1049
Db 1155 TTACCATGAGAAATGGTCTCTATGACTTCTGAAATGTGCCACCTCGGACACAGAGC 1214
Qy 1050 CCTACTCAAGTTAGCTTATCTGCTGCTGTGGTCTGTGCCACCTCCACACAGAAATTA 1109
Db 1215 CCTACTCAAGTTAGCTTATCTGCTGCTGTGGTCTGTGCCACCTCCACACAGAAATTA 1274
Qy 1110 TGGCACGCAAGGCAAGCCTGCAATTTGCTCATCGAGACCTGAAGAGCAAAACATCCTTAT 1169
Db 1275 TGGCACGCAAGGCAAGCCTGCAATTTGCTCATCGAGACCTGAAGAGCAAAACATCCTTAT 1334
Qy 1170 TAAGAAAATGGTAGTTGCTGTATGTGACTCGGCTAGCTGTAAATTTCAACAGTGA 1229
Db 1335 TAAGAAAATGGTAGTTGCTGTATGTGACTCGGCTAGCTGTAAATTTCAACAGTGA 1394
Qy 1230 CACAAATGAAGTTACATACCTTTGAACACAGAGTGGGACAGCGGTACATGGCTCC 1289
Db 1395 CACAAATGAAGTTACATACCTTTGAACACAGAGTGGGACAGCGGTACATGGCTCC 1454
Qy 1290 AGAAGTCTGGACGAGACCTTGAGTAAACCAATTTCCAGCCCTACATCATGCTGCATCAT 1349
Db 1455 AGAAGTCTGGACGAGACCTTGAGTAAACCAATTTCCAGCCCTACATCATGCTGCATCAT 1514
Qy 1350 CTACAGCTTTGGTTTGATCAATTTGGGAGATGGCCCGCTGCTGTATTACAGAGGAATCGT 1409
Db 1515 CTACAGCTTTGGTTTGATCAATTTGGGAGATGGCCCGCTGCTGTATTACAGAGGAATCGT 1574
Qy 1410 GGAGGAATCAATTTACCATATTACACATGGTGCCTAGTGACCCATCTTATGAGACAT 1469
Db 1575 GGAGGAATCAATTTACCATATTACACATGGTGCCTAGTGACCCATCTTATGAGACAT 1634
Qy 1470 GCGTGAGGTGCTGTGTGTAACCCCTTGGCGCCCAATCGTCTTAACCGCTGGAAACAGTGA 1529
Db 1635 GCGTGAGGTGCTGTGTGTAACCCCTTGGCGCCCAATCGTCTTAACCGCTGGAAACAGTGA 1694
Qy 1530 TGAATGCTTCGAGCCGTTTGAAGCTGTATGTCAGAAATGCTGGGCCCAATATCCAGCATC 1589
Db 1695 TGAATGCTTCGAGCCGTTTGAAGCTGTATGTCAGAAATGCTGGGCCCAATATCCAGCATC 1754
Qy 1590 CAGACTCACAGCTTTGAGATCAGAGAGCGCTCGCAAGATGGTTGAATCCAGGATGT 1649
Db 1755 CAGACTCACAGCTTTGAGATCAGAGAGCGCTCGCAAGATGGTTGAATCCAGGATGT 1814
Qy 1650 AAAGATTGACAAACAGTTTGGAAAAGAAATTTAGACTGCAAGAAATTCACCCGAGGAAG 1709
Db 1815 AAAGATTGACAAACAGTTTGGAAAAGAAATTTAGACTGCAAGAAATTCACCCGAGGAAG 1874
Qy 1710 GGTGGAGTTAGCATGGACTAGGATGTCCGCTTGGTTTCCAGACTCTCTCTCTTACCATCT 1769
Db 1875 GGTGGAGTTAGCATGGACTAGGATGTCCGCTTGGTTTCCAGACTCTCTCTCTCTA-CATCT 1933

Qy 1770 TCACAGGCTCTACAGTAAACCTTTTCAGGACTCTCGAGATGC 1813
Db 1934 TCACAGGCTCTACAGTAAACCTTTTCAGGACTCTCGAGATGC 1976

RESULT 7
ID ADX97429
XX ADX97429 standard; DNA; 3167 BP.
AC ADX97429;
XX
DT 05-MAY-2005 (first entry)
XX
DE Rat bone morphogenic protein type I receptor encoding DNA, SEQ ID 89.
XX
KW antibody; sclerostin; SOST; bone morphogenic protein receptor;
KW Transforming Growth Factor; osteopathic; gene therapy; bone repair;
XX osteopenia; osteoporosis; bone injury; gene; ds.
OS Rattus norvegicus.
XX
PH Key Location/Qualifiers
FT CDS 226..1824
FT /*tag= a
FT /product= "Rat bone morphogenic protein type I receptor"
XX
PN WO2005014650-A2.
XX
PD 17-FEB-2005.
XX
PF 15-JUN-2004; 2004WO-US018912.
XX
PR 16-JUN-2003; 2003US-0478977P.
XX
PA (CLLT) CELLTECH R & D INC.
XX
PI Winkler DG, Shi J, Latham J;
XX
DR WPI; 2005-163219/17.
DR P-PSDB; ADX97415.
XX
XX New isolated antibody specific for a sclerostin polypeptide, useful for increasing bone mineralization or for treating or preventing conditions associated with low bone mineral density, e.g. osteoporosis or osteopenia.
XX
PS Disclosure; SEQ ID NO 89; 157pp; English.
XX
CC The invention relates to a novel isolated antibody, or its antigen-binding fragment, which binds specifically to a sclerostin (SOST) polypeptide. The SOST polypeptide comprises any of 6 sequences having 190 or 213 amino acids, fully defined in the specification (ADX97341, ADX97360, ADX97398, ADX97400, ADX97402 or ADX97408). The antibody competitively inhibits binding of the SOST polypeptide to a bone morphogenic protein (BMP) Type I Receptor binding site and a BMP Type II Receptor binding site, where the BMP Type I Receptor binding site is capable of binding to a BMP Type I Receptor polypeptide. The invention further comprises: a hybridoma cell producing the new antibody; a host cell that is capable of expressing the new antibody; a composition comprising the new antibody, or its antigen-binding fragment, and a physiological carrier; an immunogen comprising a peptide comprising 6, 7, 8, 9, 10, 11, 12, or at least 21-50 or 20-75 consecutive amino acids of the SOST polypeptide; methods for producing an antibody that specifically binds to the SOST polypeptide; and methods for identifying an antibody that modulates a Transforming Growth Factor (TGF)-beta signaling pathway, that impairs binding of a BMP to the SOST polypeptide, that impairs SOST homodimer formation, or that increases bone mineral content. The novel antibody and compositions have osteopathic activity. The SOST nucleic acids may be used in gene therapy. The composition and methods are useful for increasing bone mineralization, which may treat or prevent diseases or conditions associated with low bone mineral density, such as osteopenia, osteoporosis or bone fractures. This polynucleotide sequence

CC represents a rat bone morphogenic protein type I receptor encoding DNA of CC the invention.

Sequence 3167 BP; 908 A; 647 C; 688 G; 924 T; 0 U; 0 Other;
XX
SQ

Query Match 96.5%; Score 1750.4; DB 14; Length 3167;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

Qy	30	TGCGGCGCCAGGACACGTCGGAATTTGGA	CAATGACTCAGCTATACACTTACATCAGATT	89		
Db	195			254		
		TGGCCCGGACAGGACACGTCGGAATTTGGA	CAATGACTCAGCTATACACTTACATCAGATT			
Qy	90	ACTGGGAGCCGTCTGTTCATTCATTTCTCAT	TGTTCAAGGGCAGAACTCTAGATAGTATGCT	149		
Db	255			314		
		ACTGGGAGCCGTCTGTTCATTCATTTCTCAT	TGTTCAAGGGCAGAACTCTAGATAGTATGCT			
Qy	150	CCATGGTACTGGTATGA	AAATCAGACGCTGGAC	CAGAAGCCGGAAATCGAGTACGCTT	209	
Db	315			374		
		CCATGGTACTGGTATGA	AAATCAGACGCTGGAC		CAGAAGCCGGAAATCGAGTACGCTT	
Qy	210	AGCACGAGGACACCTTACCTTCTTAA	ATGCTATTGCTCAGGACACATGCCCAGATGA	269		
Db	375			434		
		AGCACGAGGACACCTTACCTTCTTAA	ATGCTATTGCTCAGGACACATGCCCAGATGA			
Qy	270	CGCTATTAAATAACACATGCATACTAAT	TGGCCATTGCTTGGCCAAATATAGAAGAAGATGA	329		
Db	435			494		
		CGCTATTAAATAACACATGCATACTAAT	TGGCCATTGCTTGGCCAAATATAGAAGAAGATGA			
Qy	330	TCAGGGAGAAACCACTGTTAACTTCT	TGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATG	389		
Db	495			554		
		TCAGGGAGAAACCACTGTTAACTTCT	TGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATG			
Qy	390	CAAGGATTCA	CAAAAGCCAGCTACG	CAGGACAATAGAAATGTTGTCGACCAATTTGTG	449	
Db	555			614		
		CAAGGATTCA	CAAAAGCCAGCTACG		CAGGACAATAGAAATGTTGTCGACCAATTTGTG	
Qy	450	CAACCAATATTTGCAGCCTACAC	TGCCCTGTCGTTATAGGCCCATCTTTGATGGCAG	509		
Db	615			674		
		CAACCAATATTTGCAGCCTACAC	TGCCCTGTCGTTATAGGCCCATCTTTGATGGCAG			
Qy	510	CGTCCGATGGCTGTGCTCATCTCTAT	TGGCTGTCTGTATTGTCGCCATGATCGTCTT	569		
Db	675			734		
		CGTCCGATGGCTGTGCTCATCTCTAT	TGGCTGTCTGTATTGTCGCCATGATCGTCTT			
Qy	570	CTCAGCTGCTTCTGTTA	CAAAACATTA	CTGTAAGAGTATCTCAAGCAGAGGTCTGTTACAA	629	
Db	735			794		
		CTCAGCTGCTTCTGTTA	CAAAACATTA		CTGTAAGAGTATCTCAAGCAGAGGTCTGTTACAA	
Qy	630	CCGTGACTTGGAA	CAGGATGAAGCATTTATTC	CAAGTAGGAGAACTCACTGAAGACCTGAT	689	
Db	795			854		
		CCGTGACTTGGAA	CAGGATGAAGCATTTATTC		CAAGTAGGAGAACTCACTGAAGACCTGAT	
Qy	690	TGACCAGTCA	AAAGCTCTGGTAGTGGATCTGGA	TATACCTTTATGGTTTCAGCGAACTAT	749	
Db	855			914		
		TGACCAGTCA	AAAGCTCTGGTAGTGGATCTGGA		TATACCTTTATGGTTTCAGCGAACTAT	
Qy	750	TGCCAAACAGATTCAGATG	GTTCGGCAGGTTGGTAAAGGCCGCGTATCG	GAGAGTATGGAT	809	
Db	915			974		
		TGCCAAACAGATTCAGATG	GTTCGGCAGGTTGGTAAAGGCCGCGTATCG		GAGAGTATGGAT	
Qy	810	GGGTAAATGGCGTGA	AAAGTGGCTGTCAAAAGTATTTTTT	TACCACTGAAGAGCTAG	869	
Db	975			1034		
		GGGTAAATGGCGTGA	AAAGTGGCTGTCAAAAGTATTTTTT		TACCACTGAAGAGCTAG	
Qy	870	CTGGTTTAGAAAA	CAGAAATCTAC	CAGACGCGTCTAATCGCTCATGAAATATAC	TCTGG	929
Db	1035			1094		
		CTGGTTTAGAAAA	CAGAAATCTAC		CAGACGCGTCTAATCGCTCATGAAATATAC	TCTGG
Qy	930	TTTTATAGCTCAGACATTA	AAAGGACCGGTTCTCG	ACTCAGCTGATTTGATTA	CTGA	989
Db	1095			1154		
		TTTTATAGCTCAGACATTA	AAAGGACCGGTTCTCG		ACTCAGCTGATTTGATTA	CTGA

FH	Key	Location/Qualifiers	
FT	CDS	217..1815	
FT		/*tag= a	
FT		/product= "mALK-3"	
XX	WO9946386-A1.		
XX			
PD	16-SEP-1999.	99WO-US005735.	
XX			
PF	12-MAR-1999;		
XX			
PR	13-MAR-1998;	98US-00039177.	
XX			
PA	(LUDW-) LUDWIG INST CANCER RES.		
XX			
PI	Miyazono K, Imamura T, Ten Dijke P;		
XX			
DR	WPI; 1999-551413/46.		
DR	P-PSDB; AAY33305.		
XX			
PT	New isolated activin receptor-like kinases, used to develop products for		
PT	treating e.g. fibrosis, cancer, rheumatoid arthritis and		
PT	glomerulonephritis.		
XX			
PS	Disclosure; Page 88-91; 110pp; English.		
XX			
CC	This invention describes novel human and murine activin receptor-like		
CC	kinases (ALK's). The novel ALK products can be used in therapy, e.g. to		
CC	modulate conditions associated with activin or TGF-beta activity, such as		
CC	fibrosis, e.g. liver cirrhosis and pulmonary fibrosis, cancer, rheumatoid		
CC	arthritis and glomerulonephritis. The products can also be used for		
CC	detection, diagnosis and drug screening. This sequence encodes the murine		
CC	mALK-3 protein isolated from clones ME-7 and ME-D		
XX			
SQ	Sequence 2070 BP; 592 A; 414 C; 480 G; 584 T; 0 U; 0 Other;		
	Query Match 87.2%; Score 1581.4; DB 2; Length 2070;		
	Best Local Similarity 94.1%; Pred. No. 0;		
	Matches 1678; Conservative 0; Mismatches 96; Indels 9; Gaps 3;		
QY	39 CAGGACACGTGGCAATTGGCAATGACTCAGCTATACACTTACATCAGATTACTGGGAGC 98		
DB	195 CAGGACGCGTGGCAATCAGCAATGACTCAGCTATACACTTACATCAGATTACTGGGAGC 254		
QY	99 CTGCTGTTTCATCATTTCTCATGTTCAAGGGCAGAACTAGATAGTAGTGCCTCCATGGTAC 158		
DB	255 CTGCTGTTTCATCATTTCTCATGTTCAAGGGCAGAACTAGATAGTAGTGCCTCCATGGCAC 314		
QY	159 TGGTATGAAATCAGACGTGGACAGAGGACCGGAAATGGAGTGACGTTAGCACACAGA 218		
DB	315 TGGTATGAAATCAGACTTTGGACAGAGGACCGGAAATGGAGTGACGTTAGCACACAGA 374		
QY	219 GGCACCTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCAGATGACGCTATTAA 278		
DB	375 GGATACCTTGCCCTTTCTTAAAGTGCTATTGCTCAGGACACTGCCAGATGATGCTATTAA 434		
QY	279 TAACACATGCATAACTAATGGCCATTCCTTTGGCATATAGAGAGAGATGATCAGGAGA 338		
DB	435 TAACACATGCATAACTAATGGCCATTCCTTTGGCATATAGAGAGAGATGATCAGGAGA 494		
QY	339 AACCACTTAACCTTCTGGGTGATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTTC 398		
DB	495 AACCACTTAACCTTCTGGGTGATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTTC 554		
QY	399 ACCAAAGCCAGCTACGAGGACAAATAGAAATGTTGTCGACCAATTTGTGCAACCAATA 458		
DB	555 ACCGAAAGCCAGCTACGAGGACAAATAGAAATGTTGTCGACCAATTTGTGCAACCAATA 614		
QY	459 TTTTGACGCTTACACTGCCCTCTGTTTATAGGCCCATTTCTTTGATGGCAGCTCCGATG 518		
DB	615 TTTTGACGCTTACACTGCCCTCTGTTTATAGGCCCATTTCTTTGATGGCAGCTCCGATG 674		
QY	519 GCTGGGTGCTCATCTCTATGGCTGCTGTATTTGTTCGCCATGATCGTCTTCTCCAGCTG 578		

DB	675 GCTGGTGTGCTCATTTTCATGGCTGCTGTATAGTTGCTATGATCATCTTCTCCAGCTG 734	
QY	579 CTTCTGTTTACAAACATTACTGTAAGAGTATCTCAAGCAGAGGTCGTTTACACCGTACTT 638	
DB	735 CTTTTCGTATAAGCATTTATTTGAAGAGTATCTCAAGCAGGCGTCTTACAAACCGTATTT 794	
QY	639 GGAACAGGATGAAGCATTTATTCCAGTAGAGAACTCACTGAAAGACTGATTGACCAAGTC 698	
DB	795 GGNACAGGATGAAGCATTTATTCCAGTAGAGAACTCACTGAAAGACTGATTGACCAAGTC 854	
QY	699 ACAAGCTCTGCTGAGTGGATCTGGATTACCTTTATTGGTTTCAGCGAACTATTTCCAAACA 758	
DB	855 CCAAAGCTCTGGGAGTGGATCTGGATTGCTTTATTGGTTTCAGCGAACTATTTCCAAACA 914	
QY	759 GATTTCAGATGGTTCGGCAGCTGGTAAAGCGGCTATGGAGAACTATGATGGTAAATG 818	
DB	915 GATTTCAGATGGTTCGGCAGCTGGTAAAGCGGCTATGGAGAACTATGATGGTAAATG 974	
QY	819 GCGTGTGAAAAAGTGGCTGTCAAAGTATTTTTTACCACCTGAAAGAGCTAGCTGGTTTAG 878	
DB	975 GCGTGTGAAAAAGTGGCTGTCAAAGTATTTTTTACCACCTGAAAGAGCTAGCTGGTTTAG 1034	
QY	879 AGAAACAGAAATCTACCAGACGGTGTAAATGCGTCTATGAAATATATCTTGGTTTATAGC 938	
DB	1035 AGAAACAGAAATCTACCAGACGGTGTAAATGCGTCTATGAAATATATCTTGGTTTATAGC 1094	
QY	939 TGCAGACATTAAGGCACCGGTTCTGGACTAGCTAGCTGTATTTGATTTACTGATTACCATGA 998	
DB	1095 TGCAGACATTAAGGCACCGGTTCTGGACTAGCTAGCTGTATTTGATTTACTGATTACCATGA 1154	
QY	999 GAATGGCTCTCTATGACTCTCTGAAATGTCACCCCTGGACACACAGACCCCTACTCAA 1058	
DB	1155 AAATGGATCTCTATGACTCTCTGAAATGTCACCCCTAGACACACAGACCCCTACTCAA 1214	
QY	1059 GTTAGCTATTCTGCTGCTGCTGTGTCACACCTCTCCACACAGAAATTTATGGCACGA 1118	
DB	1215 GTTAGCTATTCTGCTGCTGCTGTGTCACACCTCTCCACACAGAAATTTATGGTACCCA 1274	
QY	1119 AGGCAAGCCTGCAATTTGCTATCGAGACCTGAAGAGCAAAAAACATCTTTTAAAGAAAA 1178	
DB	1275 AGGCAAGCCTGCAATTTGCTATCGAGACCTGAAGAGCAAAAAACATCTTTTAAAGAAAA 1334	
QY	1179 TCGTAGTTGCTGCTATTGCTGACCTGGGCTAGCTGTTAAATTCACACAGTGACACAATGA 1238	
DB	1335 TCGAAGTTGCTGCTATTGCTGACCTGGGCTAGCTGTTAAATTCACACAGTGACACAATGA 1394	
QY	1239 AGTTGACATACCTTTGAACACACAGGCTGGGCACCGGCTACATGGCTCCAGAAAGTCT 1298	
DB	1395 AGTTGACATACCTTTGAATACACAGGCTGGGCACCAAGCGGTACATGGCTCCAGAAAGTCT 1454	
QY	1299 GGACAGAGCCTGAGTAAACCAATTTCCAGCCCTACATCATGGCTGGTACATCTACAGCTT 1358	
DB	1455 GGATGAAAGCCTGAAATAAAAAACCAATTTCCAGCCCTACATCATGGCTGACATCTATAGCTT 1514	
QY	1359 TCGTTTGTATCATTTTCGGAGATGGCCGCTGCTGTATTACAGAGGAAATCGTGAGGAAATA 1418	
DB	1515 TCGTTTGTATCATTTTCGGGAAATGGCTGCTGTATTACAGAGGAAATCGTGAGGAAATA 1574	
QY	1419 TCAATTACCATATTACAACATGGTGCCTAGTGACCCCATCTTATGAAGACATGCGTGAGGT 1478	
DB	1575 TCAATTACCATATTACAACATGGTGCCTAGTGACCCCATCTTATGAGGACATGCGTGAGGT 1634	
QY	1479 CGTGTGTGAAACCGTTTCGGGCCAATCGTCTCTAAACCGCTGGAAACAGTGATGAATGTCT 1538	
DB	1635 TGTGTGTGAAACCGTTTCGGGCCAATCGTGTCTAAACCGCTGGAAACAGTGATGAATGTCT 1694	
QY	1539 TCGAGCCGTTTTGAAGCTGATGTCAGAAATGCTGGGCCCAATATCCAGCATCCAGACTCAC 1598	
DB	1695 TCGAGCAGTTTTGAAGCTGATGTCAGAAATGTTGGGCCCAATATCCAGCATCCAGACTCAC 1754	
QY	1599 AGCTTTGAGAATCAAGAAAGACCGCTCGCAAAAGATGGTTGAATCCCAAGGATGTAAGATTG 1658	

QY 39 CAGGACACGCTGCGAATTGGCAATGACTCAGCTATATACACTTACATCAGATTACTGGGAGC 98
Db 195 CAGGACGCGTGGCAATCAGACAATGACTCAGCTATATACACTTACATCAGATTACTGGGAGC 254
QY 99 CTGCTGTTTCATCATTTCTCATGTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGGTAC 158
Db 255 CTGCTGTTTCATCATTTCTCATGTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGGCAC 314
QY 159 TGGTATGAAATCAGACGCTGGACAGAGAAGACCGGAAAAATGGAGTGCAGCTTAGCACCGAGA 218
Db 315 TGGTATGAAATCAGACTTGGACAGAGAAGACCGGAAAAATGGAGTGCAGCTTAGCACCGAGA 374
QY 219 GGAACCTTTACCTTTCTTAAATGCTTATTGCTCAGGACACTGCCAGATGAGCGTATTAA 278
Db 375 GGATACCTTTGCCCTTTCTTAAAGTGTATTGCTCAGGACACTGCCAGATGAGTATTAA 434
QY 279 TAAACATGCAATAACTTAATGGCCATTGCTTGGCCATTATAGAAGAAGATGATCAGGGAGA 338
Db 435 TAAACATGCAATAACTTAATGGCCATTGCTTGGCCATTATAGAAGAAGATGATCAGGGAGA 494
QY 339 AACCAAGTTAACTTCTGGGTGATGAAGTATGAAGCTCTGATTTTCAATGCAAGGATTC 398
Db 495 AACCAATTAACCTTCTGGGTGATGAAGTATGAAGCTCTGATTTTCAATGCAAGGATTC 554
QY 399 ACCAAAAGCCGCTACGACGAGCAATAGAAATGTTGTCGGAACAATTTGTGCAACCAATA 458
Db 555 ACCGAAAGCCGCTACGACGAGCAATAGAAATGTTGTCGGAACAATTTGTGCAACCAATA 614
QY 459 TTGACGCTTACACTGCCCTCTGCTTATAGGCCCAATTTCTTGTAGGGCAGGCTCCGATG 518
Db 615 TTGACGCTTACACTGCCCTCTGCTTATAGGCCCAATTTCTTGTAGGGCAGGCTCCGATG 674
QY 519 GCTGGCTGTGCTCATCTATGGCTGTCTGTATTTGTCGCCATGATCGTCTTCTCCAGCTG 578
Db 675 GCTGGTGTGCTCATTTCCATGGCTGTCTGTATAGTTGCTATGATCATCTTCTCCAGCTG 734
QY 579 CTTCCTGTTACAAACATTACTGTAAGAGTATCTCAAGCAGAGGTCGTTACAAACGCTGACTT 638
Db 735 CTTTTCTGTTAAGCATTTATGTAAGAGTATCTCAAGCAGGCGTCTTACAAACGCTGATTT 794
QY 639 GGAACAGGATGAAGCATTTATCCAGTACGAGAACTCACTGAAAGACCTCATTTGACCACTC 698
Db 795 GGAACAGGATGAAGCATTTATCCAGTACGAGAACTCACTGAAAGACCTCATTTGACCACTC 854
QY 699 ACAAGCTCTGSPAGTGGATCTGGATTACCTTTATTGTTTCAGCGAACTATTGCCAAACA 758
Db 855 CCAAGCTCTGGAGTGGATCTGGAATTGCTTTATTGTTTCAGCGAACTATTGCCAAACA 914
QY 759 GATTACAGATGGTTCGGCAGGTTGGTAAAGCCCGGTATGGAGAAGTATGGATGGTAAATG 818
Db 915 GATTACAGATGGTTCGGCAGGTTGGTAAAGCCCGGTATGGAGAAGTATGGATGGTAAATG 974
QY 819 GCGTGTGAAAAAGTCGCTGCAAACTATTTTACCACCTGAAGAAGCTAGCTGGTTTAG 878
Db 975 GCGTGTGAAAAAGTCGCTGCAAACTATTTTACCACCTGAAGAAGCTAGCTGGTTTAG 1034
QY 879 AGAAACAGAAATCTACCAGACGGTGTAAATGCGTCAATGAAATATATCTTGGTTTTATAGC 938
Db 1035 AGAAACAGAAATCTACCAGACGGTGTAAATGCGTCAATGAAATATATCTTGGTTTTATAGC 1094
QY 939 TGCAGACATTTAAAGGACCGGTTCTCGGACTCAGCTGATTTGATTTACTGATTACCATGA 998
Db 1095 TGCAGACATTTAAAGGACCTGGTTCTCGGACTCAGCTGATTTGATTTACTGATTACCATGA 1154
QY 999 GAATGGTCTCTCTATGACTTCTGAAATGTGCCACCTGGACACCCAGAGCCCTACTCAA 1058
Db 1155 AAATGATCTCTATGACTTCTGAAATGTGCCACCTAGACACCCAGAGCCCTACTCAA 1214
QY 1059 GTTAGCTTATTCGTGCTGCTGTGCTGCTGCCACCTCCACACAGAAATTTATGGCAGCA 1118
Db 1215 GTTAGCTTATTCGTGCTGCTGTGCTGCTGCCACCTCCACACAGAAATTTATGGTACCCA 1274

QY 1119 AGGCAAGCTCGCAATTGCTCATTCGAGACCTGAAGACGAAAAACATCCCTTATTAAAGAAAA 1178
Db 1275 AGGCAAGCTCGCAATTGCTCATTCGAGACCTGAAGACGAAAAACATCCCTTATTAAAGAAAA 1334
QY 1179 TGGTAGTTGCTGTATTGCTGACCTGGGCTAGCTGTTAAATTTCAACAGTGACACAAATGA 1238
Db 1335 TGGAAAGTTGCTGTATTGCTGACCTGGGCTAGCTGTTAAATTTCAACAGTGATACAAATGA 1394
QY 1239 AGTTGACATACCCCTTTGAAACACAGGGTGGGCACACAGGGGTACATGGCTCCAGAAATGCT 1298
Db 1395 AGTTGACATACCCCTTTGAAATACAGGGTGGGCACACAGGGGTACATGGCTCCAGAAATGCT 1454
QY 1299 GGACAGAGCCTGAGTAAACCAATTTCCAGCCCTACATCATGCTGACATCTACAGCTT 1358
Db 1455 GGATGAAAGCCCTGAAATAAAACCAATTTCCAGCCCTACATCATGCTGACATCTATAGCTT 1514
QY 1359 TGGTTTGATCATTTGGGAGATGGCCCGTCTGTATTATCAGGAGGAATCGTGAGGAATA 1418
Db 1515 TGGTTTGATCATTTGGGAAATGGCTCGTCTGTATTATCAGGAGGAATCGTGAGGAATA 1574
QY 1419 TCAATTCATATATCAACATGGTCCCTAGTAGACCCATCTTATGAAGACATCGCTGAGGT 1478
Db 1575 TCAATTCATATATCAACATGGTCCCTAGTAGACCCATCTTATGAGGACATCGCTGAGGT 1634
QY 1479 CGTGTGTGTGAAACGCTTTGCGGCCAATCGTCTTAACCGCTGGAACAGTGATGTCT 1538
Db 1635 TGTGTGTGTGAAACGCTTTGCGGCCAATCGTGTCTAAACCGCTGGAACAGTGATGTCT 1694
QY 1539 TCGAGCCGCTTTTGAAGCTGATGTCAGAATGCTGGGCCCATTAATCCAGCATCCAGACTCAC 1598
Db 1695 TCGAGCAGTTTGAAGCTAAATGTCAGAATGTTGGGCCCATTAATCCAGCTCCAGACTCAC 1754
QY 1599 AGCTTTGAGAAATCAAGAAAGACGCTCGCAAGAGTGTGAATCCCAAGGATGTAAGATTG 1658
Db 1755 AGCTTTGAGAAATCAAGAAAGACACTTTGCAAAAATGTTGAATCCCAAGGATGTAAGATTG 1814
QY 1659 AC----AAACAGTTTTGAGAAAGAAATTTAGACTGCAAGAAATTC----ACCCGAGGAAG 1710
Db 1815 ACAATTAACAATTTTGAAGGAGAAATTTAGACTGCAAGAACTTCTTCAACCAAGGAATGG 1874
QY 1711 GTGGAGTTAGCATGACCTAGGATGTCGGCTTGGTTTCCAGACTCTCTCTTACCATCTT 1770
Db 1875 GTGGAGTTAGCATGGAATAGGATGTTGACTTGGTTTCCAGACTCTCTCTCTA-CATCTT 1933
QY 1771 CACAGGCTGCTAAACAGTAAACCTTTTCAGGACTCTCGAGAAATGC 1813
Db 1934 CACAGGCTGCTAAACAGTAAACCTTACCCTACTCTACAGAATAC 1976

RESULT 11

AAQ90184
ID AAQ90184 standard; DNA; 2402 BP.

XX AC AAQ90184;

XX AC AAQ90184;

DT 25-MAR-2003 (revised)

DT 01-NOV-1995 (first entry)

XX DE BRK-1 DNA.

XX KW BRK-1; BMP receptor kinase protein-1; bone morphogenetic protein; ds.

XX OS Mus sp.

XX FH Key Location/Qualifiers

FT CDS 11..1609 /*tag= a

FT sig_peptide 11..79 /*tag= b

FT mat_peptide 80..1606 /*tag= c

XX FT

XX FT

XX FT

XX W09514778-A2.

XX 01-JUN-1995.
XX 23-NOV-1994; 94WO-US013534.
XX 24-NOV-1993; 93US-00158735.
XX (PROC) PROCTER & GAMBLE CO.
XX Cook JS, Correa PE, Koenig BB, Rosenbaum JS, Ting J;
XX WPI; 1995-206935/27.
XX P-PSDB; AAR74343.
XX New bone morphogenetic protein receptor kinase protein - used for
PT identifying cpds. capable of binding it and for developing therapeutic
PT cpds. and detection system(s).
XX Claim 3; Page 29-32; 49pp; English.
XX A cDNA library prepared from NIH3T3 poly-A RNA was screened with J159 PCR
CC fragment to isolate clone BRK-1 (sequence given in AAQ90184) encoding the
CC full-length BMP receptor kinase protein (AAR74343). Vectors including the
CC DNA were used to express recombinant BRK-1 in CHO and COS-7 hosts.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 2402 BP; 676 A; 482 C; 540 G; 704 T; 0 U; 0 Other;
SQ
Query Match 86.8%; Score 1574.2; DB 2; Length 2402;
Best Local Similarity 94.2%; Pred. No. 0;
Matches 1669; Conservative 0; Mismatches 93; Indels 9; Gaps 3;
QY 51 GAATTCAGCAATGACCTCAGCTATACCTTACATCAGATTAATCTGGAGCCCTGCTGTTTCAT 110
DB 1 GAATCAGCAATGACCTCAGCTATACCTTACATCAGATTAATCTGGAGCCCTGCTGTTTCAT 60
QY 111 CATTTCTCATGTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGGTACTGGTATGAATC 170
DB 61 CATTTCTCATGTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGGTACTGGTATGAATC 120
QY 171 AGACGTGGACCAAGAACGGGAAATGGAGTGACGTTAGACACAGAGACACCTTACC 230
DB 121 AGACCTGGACCAAGAACGGGAAATGGAGTGACGTTAGACACAGAGGATACCTTGCC 180
QY 231 TTTCTTAAATGCTATTGCTCAGACACTGCCAGATGACGCTATTAAATACACATGCAT 290
DB 181 TTTCTTAAATGCTATTGCTCAGACACTGCCAGATGATGCTATTAAATACACATGCAT 240
QY 291 AACTAATGGCCATTGCTTGGCCATTATAGAAGAGATGATCAGGGAGAAACCAACGTTAAC 350
DB 241 AACTAATGGCCATTGCTTGGCCATTATAGAAGAGATGATCAGGGAGAAACCAACATTAAC 300
QY 351 TTTCTGGGTGATGAAGTATGAAGCTCTGATTTTCAATGCAAGGATTCACCAAAAGCCCA 410
DB 301 TTTCTGGGTGATGAAGTATGAAGCTCTGATTTTCAATGCAAGGATTCACCAAAAGCCCA 360
QY 411 GCTACCCAGACAAATAGATGTTGTCGGACCAATTTGTGCAACCAATATTTCAGAGCTAC 470
DB 361 GCTACCCAGACAAATAGATGTTGTCGGACCAATTTGTGCAACCAATATTTCAGAGCTAC 420
QY 471 ACTGCCCTCTGCTGTTATAGGCCCAATTTTGTGATGGCAGCGTCCGATGGCTGCTGTGCT 530
DB 421 ACTGCCCTCTGTTTATAGGTCGGTTCCTTTGATGGCAGCATCCGATGGCTGGTGTGCT 480
QY 531 CATCTCTATGGCTGCTGTATTTGTCGCCATGATGCTCTTCTCCAGTGTCTTCTGTTTACAA 590
DB 481 CATTTCCATGGCTGCTGTATGTTGCTATGATCATCTTCTCCAGCTGCTTTTGTCTATAA 540
QY 591 ACATTACTGTAAAGATATCTCAAGCAGAGCTCGTTACACCCGTGACTTGGACAGGATGA 650
DB 541 GCATTATTGAAGATATCTCAAGCAGAGGCTCGTTACACCCGTGATTTGGAAACAGGATGA 600
QY 651 AGCAATTTATCCAGTAGGAGAAATCACTGAAAGACCTGATTTGACCAAGCTCTCTGG 710

DB 601 AGCAATTTATCCAGTAGGAGAAATCAATTGAAAGACCTGATTGACCAAGTCCCAAAGCTCTGG 660
QY 711 TAGTGGATCTGGATTACCTTTTATTGGTTCAGCGAACTATTGCCAAACAGATTTCAGATGGT 770
DB 661 GAGTGGATCTGGATTGCTTTTATTGGTTCAGCGAACTATTGCCAAACAGATTTCAGATGGT 720
QY 771 TCGGCAGGTTGGTAAAGGGCCGGTATGAGAGAGTATGAGTGGGTAATTTGGCGTGGTGAATA 830
DB 721 TCGGCAGGTTGGTAAAGGGCCGGTATGAGAGAGTATGAGTGGGTAATTTGGCGTGGTGAATA 780
QY 831 AGTGGCTGTCAAAGTATTTTTTACCCTCAAGAGCTAGCTGGTGTAGAGAAACAGAGAAAT 890
DB 781 AGTGGCTGTCAAAGTATTTTTTACCCTCAAGAGCTAGCTGGTGTAGAGAAACAGAGAAAT 840
QY 891 CTACACAGCGGTGTTAATCGGTCATGAAATATACCTTGGTGTATAGCTGCACACATTAA 950
DB 841 CTACACAGCGGTGTTAATCGGTCATGAAATATACCTTGGTGTATAGCTGCACACATTAA 900
QY 951 AGGCACCGGTTCTGAGCTCAGCTGTATTTGATTACTGATTACCATGAGAAATGGGTCTCT 1010
DB 901 AGGCACCTGGTTCCTGAGCTCAGCTGTATTTGATTACTGATTACCATGAAATGGAATCTCT 960
QY 1011 CTATGACTTCTGAAATGTGCCACCTGGACACACAGAGCCCTACTCAAGTTAGCTTATTC 1070
DB 961 CTATGACTTCTGAAATGTGCCACCTAGACACACAGAGCCCTACTCAAGTTAGCTTATTC 1020
QY 1071 TCGTGGCTGTGGTCTGTGCCACTCCACACAGAAATTTATGGCACCCAGGCAAGCTGC 1130
DB 1021 TCGTGGCTGTGGTCTGTGCCACTCCACACAGAAATTTATGGTACCAAGGGAAGCTGC 1080
QY 1131 AATTGCTCATCGAGACCTGAAGAGCAAAACATCTTTATTAGAAAAATGGTATGTGCTG 1190
DB 1081 AATTGCTCATCGAGACCTGAAGAGCAAAACATCTTTATTAGAAAAATGGAAAGTTGCTG 1140
QY 1191 TATTGCTGACCTGGGCTAGCTGTTTAAATTCACAGTACACAAATGAAAGTTGACATACC 1250
DB 1141 TATTGCTGACCTGGGCTAGCTGTTTAAATTCACAGTACACAAATGAAAGTTGACATACC 1200
QY 1251 CTTGACACACAGGTTGGGACCCAGCGGTACATGGCTCAGAGTGCCTGCAGAGAGCCT 1310
DB 1201 CTTGAAATACCGGGTGGGACCAAGCGGTACATGGCTCCAGAAAGTCTGGATGAAAGCCT 1260
QY 1311 GAGTAAAAACCAATTTCCAGCCCTACATCATGGCTGACATCTACAGCTTTGGTTGATCAT 1370
DB 1261 GAATAAAAACCAATTTCCAGCCCTACATCATGGCTGACATCTATAGCTTTGGTTGATCAT 1320
QY 1371 TTGGGAGATGGCCCTGCTGCTATTACAGAGGAAATCGTGGAGGAATATCAATTACCATA 1430
DB 1321 TTGGGAAATGGGCTCGTGTGTTATTACAGGAGGAATCGTGGAGGAATATCAATTACCATA 1380
QY 1431 TTACAACATGGTGCCTAGTGACCCCATCTTATGAAGACATCCGCTGAGGTCGTGTGTGAA 1490
DB 1381 TTACAACATGGTGCCTAGTGACCCCATCTTATGAGGACATGCGGTGAGGTTGTGTGTGAA 1440
QY 1491 AGCTTTGGCGCCAAATCGTCTCTAAACCGCTGGAACAGTGAATGATGCTTTCGAGCCGTTT 1550
DB 1441 AGCTTTGGCGCCAAATCGTGTCTTAAACCGCTGGAACAGGATGAATGCTTTCGAGCAGTTT 1500
QY 1551 GAAGCTGATGTGAGAAATGCTGGGCCCAATTAATCCAGCATCCAGACTCACAGCTTTGAGAAT 1610
DB 1501 GAAGCTAATGTGAGAAATGTTGGGCCCAATTAATCCAGCTCCAGACTCACAGCTTTGAGAAT 1560
QY 1611 CAAGAAGACCTCGCAAGATGTTGAATCCAGGATGTAAGATTTGAC----AAACAG 1666
DB 1561 CAAGAAGACACTTGCAAAATGTTGAATCCAGGATGTAAAGATTTGCAATTAACAA 1620
QY 1667 TTTTCAGAAAGAAATTTAGACTGCAAGAAATTC----ACCCGAGGAGGGTGGAGTTAGCA 1722
DB 1621 TTTTCAGGAGAAATTTAGACTGCAAGAAATTTCTTACCCCAAGAAATGGGTGGGATTAGCA 1680
QY 1723 TCGACTAGGATGTCGGCTTGGTTTCCAGACTCTCTCTCTCTACATCTTTCCAGAGCTGCTA 1782

Db 1681 TGAATAGGATGTTGACTTGGTTTCCAGACTCCTTCCCTA-CACTTCCAGGCTGCTA 1739
QY 1783 ACAGTAAACCTTTCAGGACTGCGAGAATGC 1813
Db 1740 ACAGTAAACCTTACCAGCACTCTACAGAAATAC 1770

RESULT 12
AAT27228
ID AAT27228 standard; cDNA; 2402 BP.
XX AC AAT27228;
XX 22-AUG-1996 (first entry)
DE Bone morphogenetic protein type-I receptor kinase-1 gene.
XX KW Mouse; bone morphogenetic protein receptor kinase-1;
KW bone morphogenetic protein receptor kinase-3; antibody; diagnostic;
KW bone disorder; osteogenic; bone morphogenetic protein-agonist;
KW drug screening; reporter gene; bone morphogenetic protein-antagonist;
KW hormone-responsive element; ds.
XX OS Mus musculus.
XX
XX Key Location/Qualifiers
FH 11..1609
FT CDS /*tag= a
FT /product= "Bone morphogenetic protein receptor kinase-1"
XX
XX W09614412-A2.
XX
XX 17-MAY-1996.
XX 30-OCT-1995; 95WO-US014085.
XX 04-NOV-1994; 94US-00334179.
XX (PROC) PROCTER & GAMBLE CO.
XX
XX Rosenbaum JS, Nohno T;
XX WPI: 1996-251762/25.
XX P-PSDB; AAR96201.
XX
XX Isolated bone morphogenic protein receptor kinase protein - used to
XX determine if a test cpd. is capable of binding to, or is (ant)agonist of
XX BMP receptor kinase protein transcription.
XX
XX Example 4; Page 61-63; 87pp; English.
XX
XX The sequence encodes mouse bone morphogenetic protein (BMP) receptor type
XX -I kinase-1 (BRK-1), which induces cellular differentiation in response
XX to BMP. The gene may be inserted in plasmid pJT4, to form plasmid pJT4-
XX J159F, and co-expressed with a type-II BRK-3 gene to study complex
XX formation between the 2 receptor types. The BRK-3 receptor and antibodies
XX against it may be used in diagnostic assays for BMP disorders, or in
XX therapy to bind or scavenge BMPs. In addition, expression of the BRK-3
XX gene along with a reporter gene under the control of a hormone-
XX responsive element in a cell culture may be used to screen compounds for
XX BRK-agonist or -antagonist activity, by monitoring reporter gene
XX expression
XX
XX Sequence 2402 BP; 676 A; 482 C; 540 G; 704 T; 0 U; 0 Other;
Query Match 86.8%; Score 1574.2; DB 2; Length 2402;
Best Local Similarity 94.2%; Pred. No. 0;
Matches 1669; Conservative 0; Mismatches 93; Indels 9; Gaps 3;
QY 51 GAATGGACAATGACTCAGCTATACATCTTACATGATTCTGGAGCCCTGCTGTTTCAT 110
Db 1 GAATCAGACAATGACTCAGCTATACATCTTACATGATTCTGGAGCCCTGCTGTTTCAT 60

QY 111 CATTTCTCATGTTCAAGGGCAGAAATCTAGATAGTATGCTCCTCATGCTGCTATGATGAATC 170
Db 61 CATTTCTCATGTTCAAGGGCAGAAATCTAGATAGTATGCTCCTCATGCTGCTATGATGAATC 120
QY 171 AGACGTGACCAAGAAAGCCGGAATATGGAGTGCACGTTAGCACCCAGAGGACACCTTACC 230
Db 121 AGACTTGGACCAAGAAAGCCGGAATATGGAGTGCACGTTAGCACCCAGAGGATACCTTGCC 180
QY 231 TTTCTTAAATGCTATTGCTCAGGACACTGCCCCAGATGACGCTATTATAACACATGAT 290
Db 181 TTTCTTAAAGTCTATTGCTCAGGACACTGCCCCAGATGATGCTATTATAACACATGAT 240
QY 291 AACTAAATGGCCATTGCTTTGCCATTATAGAAAGATGATCAGGAGAGAAACACGTTAAC 350
Db 241 AACTAAATGGCCATTGCTTTGCCATTATAGAAAGATGATCAGGAGAGAAACACATTAAC 300
QY 351 TTCTGGGTGATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCAAAAGCCCA 410
Db 301 TTCTGGGTGATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCGAAAGCCCA 360
QY 411 GCTACGCAAGCAATAGAAATGTTGCGACCAATTTGTGCAACCAATATTTGACGCTTAC 470
Db 361 GCTACGCAAGCAATAGAAATGTTGCGACCAATTTGTGCAACCAATATTTGACGCTTAC 420
QY 471 ACTGCCCCCTGCTGTTATAGGCCCATTTCTTTGATGGCAGCGTCCGATGGCTGGCTGCT 530
Db 421 ACTGCCCCCTGCTGTTATAGGTCCTTTTGTGATGGCAGCATCCGATGGCTGGCTGCT 480
QY 531 CATCTATGCTGCTGCTATTTGTCGCATGATGCTCTTCTCCAGCTGCTTCTGTTTACAA 590
Db 481 CATTTCCATGCTGCTGCTATAGTTGCTATGATCATCTTCTCCAGCTGCTTTTGTATAA 540
QY 591 ACATTACTGTAAGAGTATCTCAAGCAGAGGTCGTTTACAAACCTGATCTTGGAAACAGATGA 650
Db 541 GCATTTATTTGAAGAGTATCTCAAGCAGGGTCGTTTACAAACCTGATTTGGAAACAGATGA 600
QY 651 AGCATTTATTTCCAGTAGGAGAAATCACTGAAAGACCTGATTCACCAAGTACCAAGCTCTGG 710
Db 601 AGCATTTATTTCCAGTAGGAGAAATCACTGAAAGACCTGATTCACCAAGTACCAAGCTCTGG 660
QY 711 TAGTGGATCTGGATTTACCTTTTATTTGTTTACAGCAACTATTGCCAAACAGATTCAGATGCT 770
Db 661 GAGTGGATCTGGATTTGCTTTTATTTGTTTACAGCAACTATTGCCAAACAGATTCAGATGCT 720
QY 771 TCGCAGGTTGCTTAAAGGCCCGGTATGGAGAGTATGGATGGGTAAATGGCGTGGTGA AAA 830
Db 721 TCGCAGGTTGCTTAAAGGCCCGGTATGGAGAGTATGGATGGGTAAATGGCGTGGTGA AAA 780
QY 831 AGTGGCTGTCAAAGTATTTTATTTTACCACTGAAAGAGCTAGCTGGTTTACAGAGAAACAGAAAT 890
Db 781 AGTGGCTGTCAAAGTATTTTATTTTACCACTGAAAGAGCTAGCTGGTTTACAGAGAAACAGAAAT 840
QY 891 CTACAGACGGTGTAAATGCTCATGAAATATATCTTGGTTTATAGCTGCAGACATTA 950
Db 841 CTACAGACGGTGTAAATGCTCATGAAATATATCTTGGTTTATAGCTGCAGACATTA 900
QY 951 AGGCACCGGTTCTCGGACTCAGCTGATTTGATTTAGTATGATTAACCATGAGATGGGTCTCT 1010
Db 901 AGGCACCGGTTCTCGGACTCAGCTGATTTGATTTAGTATGATTAACCATGAGATGGGTCTCT 960
QY 1011 CTATGACTTCTGAAATGTGCCCACCTGGACACCAAGAGCCCTACTCAAGTTAGCTTATTC 1070
Db 961 CTATGACTTCTGAAATGTGCCCACCTAGACACCAAGAGCCCTACTCAAGTTAGCTTATTC 1020
QY 1071 TGCTGCCTGTGCTGTGTCACCTCCACACAGAAATTTATGGCAGCGCAAGGCAAGCCCTGC 1130
Db 1021 TGCTGCCTGTGCTGTGTCACCTCCACACAGAAATTTATGGTACCCCAAGGAGCCCTGC 1080
QY 1131 AATTGCTCATCGAGACCTGAAGAGCAAAAATCATCTTTATTAAGAAAAATGTTAGTTGCTG 1190
Db 1081 AATTGCTCATCGAGACCTGAAGAGCAAAAATCATCTTTATTAAGAAAAATGTTAGTTGCTG 1140
QY 1191 TATTGCTGACCTGGGCTAGCTGTTTAAATTTCAAGTCACCAAAATGAAGTTGACATACC 1250

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Db 1141 TATTGCTGACCTGGCGCTAGCTGTTAAATTCACACAGTGATACAAATGAAGTTGACATACC 1200
Qy 1251 CTTGAACACAGGCTGGGACACAGCGGTACATGGCTCCAGAGTCTCGAGAGAGCCT 1310
Db 1201 CTTGAATACAGGCTGGGACCAAGCGGTACATGGCTCCAGAGTCTCGATGAAGCCT 1260
Qy 1311 GAGTAAAAACCAATTTCCAGCCCTACACATCATGGCTGACATCTACAGCTTTGGTTGATCAT 1370
Db 1261 GAATAAAAACCAATTTCCAGCCCTACACATCATGGCTGACATCTATAGCTTTGGTTGATCAT 1320
Qy 1371 TTGGAGATAGGCCCGCTGGCTGTATTATACAGAGAAATCGTGGAGGAATATCAATTACCATA 1430
Db 1321 TTGGGAAATGGCTGCTGTTGTTATTACAGAGGAATCGTGGAGGAATATCAATTACCATA 1380
Qy 1431 TTACAAACATGGTGGCTAGTACCCATCTTATGAAGACATGCGTGAGGTGCTGTGTGAA 1490
Db 1381 TTACAAACATGGTGGCCAGTGACCCATCTTATGAGGACATGCGTGAGGTGCTGTGTGAA 1440
Qy 1491 ACGCTTGGCGCCCAATCGTCTCTAAACCGCTCGAACAGTGATGAATGTCTTCGAGCCGTTTT 1550
Db 1441 ACGCTTGGCGCCCAATCGTCTCTAAACCGCTGGAACAGCGATGAATGTCTTCGAGCAGTTTT 1500
Qy 1551 GAAGCTGATGTCAGAAATGCTGGGCCCAATTAATCCAGCATCCAGACTCACAGCTTTGAGAAT 1610
Db 1501 GAAGCTAATGTGAGAAATGTTGGGCCCAATTAATCCAGCCTCCAGACTCACAGCTTTGAGAAT 1560
Qy 1611 CAAGAAGACGCTCGCAAGACATGGTGAATCCAGGATGTAAGATTTGAC----BAACAG 1666
Db 1561 CAAGAAGACACATTGCAAAATGGTGAATCCAGGATGTAAGATTTGACAAATTAACAA 1620
Qy 1667 TTTTGAAGAAAGATTTAGACTGCAAGAAATTC----ACCCGAGGAGGCTGGAGTTAGCA 1722
Db 1621 TTTTGAAGGAGAAATTTAGACTGCAAGAACTTTTACCCCAAGGAATGGTGGGATTAGCA 1680
Qy 1723 TGGACTAGGATGTGGCTTTGGTTTCCAGACTCTCTCTCTACCATCTTCCAGAGGTGCTA 1782
Db 1681 TGGAAATAGGATGTGACTTTGGTTTCCAGACTCTCTCTCTA-CATCTTCACAGGCTGCTA 1739
Qy 1783 ACAGTAAACCTTTACAGGACTTCGAGAATGC 1813
Db 1740 ACAGTAAACCTTTACCGCACTTACAGAAATAC 1770
```

RESULT 13

ID AAT28021 standard; cDNA; 2402 BP.

AC AAT28021;

XX 31-DEC-1996 (first entry)

DE Mouse BMP type I receptor kinase (BRK-1) cDNA.

XX BMP type II receptor kinase-3; BRK-3; bone morphogenetic protein;

KW BMP type I receptor kinase; BRK-1; BMP receptor; ds.

XX Mus sp.

OS

XX Key

FT CDS 11..1609

FT /*tag= a

XX Location/Qualifiers

XX WO9614579-Al.

XX 17-MAY-1996.

XX 30-OCT-1995; 95WO-US014027.

XX 04-NOV-1994; 94US-003341178.

PR 05-JUN-1995; 95US-00462467.

XX (PROC) PROCTER & GAMBLE CO.

XX Rosenbaum JS;
PI WPI; 1996-251987/25.
XX P-PSDB; AAR95225.
PT Assays for bone morphogenetic protein activities - using complex of BMP
type I receptor kinase protein and BMP receptor kinase protein BRK-3.
PS Claim 5; Page 64-66; 101pp; English.
XX A cDNA clone (AAT28021) codes for full-length mouse bone morphogenetic
protein (BMP) type I receptor kinase protein-1 (BRK-1) (AAR95225), a
CC receptor capable of binding BMP and transducing a signal initiated by the
CC binding. Host cells co-transfected with vectors carrying full-length,
CC incomplete or soluble BMP type I receptor kinase protein cDNA and full-
CC length, incomplete, soluble or truncated BMP type II receptor kinase
CC protein-3 (BRK-3) cDNA (see also AAT28018-20 and AAT28022-30) express a
CC BMP receptor complex useful for screening cpds. for BMP receptor affinity
CC or for determining the concentration of a BMP receptor ligand in a
CC clinical sample

XX Sequence 2402 BP; 676 A; 482 C; 540 G; 704 T; 0 U; 0 Other;

XX Query Match 86.8%; Score 1574.2; DB 2; Length 2402;

XX Best Local Similarity 94.2%; Pred. No. 0;

XX Matches 1669; Conservative 0; Mismatches 93; Indels 9; Gaps 3;

Qy 51 GAATTTGGACAATGACTCAGCTATACATTTACATCAGATTACTGGGAGCCTGCTGTTCAT 110

Db 1 GAATCAGACAATGACTCAGCTATACATTTACATCAGATTACTGGGAGCCTGCTGTTCAT 60

Qy 111 CATTTCTCATGTTCAAGGCGCAATCTAGATAGTAGTCTCCATGTTAGTGGTATGAATC 170

Db 61 CATTTCTCATGTTCAAGGCGCAATCTAGATAGTAGTCTCCATGTTAGTGGTATGAATC 120

Qy 171 AGACGTGGACCAAGAAAGCCGGAATGAGTGTAGCTTTAGCACACAGAGACACCTTACC 230

Db 121 AGACTTGGACCAAGAAAGCCGGAATGAGTGTAGCTTTAGCACACAGAGATACCTTGC 180

Qy 231 TTTCTTAAATGCTATTGCTCAGGACACTGCCCAGATGATGCTATTAATAACACATGCAT 290

Db 181 TTTCTTAAATGCTATTGCTCAGGACACTGCCCAGATGATGCTATTAATAACACATGCAT 240

Qy 291 AACTTAATGGCCATTCGTTTGGCCATTATAGAAGAATGATCAGGAGAAACACCGTTAC 350

Db 241 AACTTAATGGCCATTCGTTTGGCCATTATAGAAGAATGATCAGGAGAAACACCAATAC 300

Qy 351 TTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTTCAACCAAGCCCA 410

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Qy 411 GCTACGAGGACAATAGAAATGTTGCGGACCAATTTGTGCAACCAATATTTGAGGCTTAC 470

Db 361 GCTACGAGGACAATAGAAATGTTGCGGACCAATTTGTGCAACCAATATTTGAGGCTTAC 420

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Db 1740 ACAGTAAACCTTTACCGCACTCTACAGAATAC 1770

RESULT 15

AAQ90183
ID AAQ90183 standard; DNA; 2056 BP.

XX AAQ90183;
AC

XX 25-MAR-2003 (revised)

DT 01-NOV-1995 (first entry)

XX Truncated BRK-1.

XX BRK-1; BMP receptor kinase protein-1; bone morphogenetic protein; ds.

XX Mus sp.

XX Key Location/Qualifiers
FH CDS 291..1793

FT sig_peptide /*tag= a

FT mat_peptide /*tag= b

FT /*tag= c

XX WO9514778-A2.

XX 01-JUN-1995.

XX 23-NOV-1994; 94WO-US013534.

XX 24-NOV-1993; 93US-00158735.

XX (PROC) PROCTER & GAMBLE CO.

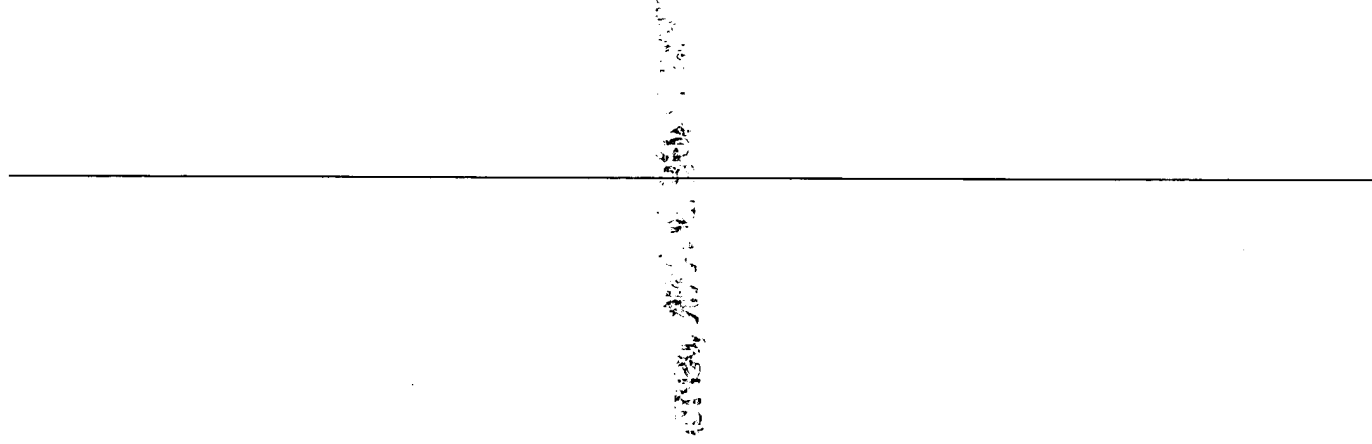
XX Cook JS, Correa PE, Koenig BB, Rosenbaum JS, Ting J;

DR WPI: 1995-206935/27.
DR P-PSDB; AAR74342.
XX New bone morphogenetic protein receptor kinase protein - used for
PT identifying cpds. capable of binding it and for developing therapeutic
PT cpds. and detection system(s).
XX
XX
PS Claim 6; Page 25-28; 49pp; English.
XX
CC PCR primers (given in AAQ90186-89) based on unique sequences present in
CC activin and DpF-1 receptor kinase domain VI were used to amplify cDNA
CC derived from NIH3T3 cells. A 300 bp PCR fragment obtd. was used to screen
CC a cDNA library prepd. from NIH3T3 cells in lambda ZapII to obtain clone
CC J159 containing DNA (AAQ90183) encoding truncated BRK-1 (AAR74342).
CC Vectors including the DNA were used to express recombinant EBRK-1 in CHO
CC and COS-7 hosts. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 2056 BP; 573 A; 436 C; 506 G; 541 T; 0 U; 0 Other;

Query Match 78.6%; Score 1424.4; DB 2; Length 2056;
Best Local Similarity 90.3%; Pred. No. 0;
Matches 1584; Conservative 0; Mismatches 76; Indels 94; Gaps 2;

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QY 99 CTGCTGTTTCATCAATTTCTCATGTTCAAGGGCAGAACTCTAGATAGTAGTCTCATGGTAC 158
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QY 329 CTGCTGTTTCATCAATTTCTCATGTTCAAGGGCAGAACTCTAGATAGTAGTCTCATGGCAGC 388
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QY 389 TGGTATGAATCAGAGCTGGACAGAGAAAGCGGAAATGGAGTGAGCTTAGCACCCAGA 448
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QY 1685 ACTGCAAGAAATTC 1698
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DB 2009 ACTGCAAGAACTTC 2022



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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1581.4	87.2	2070	3	US-09-395-115-13
6	1581.4	87.2	2070	3	US-08-436-265-13
7	1581.4	87.2	2070	3	US-09-679-187-13
8	1581.4	87.2	2070	3	US-09-267-963D-13
9	1574.2	86.8	2402	3	US-08-462-467B-11
10	1574.2	86.8	2402	3	US-08-158-735A-3
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36	690.6	38.1	1765	3	US-09-949-016-4525	Sequence 4525, Ap
37	673	37.1	2252	3	US-08-462-467B-13	Sequence 13, Appl
38	673	37.1	2252	3	US-08-334-179A-13	Sequence 13, Appl
39	647	35.7	706	3	US-08-462-467B-19	Sequence 19, Appl
40	440.8	24.3	469	3	US-08-462-467B-15	Sequence 15, Appl
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ALIGNMENTS

RESULT 1
US-08-123-934A-1
; Sequence 1, Application US/08123934A
; Patent No. 6291206
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; APPLICANT: CELESTE, Anthony J.
; APPLICANT: THIES, R. Scott
; APPLICANT: YAMAJI, No. 6291206oru
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute Inc. - Legal Affairs
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,934A
; FILING DATE: 17-SEP-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, Steven R
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 876 1170
; TELEFAX: 617 876 5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: CFK1-23a
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 61..1656
US-08-123-934A-1

Query Match									
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481	GTGCTTATAGGCCCATTTCTTATGAGCGAC	CGCTCCGATGGCTGCTCATCTATG	540						
481	GTGCTTATAGGCCCATTTCTTATGAGCGAC	CGCTCCGATGGCTGCTCATCTATG	540						
541	GCTGCTGTATTGTGCGCATGATCGTCTTCT	CGAGCTGCTTGTACAAACATTACTGT	600						
541	GCTGCTGTATTGTGCGCATGATCGTCTTCT	CGAGCTGCTTGTACAAACATTACTGT	600						
601	AAGAGTATCTCAAGCAGAGGTCGTTACAA	CCGTCACCTTGGAAACAGGATGAAGCAATTTAT	660						
601	AAGAGTATCTCAAGCAGAGGTCGTTACAA	CCGTCACCTTGGAAACAGGATGAAGCAATTTAT	660						
661	CCAGTAGGAGAAATCACTGAAAGACCTGAT	TGACCAAGCTCTGGTAGTGATCT	720						
661	CCAGTAGGAGAAATCACTGAAAGACCTGAT	TGACCAAGCTCTGGTAGTGATCT	720						
721	GGATTACCTTTATTGGTTCAGCGAACTATT	TGCCAAACAGATTGATGTTCCGCGAGTT	780						
721	GGATTACCTTTATTGGTTCAGCGAACTATT	TGCCAAACAGATTGATGTTCCGCGAGTT	780						
781	GCTAAGGCGCGGTATGGAGAAGTATGGAT	TGGAATGGCGTGGTGAAGAAAGTGGCTGTC	840						
781	GCTAAGGCGCGGTATGGAGAAGTATGGAT	TGGAATGGCGTGGTGAAGAAAGTGGCTGTC	840						
841	AAAGTATTTTTTACCACCTGAAGACCTAGCT	GTTTATAGAGAAACAGAAATCTACAGACG	900						
841	AAAGTATTTTTTACCACCTGAAGACCTAGCT	GTTTATAGAGAAACAGAAATCTACAGACG	900						
901	GTGTTAATCGCTCATGAAATATACTTGTGTT	TATAGCTGCGAGACATTAAGGCGACCGGT	960						
901	GTGTTAATCGCTCATGAAATATACTTGTGTT	TATAGCTGCGAGACATTAAGGCGACCGGT	960						
961	TCCTGGACTCAGCTGTATTGATTACTGATTAC	CATGAGAAATGGGTCTCTTATGACTTC	1020						
961	TCCTGGACTCAGCTGTATTGATTACTGATTAC	CATGAGAAATGGGTCTCTTATGACTTC	1020						

Qy	1021	CTGAATGTGCCACCTCGACACAGAGCCCTACTCAAGTTAGCTTATTTCTGCTGCTCTGT	1080
Db	1021	CTGAATGTGCCACCTCGACACAGAGCCCTACTCAAGTTAGCTTATTTCTGCTGCTCTGT	1080
Qy	1081	GGTCTGTGCCACCTCCACACAGAAAATTTATGGCACGCAAGGCAAGCCTGCAATTTGCTCAT	1140
Db	1081	GGTCTGTGCCACCTCCACACAGAAAATTTATGGCACGCAAGGCAAGCCTGCAATTTGCTCAT	1140
Qy	1141	CGAGACCTGAAGAGCAAAAAATCCTTTATTAAGAAAAATGGTAGTTGCTGTATTTGCTGAC	1200
Db	1141	CGAGACCTGAAGAGCAAAAAATCCTTTATTAAGAAAAATGGTAGTTGCTGTATTTGCTGAC	1200
Qy	1201	CTGGGCTAGCTGTTAAATTCACAGTCACACAAATGAAGTTGCATACCCCTTGAACACC	1260
Db	1201	CTGGGCTAGCTGTTAAATTCACAGTCACACAAATGAAGTTGCATACCCCTTGAACACC	1260
Qy	1261	AGGTTGGGCAACAGGCGGTACATGGCTCCAGAAAGTCTGGACGAGAGCCTGAGTAAAAAC	1320
Db	1261	AGGTTGGGCAACAGGCGGTACATGGCTCCAGAAAGTCTGGACGAGAGCCTGAGTAAAAAC	1320
Qy	1321	CATTTCCAGCCCTACATCATGGCTGACATCTACAGCTTTGGTTTGTATTTGGGAGATG	1380
Db	1321	CATTTCCAGCCCTACATCATGGCTGACATCTACAGCTTTGGTTTGTATTTGGGAGATG	1380
Qy	1381	GCCGTCGCTGTTTACAGAGGAATCTGGAGGAATATCAATTTACCATATTACAACATG	1440
Db	1381	GCCGTCGCTGTTTACAGAGGAATCTGGAGGAATATCAATTTACCATATTACAACATG	1440
Qy	1441	GTGCTTAGTGACCCATCTTATGAAGACATGCGTGGAGTCTGTGTGTGAAACGCTTCGGG	1500
Db	1441	GTGCTTAGTGACCCATCTTATGAAGACATGCGTGGAGTCTGTGTGTGAAACGCTTCGGG	1500
Qy	1501	CAATCGTCTTAACCGCTGGAAACAGTGAATGCTTCGAGCGCTTTTGAAGCTGATG	1560
Db	1501	CAATCGTCTTAACCGCTGGAAACAGTGAATGCTTCGAGCGCTTTTGAAGCTGATG	1560
Qy	1561	TCAGAAATCTGGGCCCAATAATCCAGACTCCAGACTTTCAGAAATCAAGAGAGC	1620
Db	1561	TCAGAAATCTGGGCCCAATAATCCAGACTCCAGACTTTCAGAAATCAAGAGAGC	1620
Qy	1621	CTCGCAAGATGTTGAATCCAGGATGTAAGATTTGACAAACAGTTTTCAGAAAGAAAT	1680
Db	1621	CTCGCAAGATGTTGAATCCAGGATGTAAGATTTGACAAACAGTTTTCAGAAAGAAAT	1680
Qy	1681	TTAGACTGCAAGAAATTCACCGAGGAAGGGTGGAGTTAGCATAGGATGTCGGCT	1740
Db	1681	TTAGACTGCAAGAAATTCACCGAGGAAGGGTGGAGTTAGCATAGGATGTCGGCT	1740
Qy	1741	TGGTTTCCAGACTCTCTCTCTTACCATCTTACAGGCTGCTAACAGTAAACCTTTCAGGA	1800
Db	1741	TGGTTTCCAGACTCTCTCTCTTACCATCTTACAGGCTGCTAACAGTAAACCTTTCAGGA	1800
Qy	1801	CTCTGCAGAAATGC	1813
Db	1801	CTCTGCAGAAATGC	1813

RESULT 2

US-09-874-628-1
; Sequence 1, Application US/09874628
; Patent No. 6610513
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; CELESTE, Anthony J.
; THIES, R. Scott
; YAMAJI, No. 6610513oru
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute Inc.- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA

COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 05-Jun-2001
APPLICATION NUMBER: US/09/874,628
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,934
FILING DATE: 17-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5203
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 876 1170
TELEFAX: 617 876 5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1813 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: CFK1-23a
FEATURE:
NAME/KEY: CDS
LOCATION: 61..1656
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-874-628-1

Query Match 100.0%; Score 1813; DB 3; Length 1813;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CTAGTGGATCCCGGGCTGCAGGAATTCGCGGCGCCAGGACACGTGGGAATTTGGACA	60
DB	1	CTAGTGGATCCCGGGCTGCAGGAATTCGCGGCGCCAGGACACGTGGGAATTTGGACA	60
QY	61	ATGACTCAGCTATACACTTACATCAGATTACTGGGAGCCCTGCTGTTTCATCTTCAT	120
DB	61	ATGACTCAGCTATACACTTACATCAGATTACTGGGAGCCCTGCTGTTTCATCTTCAT	120
QY	121	GTTCAGGGCAGAACTAGATAGTATGCTCCATGGTACTGGTATGAAATCAGACGTGGAC	180
DB	121	GTTCAGGGCAGAACTAGATAGTATGCTCCATGGTACTGGTATGAAATCAGACGTGGAC	180
QY	181	CAGAAAGCCGGAATGGAGTGACGTTAGCACAGAGACACCTTACCTTTCTTAAAA	240
DB	181	CAGAAAGCCGGAATGGAGTGACGTTAGCACAGAGACACCTTACCTTTCTTAAAA	240
QY	241	TGCTATTGCTCAGACACTGCCAGATGAGCTATTAAACACATGCATTAACCTATGCG	300
DB	241	TGCTATTGCTCAGACACTGCCAGATGAGCTATTAAACACATGCATTAACCTATGCG	300
QY	301	CATTGCTTTGCCATTATAGAAGAGATGATCAGGAGAAACACGTTAACTTCGGGTGT	360
DB	301	CATTGCTTTGCCATTATAGAAGAGATGATCAGGAGAAACACGTTAACTTCGGGTGT	360
QY	361	ATGAAGTATGAAGGCTCTGATTTTCAATGAAGATTCACCAAAAGCCAGCTACGAG	420
DB	361	ATGAAGTATGAAGGCTCTGATTTTCAATGAAGATTCACCAAAAGCCAGCTACGAG	420
QY	421	ACAATAGATGTTGTCGGACCAATTTGTGCAACCAATTTTGCAGCTACCTGCCCCCT	480
DB	421	ACAATAGATGTTGTCGGACCAATTTGTGCAACCAATTTTGCAGCTACCTGCCCCCT	480
QY	481	GTGTTATAGGCCCATTTCTTTGATGGCAGCGTCCGATGGCTGTGCTCATCTCTATG	540

Db	481	GTGTTATAGGCCCATTTCTTTGATGGCAGCGTCCGATGGCTGTGCTCATCTCTATG	540
QY	541	GCTGCTGTATTGTCGCCCATGCTCTTCTCAGCTGCTCTTGTACAAACATTACTGT	600
Db	541	GCTGCTGTATTGTCGCCCATGCTCTTCTCAGCTGCTCTTGTACAAACATTACTGT	600
QY	601	AAGAGTATCTCAAGCAGAGGTCCTTACAAACCGTGACTTGGAAACAGGATGAAGCATTTATT	660
Db	601	AAGAGTATCTCAAGCAGAGGTCCTTACAAACCGTGACTTGGAAACAGGATGAAGCATTTATT	660
QY	661	CCAGTAGGAGATCACTGAAAGACCTGATTGACAGCTCACAAGCTCTGTTAGTGATCT	720
Db	661	CCAGTAGGAGATCACTGAAAGACCTGATTGACAGCTCACAAGCTCTGTTAGTGATCT	720
QY	721	GGATTACCTTTATTGCTCAGCGAACTATTGCCCCAAGATTTGCCCCAAGATTTGCGCAGGTT	780
Db	721	GGATTACCTTTATTGCTCAGCGAACTATTGCCCCAAGATTTGCCCCAAGATTTGCGCAGGTT	780
QY	781	GGTAAGGGCGGTATGGAGAAGTATGATGGGTAAATGGCGTGGTGAAGAGTGGCTGTC	840
Db	781	GGTAAGGGCGGTATGGAGAAGTATGATGGGTAAATGGCGTGGTGAAGAGTGGCTGTC	840
QY	841	AAAGTATTTTACCCTGAAAGAGCTAGCTGCTGTTAGAGAAAACAGAAATCTACACAGC	900
Db	841	AAAGTATTTTACCCTGAAAGAGCTAGCTGCTGTTAGAGAAAACAGAAATCTACACAGC	900
QY	901	GTGTTAATGCGTCATGAAAATATATCTGTTTATAGCTGCAGACATTAAGGCACCGGT	960
Db	901	GTGTTAATGCGTCATGAAAATATATCTGTTTATAGCTGCAGACATTAAGGCACCGGT	960
QY	961	TCCTGGACTCAGCTGATTGTTGTTACTGATTACCATGAGAAATGGGTCTCTCTATGACTTC	1020
Db	961	TCCTGGACTCAGCTGATTGTTGTTACTGATTACCATGAGAAATGGGTCTCTCTATGACTTC	1020
QY	1021	CTGAAATGTGCCACCTCGACACACAGAGCCCTACTCAAGTTAGCTTATTCTGCTGCTGT	1080
Db	1021	CTGAAATGTGCCACCTCGACACACAGAGCCCTACTCAAGTTAGCTTATTCTGCTGCTGT	1080
QY	1081	GGTCTGTGCCACCTCCACACAGAAATTTATGGCAGCAAGGCAAGCTGCAATGCTCAT	1140
Db	1081	GGTCTGTGCCACCTCCACACAGAAATTTATGGCAGCAAGGCAAGCTGCAATGCTCAT	1140
QY	1141	CGAGACTCAGAGCAAAACATCTTATTAAGAAAATGGTGTGCTGTATTGCTGAC	1200
Db	1141	CGAGACTCAGAGCAAAACATCTTATTAAGAAAATGGTGTGCTGTATTGCTGAC	1200
QY	1201	CTGGGCTAGCTGTTAAATTTCAACAGTGAACAAATGAAAGTTGACATACCTTTGAACACC	1260
Db	1201	CTGGGCTAGCTGTTAAATTTCAACAGTGAACAAATGAAAGTTGACATACCTTTGAACACC	1260
QY	1261	AGGTTGGGCAACGCGGTACATGGCTCCAGAGTCTGGACGAGACCTGAGTAAAC	1320
Db	1261	AGGTTGGGCAACGCGGTACATGGCTCCAGAGTCTGGACGAGACCTGAGTAAAC	1320
QY	1321	CATTTCCAGCCCTACATCATGCTGACATCTCAGCTTTGGTTTGTATCATTTGGGAGATG	1380
Db	1321	CATTTCCAGCCCTACATCATGCTGACATCTCAGCTTTGGTTTGTATCATTTGGGAGATG	1380
QY	1381	GCCCGTGCCTGATTACAGGAGAAATCGTGGAGGAAATCAATTTACCATAATTACAACATG	1440
Db	1381	GCCCGTGCCTGATTACAGGAGAAATCGTGGAGGAAATCAATTTACCATAATTACAACATG	1440
QY	1441	GTGCTAGTGACCATCTTATGAAGACATGCGTGAGCTGCTGTGTGAACCTTGGCG	1500
Db	1441	GTGCTAGTGACCATCTTATGAAGACATGCGTGAGCTGCTGTGTGAACCTTGGCG	1500
QY	1501	CCAACTGCTCTAAACCGCTGGAACAGTGAATGCTTCGAGCCGCTTTTGAAGCTGATG	1560
Db	1501	CCAACTGCTCTAAACCGCTGGAACAGTGAATGCTTCGAGCCGCTTTTGAAGCTGATG	1560
QY	1561	TCAGATGCTGGGCCCATTAATCCAGCATCCAGCTCAGACTTTGAGAAATCAAGAAAGC	1620

Db 1561 TCAGATGCTGGCCCATTAATCCAGATCCAGACTCACAGCTTTGAGATCAAGAGAGC 1620
QY 1621 CTCGCAAGATGTTGAATCCAGGATGTAAGATTGACAAACAGTTTGTGAGAAAGAAAT 1680
Db 1621 CTCGCAAGATGTTGAATCCAGGATGTAAGATTGACAAACAGTTTGTGAGAAAGAAAT 1680
QY 1681 TTAGACTGCAAGAAATTCACCGAGGAGGTTGGAGTTAGCATGGACTAGGATGTCGGCT 1740
Db 1681 TTAGACTGCAAGAAATTCACCGAGGAGGTTGGAGTTAGCATGGACTAGGATGTCGGCT 1740
QY 1741 TGGTTTCCAGACTCTCTCCTTACCATTCTTCCAGGCTCTTAAACAGTAAACCTTTTCAGGA 1800
Db 1741 TGGTTTCCAGACTCTCTCCTTACCATTCTTCCAGGCTCTTAAACAGTAAACCTTTTCAGGA 1800
QY 1801 CTCTGCAGAAATGC 1813
Db 1801 CTCTGCAGAAATGC 1813

RESULT 3

PCT-US94-10080-1
; Sequence 1, Application PC/TUS9410080
; GENERAL INFORMATION:
; APPLICANT: GENETICS INSTITUTE, INC.
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute Inc. - Legal Affairs
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10080
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,934
; FILING DATE: 17-SEP-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, Steven R
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5203-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8260
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: CFK1-23a
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 61..1656
PCT-US94-10080-1

Query Match 100.0%; Score 1813; DB 6; Length 1813;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTAGTGGATCCCCGGCTGCGAGGAATTCCTGCGCGCCGAGGACACGTCGCAATTTGGACA 60
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Db 1 CTAGTGGATCCCCGGCTGCGAGGAATTCCTGCGCGCCGAGGACACGTCGCAATTTGGACA 60
QY 61 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCGCTGCTGTTCATCATTTCTCAT 120
|||||
Db 61 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCGCTGCTGTTCATCATTTCTCAT 120
|||||
QY 121 GTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGCTACTGGTATGAATACAGACGTCGAC 180
|||||
Db 121 GTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGCTACTGGTATGAATACAGACGTCGAC 180
|||||
QY 181 CAGAAAGAGCCGAAAAATGGAGTGACGTTAGCACCCAGAGGACACCTTACTCTTTCTTAAAA 240
|||||
Db 181 CAGAAAGAGCCGAAAAATGGAGTGACGTTAGCACCCAGAGGACACCTTACTCTTTCTTAAAA 240
|||||
QY 241 TGCTATTGCTCAGGACACTGCCCCAGATGACGCTATTATAACACATGATCATATAATGCG 300
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Db 241 TGCTATTGCTCAGGACACTGCCCCAGATGACGCTATTATAACACATGATCATATAATGCG 300
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QY 301 CATTCGTTTGCCATTATAGAAAGATGATCAGGGAGAAACCACTTAACTTCTGGGTGT 360
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Db 301 CATTCGTTTGCCATTATAGAAAGATGATCAGGGAGAAACCACTTAACTTCTGGGTGT 360
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QY 361 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCAACAAAAGCCAGCTACGCAGG 420
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Db 361 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCAACAAAAGCCAGCTACGCAGG 420
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QY 421 ACAATAGAAATGTTGTCGGAACCAATTTTGCAACCAATATTTGCGAGCTACACTGCCCCCT 480
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QY 481 GTCGTTATAGGCCCAATCTTTGATGGCAGCGTCCGATGGCTGCTGCTCATCTCTATG 540
Db 481 GTCGTTATAGGCCCAATCTTTGATGGCAGCGTCCGATGGCTGCTGCTCATCTCTATG 540
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QY 541 GCTGCTGTATTGTCGCCATGATCTCTTCCAGCTGCTTCTGTTTACAAACATTACTGT 600
Db 541 GCTGCTGTATTGTCGCCATGATCTCTTCCAGCTGCTTCTGTTTACAAACATTACTGT 600
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QY 601 AAGAGTATCTCAAGCAGAGGTCGTTTACAACCGTGACTTTGGAAACAGGATGAAGCAATTA 660
Db 601 AAGAGTATCTCAAGCAGAGGTCGTTTACAACCGTGACTTTGGAAACAGGATGAAGCAATTA 660
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QY 661 CCAGTAGGAGAAATCACTGAAAGACCTGATGACCAAGCTCACAAGCTCTGGTAGTGGATCT 720
Db 661 CCAGTAGGAGAAATCACTGAAAGACCTGATGACCAAGCTCACAAGCTCTGGTAGTGGATCT 720
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QY 721 GGATTACCTTTATTGGTTTCAAGCAACTATTGCAACACAGATTTCAGATGGTTCGGCAGGTT 780
Db 721 GGATTACCTTTATTGGTTTCAAGCAACTATTGCAACACAGATTTCAGATGGTTCGGCAGGTT 780
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QY 781 GGTAAAGGCGCGTATGGAGAAATGAGTATGGATGGGTAAATGGCGGTGGAAGGTCGCTGTC 840
Db 781 GGTAAAGGCGCGTATGGAGAAATGAGTATGGATGGGTAAATGGCGGTGGAAGGTCGCTGTC 840
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QY 841 AAGCTATTTTACCACCTGAAGAGCTAGCTGTTTAGGAAACAGAAATCTACACAGCG 900
Db 841 AAGCTATTTTACCACCTGAAGAGCTAGCTGTTTAGGAAACAGAAATCTACACAGCG 900
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QY 901 GTGTTAATGCGTCATGAAAATATCTCTGGTTTATAGCTGCAGACATTTAAAGGCCCGGT 960
Db 901 GTGTTAATGCGTCATGAAAATATCTCTGGTTTATAGCTGCAGACATTTAAAGGCCCGGT 960
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QY 961 TCCTGGACTCAGCTGATTTGATTACTGATTAACCATGAGATGGGTCTCTCTATGACTTC 1020
Db 961 TCCTGGACTCAGCTGATTTGATTACTGATTAACCATGAGATGGGTCTCTCTATGACTTC 1020
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QY 1021 CTGAAATGTCACCCCTGGACACAGAGCCCTACTCTCAAGTTAGCTTATCTCTGCTGCT 1080
Db 1021 CTGAAATGTCACCCCTGGACACAGAGCCCTACTCTCAAGTTAGCTTATCTCTGCTGCT 1080
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QY 1081 GGTCTGTGCCACCTCCACACAGAAATTTATGCGACGCAAGGCAAGCCCTGCAATTTGCTCAT 1140
Db 1081 GGTCTGTGCCACCTCCACACAGAAATTTATGCGACGCAAGGCAAGCCCTGCAATTTGCTCAT 1140
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9136099.2
; FILING DATE: 3-August-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9321344.5
; FILING DATE: 15-October-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohlei, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2070 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 217..1812
; US-09-395-115-13

Query Match
Best Local Similarity 94.1%; Pred. No. 0;
Matches 1678; Conservative 0; Mismatches 96; Indels 9; Gaps 3;

QY 39 CAGGACACGTCGCAATGGACATGACTCAGCTATACACTTACATCAGATTACTGGGAGC 98
DB 195 CAGGACGCGTGGCAATCAGACAAATGACTCAGCTATATACACTTACATCAGATTACTGGGAGC 254
QY 99 CTGCTGTTTCATCATTTCTCATGCTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGGTAC 158
DB 255 CTGCTGTTTCATCATTTCTCATGCTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGGCAC 314
QY 159 TGTATGAAATCAGACGTGGACACAGAAAGACGCGGAAATGGAGTACGCTTAGCACCAGA 218
DB 315 TGTATGAAATCAGACTTGGACACAGAAAGACGCGGAAATGGAGTACGCTTAGCACCAGA 374
QY 219 GGACACTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCCAGATGACGCTATTAA 278
DB 375 GGATACCTTGGCTTTCTTAAAGTGTATTGCTCAGGACACTGCCCAGATGATGCTATTAA 434
QY 279 TAACACATGCATAACTTAATGGCCATTGCTTTGCCATTATAGAAAGAGATGATCAGGGAGA 338
DB 435 TAACACATGCATAACTTAATGGCCATTGCTTTGCCATTATAGAAAGAGATGATCAGGGAGA 494
QY 339 AACACGCTTAACTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTTC 398
DB 495 AACACATTAACCTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTTC 554
QY 399 ACCAAAGCCCGACTACGAGGACCAATAGAAATGTTGTCGGACCAATTTGTGCAACCAATA 458
DB 555 ACCGAAAGCCCGACTACGAGGACCAATAGAAATGTTGTCGGACCAATTTGTGCAACCAATA 614
QY 459 TTTCAGGCTTACACTGCCCTGCTGTATAGGCCCATTTCTTTGATGGCAGGCTCCGATG 518
DB 615 TTTCAGGCTTACACTGCCCTGCTGTATAGGCCCATTTCTTTGATGGCAGGATCCGATG 674
QY 519 GCTGGCTGCTCATCTCTATGGCTGCTGTATTGTCGCCATGATCGTCTTCTCCAGCTG 578
DB 675 GCTGGTGTGCTCATTTCCATGCTGCTGTATAGTATGCTATGATCATCTTCTCCAGCTG 734
QY 579 CTTCTGTTACAAACATTACTGTAAAGATATCTCAAGCAGAGGTGCGTTACAAACCGTACTTT 638
DB 735 CTTTTCCTATAAGCATTTATTGTAAGAGTATCTCAAGCAGGGGTGTTTCCACCAAGGAATTT 794
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639 GGAACAGAGTGAAGCATTTATTCCAGTAGGAGAAATCACTGAAAGACCTGATTGACCAGTC 698
795 GGAACAGAGTGAAGCATTTATTCCAGTAGGAGAAATCACTGAAAGACCTGATTGACCAGTC 854
699 ACAAGCTCTGTTAGTGGATCTGGATTAACCTTTATTTGGTTTCAGCGAACTATTGCCAAACA 758
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759 GATTTCAGATGGTTTCGSCAGGTTGGTAAGGCGGTAATGGAGAGTATGGATGGTGAATG 818
915 GATTTCAGATGGTTTCGSCAGGTTGGTAAGGCGGTAATGGAGAGTATGGATGGTGAATG 974
819 GCGTGTGTAAGGAGTGGCTGTCTCAAGTATTTTTTACCACCTGAAAGAGTACGTGGTTTAG 878
975 GCGTGTGTAAGGAGTGGCTGTCTCAAGTATTTTTTACCACCTGAAAGAGTACGTGGTTTAG 1034
879 AGAAACAGAAATCTACACAGACGCTGTTAATGGCTCATGAAATATATCTTGGTTTTATAGC 938
1035 AGAAACAGAAATCTACACAGACGCTGTTAATGGCTCATGAAATATATCTTGGTTTTATAGC 1094
939 TGCAGACATTTAAGGACACCGGTTCCCTGGACTCAGCTGTATTTCGATTACTGATTACCATGA 998
1095 TGCAGACATTTAAGGACACCGGTTCCCTGGACTCAGCTGTATTTCGATTACTGATTACCATGA 1154
999 GAATGGGTCTCTCTATGACTTCTCTGAAATGTGCTCACCTGGACACACAGAGCCCTACTCAA 1058
1155 AAATGGATCTCTCTATGACTTCTCTGAAATGTGCTCACCTGGACACACAGAGCCCTACTCAA 1214
1059 GTTAGCTTATCTGCTGCTGCTGCTGTCGCAACCTTCCACACAGAAATTTATGGCAGCA 1118
1215 GTTAGCTTATCTGCTGCTGCTGCTGTCGCAACCTTCCACACAGAAATTTATGGTACCCA 1274
1119 AGGCAAGCTGCAATTTGCTCATCGAGACTGGAAGAGCAAAACATCTTTATTAAGAAAA 1178
1275 AGGCAAGCTGCAATTTGCTCATCGAGACTGGAAGAGCAAAACATCTTTATTAAGAAAA 1334
1179 TGTGATGTTGCTGTATTGCTGACTGCGGCTAGCTGTGTTAAATTTCAACAGTGACACAAATGA 1238
1335 TGTGATGTTGCTGTATTGCTGACTGCGGCTAGCTGTGTTAAATTTCAACAGTGATACAATGA 1394
1239 AGTTGACATACCTTTGAAACACACAGAGTGGGACACAGGGGGTACATGGCTCCAGAGTGTCT 1298
1395 AGTTGACATACCTTTGAAATACACAGAGTGGGACACAGGGGGTACATGGCTCCAGAGTGTCT 1454
1299 GGACAGAGCTGAGTAAACCATTTCCAGCCCTACATCATGCTGCTGACATCTACAGCTT 1358
1455 GGATGAAAGCTGAAATTAACCAATTTCCAGCCCTACATCATGCTGCTGACATCTATAGCTT 1514
1359 TGGTTTGTGATCATTTGGGAGATGGCCCGCTGCTGTATTACAGGAGGAATCGTGGAGGAATA 1418
1515 TGGTTTGTGATCATTTGGGAGATGGCCCGCTGCTGTATTACAGGAGGAATCGTGGAGGAATA 1574
1419 TCAATTTACCATAATTAACAATGGTGCCTAGTGACCCATCTTTATGAAGACATCGTGGAGGT 1478
1575 TCAATTTACCATAATTAACAATGGTGCCTAGTGACCCATCTCTATGAGGACATCGTGGAGGT 1634
1479 CGTGTGTGTGAACCGCTTGGGCCCAATCGTCTCTAACCGCTGGAACAGTGTGAATGTCT 1538
1635 TGTTGTGTGAACCGCTTGGGCCCAATCGTGTCTTAACCGCTGGAACAGGATGAATGTCT 1694
1539 TCGAGCCGTTTTTGAAGCTGTGTCAGAAATGCTGGGCCCAATTAATCAGACATCCAGACTCAC 1598
1695 TCGAGCAGTTTTTGAAGCTGTGTCAGAAATGCTGGGCCCAATTAATCAGACCTCCAGACTCAC 1754
1599 AGCTTTGAGAAATCAAGAGACGCTCGCAAGATGTTGAATCCCAAGGATGTAAGATTG 1658
1755 AGCTTTGAGAAATCAAGAGACACTTGCAGAAATGTTGAATCCCAAGGATGTAAGATTG 1814
1659 AC----AAACAGTTTTTGAGAAAGATTTTAGACTGCAAGAAATTC----ACCCAGGAAG 1710
1815 ACAATTAACCAATTTTGAGGGAGAAATTTAGACTGCAAGAACTTTCTTCCACCAAGGAATGG 1874
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QY 1711 GTGGAGTTAGCAGTACAGGATGCGGCTTGGTTCCAGACTCTCTCCTCTACCATCTT 1770
Db 1875 GTGGGATTAGCAGTAAGTAAGGATGTTGACTTGGTTTCCAGACTCTCTCCTCTA-CATCTT 1933
QY 1771 CACAGGCTCTAACAGTAAACCTTTTCAGGACTCTGCAGAAATGC 1813
Db 1934 CACAGGCTCTAACAGTAAACCTTACCGTACTCTACAGAAATAC 1976

RESULT 6
US-08-436-265-13
; Sequence 13, Application US/08436265
; Patent No. 6316217
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
; APPLICANT: Franzon, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
; TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,265
; FILING DATE: 30-October-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: 17-No. 6316217ember-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9224057.1
; FILING DATE: 17-No. 6316217ember-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304677.9
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304680.3
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9311047.6
; FILING DATE: 28-May-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9313763.6
; FILING DATE: 2-July-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9136099.2
; FILING DATE: 3-August-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9321344.5
; FILING DATE: 15-October-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohlei, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2070 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO

; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 217..1812
US-08-436-265-13
Query Match 87.2%; Score 1581.4; DB 3; Length 2070;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 1678; Conservative 0; Mismatches 96; Indels 9; Gaps 3;
QY 39 CAGGACACGTCGGAATTCGACAACTGACTCAGCTATACACTTACATCAGATTAATCGGAGC 98
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QY 99 CTGCTCTGTTTCATCTTCTCATGTTTCAAGGCGCAGAACTCTAGATAGTATGCTCCATGGTAC 158
Db 255 CTGCTCTGTTTCATCTTCTCATGTTTCAAGGCGCAGAACTCTAGATAGTATGCTCCATGGCAC 314
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Db 375 GGATACCTTGGCTTTCTTAAATGCTATGCTCAGGACACTGCCCAGATGAGCTATTAA 434
QY 279 TAACACATGCATAACTAATGCGCATTTGCTTGCCTATAGAAAGAGATGATCAGGAGA 338
Db 435 TAACACATGCATAACTAATGCGCATTTGCTTGCCTATAGAAAGAGATGATCAGGAGA 494
QY 339 AACCAAGCTTAACTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTC 398
Db 495 AACCAAGCTTAACTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTC 554
QY 399 ACCAAAGCCGACGCTACCCAGGACAAATAGAAATGTTGTCGACCAATTTGTGCAACCAATA 458
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Db 615 TTTGAGGCTACACTGCCCTCTGTTATAGGCTCGTTTGTATGATGCGAGGCTCCGATG 674
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QY 819 CGGTGGTCAAAAAGTGGCTGTCAAAGTATTTTTTACCACTCAAGAGAGTGTGCTGTTTAG 878
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Db 1035 AGAAACAGAAATCTACCAGACGGTGTAAATCGCTCATGAAATATATCTTGGTTTTATAGC 1094

Qy	939	TCGAGACATTAAAGCGCACCGGTTCTCGAGCTGATCTTTGATTA	998
		TCGAGACATTAAAGCGCACCGGTTCTCGAGCTGATCTTTGATTA	
Db	1095	TCGAGACATTAAAGCGCACCGGTTCTCGAGCTGATCTTTGATTA	1154
		TCGAGACATTAAAGCGCACCGGTTCTCGAGCTGATCTTTGATTA	
Qy	999	GAATGGGCTCTCTATGACATTCCTGAAATGTGCCACCTGGACAC	1058
		GAATGGGCTCTCTATGACATTCCTGAAATGTGCCACCTGGACAC	
Db	1155	AAATGGGATCTCTATGACATTCCTGAAATGTGCCACACTAGACAC	1214
		AAATGGGATCTCTATGACATTCCTGAAATGTGCCACACTAGACAC	
Qy	1059	GTTAGCTTATTTCTGCTCGCTGTGCTGTGCGACCTCCACACAGAA	1118
		GTTAGCTTATTTCTGCTCGCTGTGCTGTGCGACCTCCACACAGAA	
Db	1215	GTTAGCTTATTTCTGCTGTGCTGTGCGACCTCCACACAGAAATTT	1274
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Qy	1119	AGGCAAGCCCTGCAATTGCTCATCGAGACCTGAAGAGCAAAACATC	1178
		AGGCAAGCCCTGCAATTGCTCATCGAGACCTGAAGAGCAAAACATC	
Db	1275	AGGCAAGCCCTGCAATTGCTCATCGAGACCTGAAGAGCAAAACATC	1334
		AGGCAAGCCCTGCAATTGCTCATCGAGACCTGAAGAGCAAAACATC	
Qy	1179	TGGTAGTTGCTGATTTGCTGACCTGGGCGCTAGCTGTTTAAATTC	1238
		TGGTAGTTGCTGATTTGCTGACCTGGGCGCTAGCTGTTTAAATTC	
Db	1335	TGGAGTTGCTGATTTGCTGACCTGGGCGCTAGCTGTTTAAATTC	1394
		TGGAGTTGCTGATTTGCTGACCTGGGCGCTAGCTGTTTAAATTC	
Qy	1239	AGTTGACATACCCCTTGAACACCAAGGCTGGGCAACAGGCGGTAC	1298
		AGTTGACATACCCCTTGAACACCAAGGCTGGGCAACAGGCGGTAC	
Db	1395	AGTTGACATACCCCTTGAATACCAAGGCTGGGCAACAGGCGGTAC	1454
		AGTTGACATACCCCTTGAATACCAAGGCTGGGCAACAGGCGGTAC	
Qy	1299	GGACGAGAGCCTGAGTAAAAACCATTTCCAGCCCTACATCATGCT	1358
		GGACGAGAGCCTGAGTAAAAACCATTTCCAGCCCTACATCATGCT	
Db	1455	GGATGAAAGCCTGAAATAAAACCATTTCCAGCCCTACATCATGCT	1514
		GGATGAAAGCCTGAAATAAAACCATTTCCAGCCCTACATCATGCT	
Qy	1359	TGGTTTGATCATTTTGGAGATGGCCCGTCGCTGTAATTACAGGAG	1418
		TGGTTTGATCATTTTGGAGATGGCCCGTCGCTGTAATTACAGGAG	
Db	1515	TGGTTTGATCATTTTGGGAAATGGCTCGTGTGTAATTACAGGAG	1574
		TGGTTTGATCATTTTGGGAAATGGCTCGTGTGTAATTACAGGAG	
Qy	1419	TCAATTACCATATTTACAACTGCTGCTGTAGTGACCCATCTTATG	1478
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Db	1575	TCAATTACCATATTTACAACTGCTGCTGTAGTGACCCATCTTATG	1634
		TCAATTACCATATTTACAACTGCTGCTGTAGTGACCCATCTTATG	
Qy	1479	CGTGTGTGTAACCGCTTGGCGGCAATCGTCTCTAAACCGCTGGA	1538
		CGTGTGTGTAACCGCTTGGCGGCAATCGTCTCTAAACCGCTGGA	
Db	1635	TGTGTGTGTAACCGCTTGGCGGCAATCGTCTCTAAACCGCTGGA	1694
		TGTGTGTGTAACCGCTTGGCGGCAATCGTCTCTAAACCGCTGGA	
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		TCGAGCCGTTTTGAAGCTGATGTGAGAAATGCTGGGCCCAATAA	
Db	1695	TCGAGCAGTTTTGAAGCTAATGTGAGAAATGTTGGGCCCAATAA	1754
		TCGAGCAGTTTTGAAGCTAATGTGAGAAATGTTGGGCCCAATAA	
Qy	1599	AGCTTTGAGAAATCAAGAAAGCGCTCGCAAGATGGTTGAATCC	1658
		AGCTTTGAGAAATCAAGAAAGCGCTCGCAAGATGGTTGAATCC	
Db	1755	AGCTTTGAGAAATCAAGAAAGCACTTGCAAAAATGGTTGAAATC	1814
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Qy	1659	AC----AAACAGTTTTTCAGAAAGAAATTTAGACTGCAAGAAATTC	1710
		AC----AAACAGTTTTTCAGAAAGAAATTTAGACTGCAAGAAATTC	
Db	1815	ACAATTAACAAATTTGAGGAGAAATTTAGACTGCAAGAAATCTTC	1874
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Qy	1711	GTGAGGTTAGCATGGCATAGGATGTCGGCTTGGTTTTCCAGACTC	1770
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Db	1875	GTGGGATTAGCATGGAATAGGATGTCACTTGGTTTCCAGACTCCTT	1933
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Qy	1771	CACAGGCTGCTAACAGTAACACCTTTTCAGGACTCTGCAGAAATGC	1813
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Db	1934	CACAGGCTGCTAACAGTAACACCTTTACCGTACTCTACAGAAATAC	1976
		CACAGGCTGCTAACAGTAACACCTTTACCGTACTCTACAGAAATAC	

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1 STREET: 805 Third Avenue
2 CITY: New York City
3 STATE: New York
4 ZIP: 10022
5
6 COMPUTER READABLE FORM:
7 MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
8
9 COMPUTER: IBM
10 OPERATING SYSTEM: PC-DOS
11 SOFTWARE: Wordperfect
12
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/09/679,187
15 FILING DATE: 03-OCT-2000
16
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: US/08/436,265
19 FILING DATE: 30-October-1995
20
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: PCT/G93/02367
23 FILING DATE: 17-No. 6331621ember-1993
24
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: 9224057.1
27 FILING DATE: 17-No. 6331621ember-1992
28
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: 9304677.9
31 FILING DATE: 8-March-1993
32
33 PRIOR APPLICATION DATA:
34 APPLICATION NUMBER: 9304680.3
35 FILING DATE: 8-March-1993
36
37 PRIOR APPLICATION DATA:
38 APPLICATION NUMBER: 9311047.6
39 FILING DATE: 28-May-1993
40
41 PRIOR APPLICATION DATA:
42 APPLICATION NUMBER: 9313763.6
43 FILING DATE: 2-July-1993
44
45 PRIOR APPLICATION DATA:
46 APPLICATION NUMBER: 9136099.2
47 FILING DATE: 3-August-1993
48
49 PRIOR APPLICATION DATA:
50 APPLICATION NUMBER: 9321344.5
51 FILING DATE: 15-October-1993
52
53 ATTORNEY/AGENT INFORMATION:
54 NAME: Kohlei, Vineet
55
56 REGISTRATION NUMBER: 37,003
57
58 REFERENCE/DOCKET NUMBER: LUD 5298
59
60 TELECOMMUNICATION INFORMATION:
61 TELEPHONE: (212) 688-9200
62
63 TELEFAX: (212) 838-3884
64
65 INFORMATION FOR SEQ ID NO: 13:
66
67 SEQUENCE CHARACTERISTICS:
68 LENGTH: 2070 base pairs
69 TYPE: nucleic acid
70 STRANDEDNESS: unknown
71
72 TOPOLOGY: linear
73
74 MOLECULE TYPE: cDNA
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76 HYPOTHETICAL: NO
77
78 ANTI-SENSE: NO
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80 FRAGMENT TYPE: internal
81
82 ORIGINAL SOURCE:
83 ORGANISM: Mouse
84
85 FEATURE:
86
87 NAME/KEY: CDS
88
89 LOCATION: 217..1812
90
91 US-09-679-187-13

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US-09-679-187-13
; Sequence 13, Application US/09679187

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	Best Local Similarity	94.1%	Pred. No. 0		
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Db	195	CAGGACCGTGGCAATCAGACAAATGACTCAGCTATACATTACATCAGATTA	CTCTGGAGC	254	
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Db 375 GGATACCTTTCCTTTTAAAGTCTATTGCTCAGGACACTGCGCCAGATGATGCTATTAA 434
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Db 735 CTTTGTGCTAAGCAATTAATGTAAGATATCTCAAGCAGGGGTCGTTTACAAACGCTGATTT 794
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Db 1575 TCAATTAACCATATTCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1634
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Db 1815 ACAATTTAAACAAATTTTGAAGGAGAAATTTAGACTGCAAGAAATTC-----ACCCGAGGAGG 1874
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Db 1875 GTGGGATTAGCTAGGATGCTGGCTTGGTTTCCAGACTCTCTCTCTACCATCTT 1933
Qy 1771 CACAGCTCTAACAGTAAACCTTTTCAGGACTCTGCGAATGC 1813
Db 1934 CACAGCTCTAACAGTAAACCTTTTCAGGACTCTGCGAATGC 1976

RESULT 9

US-08-462-467B-11

; Sequence 11, Application US/08462467B

; Patent No. 6210899

; GENERAL INFORMATION:

; APPLICANT: Rosenbaum, Jan S

; TITLE OF INVENTION: The Use of a BMP Protein Receptor

; TITLE OF INVENTION: Complex for Screening Bone Metabolism Actives and Cells

; TITLE OF INVENTION: Co-Transfected With a Type II BMP Receptor and a Type I

; TITLE OF INVENTION: BMP Receptor

; NUMBER OF SEQUENCES: 39

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The Procter & Gamble Company

; STREET: 11810 East Miami River Road

; CITY: Ross

; STATE: OH

; COUNTRY: USA

; ZIP: 45061

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/462,467B

; FILING DATE:

; CLASSIFICATION: 435

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;
; ATTORNEY/AGENT INFORMATION:
; NAME: Hersko, Bart S.
; REGISTRATION NUMBER: 32,572
; REFERENCE/DOCKET NUMBER: 5474R
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 627-0633
; TELEFAX: (513) 627-0260
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2402 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-462-467B-11

Query Match      86.8%; Score 1574.2; DB 3; Length 2402;
Best Local Similarity 94.2%; Pred. No. 0;
Matches 1669; Conservative 0; Mismatches 93; Indels 9; Gaps 3;

QY 51 GAATTGGACAATGACTCAGCTATACACTTACATCATGATTAATGGAGGCTGTCTGTTCAT 110
Db 1 GAATCAGACAATGACTCAGCTATACACTTACATCATGATTAATGGAGGCTGTCTGTTCAT 60

QY 111 CATTTCTCATGTTCAAGGCGAGAACTAGATAGTATGCTCCATGCTGCTGATGAATC 170
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QY 291 AACTAATGCCATTCGTTTGCATTTAGAAAGATGATCAGGAGAAACACGCTTAAC 350
Db 241 AACTAATGCCATTCGTTTGCATTTAGAAAGATGATCAGGAGAAACACACATTAAC 300

QY 351 TTCTGGGTGATGAAGTGAAGGCTCTGATTTTCAATGCAAGGATTCACCAAAAGCCCA 410
Db 301 TTCTGGGTGATGAAGTGAAGGCTCTGATTTTCAATGCAAGGATTCACCGAAAGCCCA 360

QY 411 GCTACGAGGACAATAGAAATTTGTCGACCAATTTGTGCAACCAATATTTGACGCTTAC 470
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QY 471 ACTGCCCTCTGCTGTTATAGGCCCATTTCTTATGATGCGACGCTCCGATGGCTGTGCT 530
Db 421 ACTGCCCTCTGCTGTTATAGGCCCATTTCTTATGATGCGACGCTCCGATGGCTGTGCT 480

QY 531 CATCTCTATGGCTGTCTGATTTGTCGCCATGATCGTCTTCCAGCTGCTTCTGTTACAA 590
Db 481 CATTTCCATGGCTGTCTGATTTGCTATGATCATCTTCCAGCTGCTTGTGCTATAA 540

QY 591 ACATTACTGTAAGAGATATCTCAAGCAGAGGTCGTTTAAACCGTGATCTGGAAACAGGATGA 650
Db 541 GCATTTATTGTAAGAGATATCTCAAGCAGAGGTCGTTTAAACCGTGATTTGGAACAGGATGA 600

QY 651 AGCATTTATTCAGTAGGAGATCACTGAAAGACCTGATTGACCACTCACAAGCTCTGG 710
Db 601 AGCATTTATTCAGTAGGAGATCACTGAAAGACCTGATTGACCACTCACAAGCTCTGG 660

QY 711 TAGTGGATCTGATTAACCTTTATTGTTTCCAGGAACTATTGCAAAACAGATTCAGATGGT 770
Db 661 GAGTGGATCTGATTAACCTTTATTGTTTCCAGGAACTATTGCAAAACAGATTCAGATGGT 720

QY 771 TCGCAGGTTGGTAAGGCGCGGTATGGAAGATGATGGATGGGTAATGGCGTGGTGAATA 830
Db 721 TCGCAGGTTGGTAAGGCGCGGTATGGAAGATGATGGATGGGTAATGGCGTGGTGAATA 780

QY 831 AGTGGCTGTCAAAGTATTTTTTACCACCTCAAGAACTAGCTGGTTTAGAGAAACAGAAAT 890
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Db 781 AGTGGCTGTCAAAGTATTTTTTACCACCTGAAGAACTAGCTGGTTTAGAGAAACAGAAAT 840
QY 891 CTACCAGACGGTGTAAATGCGGTCAATGAAATATATCTGTTTATATAGCTGCAGACATTA 950
Db 841 CTACCAGACGGTGTAAATGCGGTCAATGAAATATATCTGTTTATATAGCTGCAGACATTA 900
QY 951 AGGCACCGGTTCTTGGACTCAGCTGTATTTGATTTACTGATTTACCATGAGAAATGGATCTCT 1010
Db 901 AGGCACCTGGTTCTTGGACTCAGCTGTATTTGATTTACTGATTTACCATGAGAAATGGATCTCT 960
QY 1011 CTATGACTTCTGAAATGTCACCTCGACACAGAGCCCTACTCAAGTTAGCTATTTC 1070
Db 961 CTATGACTTCTGAAATGTCACCTCGACACAGAGCCCTACTCAAGTTAGCTATTTC 1020
QY 1071 TGCTGCTGTGCTGTGCTCCACCTCCACACAGAAATTTATGGCAGCGCAAGCAAGCCTGC 1130
Db 1021 TGCTGCTGTGCTGTGCTCCACCTCCACACAGAAATTTATGGTACCCAAAGGAAGCCTGC 1080
QY 1131 AATTGCTCATCGAGACCTGAAAGAGCAAAACATCTCTTATTAAGAAAAATGGTAGTTGCTG 1190
Db 1081 AATTGCTCATCGAGACCTGAAAGAGCAAAACATCTCTTATTAAGAAAAATGGAAGTTGCTG 1140
QY 1191 TATTGCTGACCTGGGCTAGCTGTTAAATTCACAGTGCACACAAATGAAGTTGACATACC 1250
Db 1141 TATTGCTGACCTGGGCTAGCTGTTAAATTCACAGTGCATCAAAATGAAGTTGACATACC 1200
QY 1251 CTTGAACACCAAGGTTGGCACCAGCGGTACATGCTCCAGAAAGTGCCTGGAGAGAGCCT 1310
Db 1201 CTTGAATACCAAGGTTGGCACCAGCGGTACATGCTCCAGAAAGTGCCTGGAGAGAGCCT 1260
QY 1311 GAGTAAAAACCAATTTCCAGCCCTACATCATGGCTGACATCTACAGCTTTGGTTGATCAT 1370
Db 1261 GAATAAAAACCAATTTCCAGCCCTACATCATGGCTGACATCTATAGCTTTGGTTGATCAT 1320
QY 1371 TTGGGAGATGCCCGTCTGCTGTTTACAGGAGGATCGTGGAGGAATATCAATTAACATA 1430
Db 1321 TTGGGAAATGGCTGCTGCTGTTTATTAAGGAGGAATCGTGGAGGAATATCAATTAACATA 1380
QY 1431 TTACAACATGCTGCTAGTGACCCCATCTTATGAAGACATGCGTGAAGTCTGTGTGAA 1490
Db 1381 TTACAACATGCTGCTAGTGACCCCATCTTATGAAGACATGCGTGAAGTCTGTGTGAA 1440
QY 1491 ACGTTTGGGCAATTCGTCTCTAAACCGCTGAAACAGTGAATGATGCTTTCGAGCCGTTT 1550
Db 1441 ACGTTTGGGCAATTCGTCTCTAAACCGCTGAAACAGCGATGAATGCTTTCGAGCAGTTT 1500
QY 1551 GAAGCTGATGTCAGAAATGCTGGGCCCAATAATCCAGCATCCAGACTCCAGACTTTTGAGAT 1610
Db 1501 GAAGCTAATGTCAGAAATGTTGGGCCCAATAATCCAGCTCCAGACTCCAGACTTTTGAGAT 1560
QY 1611 CAAGAAGACGCTCGCAAGATGTTGAATCCAGGATTAAGATTTTGAC----AAACAG 1666
Db 1561 CAAGAAGACCTTCGCAAAATGTTGAATCCAGGATGTAAGATTTTGACAAATTAACAA 1620
QY 1667 TTTTGAGAAAGAAATTTAGACTGCAAGAAATTC----ACCCGAGGAGGGTGGAGTTAGCA 1722
Db 1621 TTTTGAGGAGAAATTTAGACTGCAAGAAATTCCTTCAACCCAAAGGAATGGGTGGGATAGCA 1680
QY 1723 TGGACTAGGATGTCGGCTTGGTTTCCAGACTCTCTCTCTACCATCTTTCACAGGCTGCTA 1782
Db 1681 TGGAAATAGGATGTTGACTTTGGTTTCCAGACTCTCTCTCTCTA-CATCTTTCACAGGCTGCTA 1739
QY 1783 ACAGTAAACCTTTTCAGGACTCTGCAGAAATGC 1813
Db 1740 ACAGTAAACCTTACCGCACTCTACAGAAATC 1770
```

RESULT 10
US-08-158-735A-3
; Sequence 3, Application US/08158735A
; Patent No. 6248554
; GENERAL INFORMATION:

APPLICANT: COOK, JONATHAN S.
APPLICANT: CORREA, PAUL E.
APPLICANT: KOENIG, BETH B.
APPLICANT: ROSENBAUM, JAN S.
APPLICANT: TING, JERRY
TITLE OF INVENTION: DNA SEQUENCE CODING FOR A BMP RECEPTOR
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESS: THE PROCTER & GAMBLE COMPANY
STREET: 11810 EAST MIAMI RIVER ROAD
CITY: ROSS
STATE: OH
COUNTRY: USA
ZIP: 45061
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,735A
FILING DATE: 24-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CORSTANJE, BRAHM J.
REGISTRATION NUMBER: 34,804
REFERENCE/DOCKET NUMBER: 5088
TELECOMMUNICATION INFORMATION:
TELEPHONE: (513) 627-2858
TELEFAX: (513) 627-0260
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2402 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(11...1606)
US-08-158-735A-3

Query Match 86.8%; Score 1574.2; DB 3; Length 2402;

Best Local Similarity 94.2%; Pred. No. 0;

Matches 1669; Conservative 0; Mismatches 93; Indels 9; Gaps 3;

Qy	51	GAATTGACAAATGACTCAGCTATACACTTACATCAGATTACTGGAGCCCTGCTGTTTCAT	110
Db	1	GAATCAGACAATGACTCAGCTATACACTTACATCAGATTACTGGAGCCCTGCTGTTTCAT	60
Qy	111	CATTTCATGTTTCAAGGCGAGAATCTAGATAGTATGCTCCATGGTACTGGTATGAAATC	170
Db	61	CATTTCATGTTTCAAGGCGAGAATCTAGATAGTATGCTCCATGGTACTGGTATGAAATC	120
Qy	171	AGAGTGGACAGAGAAGCGGAAATAGAGTACGCTTACGACCAAGAGACACCTTACC	230
Db	121	AGACTTGGACAGAGAAGCGGAAATAGAGTACGCTTACGACCAAGAGATACCTTACC	180
Qy	231	TTTCTTAAATGCTATTGCTCAGACACTGCCAGATGAGCTTAAATACATGCTAT	290
Db	181	TTTCTTAAATGCTATTGCTCAGACACTGCCAGATGAGCTTAAATACATGCTAT	240
Qy	291	AACATAATGGCCATTTGCTTTGCCATTATAGAGAAGATGATCAGGAGAAACACCGTTAAC	350
Db	241	AACATAATGGCCATTTGCTTTGCCATTATAGAGAAGATGATCAGGAGAAACACCATTAAC	300
Qy	351	TTCTGGGTGATGAAGTATGAAGCTCTGATTTTCAATGAAGGATTTACAAAGCCCA	410
Db	301	TTCTGGGTGATGAAGTATGAAGCTCTGATTTTCAATGAAGGATTTACCCGAAAGCCCA	360
Qy	411	GCTACCGAGACAATAGAATGTTGTCGACCAATTTGTGCAACCAATATTTCAGGCTTAC	470
Db	361	GCTACCGAGACAATAGAATGTTGTCGACCAATTTGTGCAACCAATATTTCAGGCTTAC	420

Qy	471	ACTGCCCCCTGCTGTTATAGGCCCATCTTTTGATGGCAGCGTCGATGGCTGGCTGCT	530
Db	421	ACTGCCCCCTGCTGTTATAGGCCCATCTTTTGATGGCAGCGTCGATGGCTGGCTGCT	480
Qy	531	CATCTCTATGGCTGCTGTTATGTCGCCATGATGCTCTTCCAGCTGCTTCTGTTACAA	590
Db	481	CATTTCCATGGCTGCTGTTATGTCGCCATGATGCTCTTCCAGCTGCTTCTGTTACAA	540
Qy	591	ACATTACTGTAAAGAGTATCTCAAGCAGAGTCTGTTACAACCGTGACTTGGAAACAGGATGA	650
Db	541	GCATTATTGTAAGAGTATCTCAAGCAGAGTCTGTTACAACCGTGAATTTGGAACAGGATGA	600
Qy	651	AGCATTATTCCAGTAGGAGATCACTGAAAGACCTGATTGACCACTCACAAGCTCTGG	710
Db	601	AGCATTATTCCAGTAGGAGATCACTGAAAGACCTGATTGACCACTCACAAGCTCTGG	660
Qy	711	TAGTGGATCTGGATTACCTTTTATGTTTACGCCAACTATTTGCCAAACAGATTTCAGATGGT	770
Db	661	GAGTGGATCTGGATTGCTTTTATGTTTACGCCAACTATTTGCCAAACAGATTTCAGATGGT	720
Qy	771	TCGGCAGGTTGGTAAAGGCGGTATGGAGAAGTATGGATGGGTAAATGGCGTGGTGA	830
Db	721	TCGGCAGGTTGGTAAAGGCGGTATGGAGAAGTATGGATGGGTAAATGGCGTGGTGA	780
Qy	831	AGTGGCTGTCAAAAGTATTTTTTACCACTGAAGAGCTAGCTGGTTTTAGAGAAACAGAAAT	890
Db	781	AGTGGCTGTCAAAAGTATTTTTTACCACTGAAGAGCTAGCTGGTTTTAGAGAAACAGAAAT	840
Qy	891	CTACCAAGCGTGTAAATGCGTCATGAAAATATACCTTGGTTTTATAGTCTCAGACATTAA	950
Db	841	CTACCAAGCGTGTAAATGCGTCATGAAAATATACCTTGGTTTTATAGTCTCAGACATTAA	900
Qy	951	AGGACCGGTTCTGCGACTCAGCTGATTTGATTACTGATACCATGAGATCGGCTCT	1010
Db	901	AGGACCGGTTCTGCGACTCAGCTGATTTGATTACTGATACCATGAGATCGGCTCT	960
Qy	1011	CTATGACTTCTGAAATGTGCCACCTGGACACACAGAGCCCTACTCAAGTTAGCTTATTC	1070
Db	961	CTATGACTTCTGAAATGTGCCACCTAGACACACAGAGCCCTACTCAAGTTAGCTTATTC	1020
Qy	1071	TGCTGCTGCTGCTGTCACCTCCACACAGAAATTTATGGCAGCAAGGCAAGCCTGC	1130
Db	1021	TGCTGCTGCTGCTGTCACCTCCACACAGAAATTTATGGTACCAGGGAAGCCTGC	1080
Qy	1131	AATTGCTCATCAGACCTGAAGAGCAAAACATCTTTATTAAGAAAATAGTATGCTG	1190
Db	1081	AATTGCTCATCAGACCTGAAGAGCAAAACATCTTTATTAAGAAAATAGTATGCTG	1140
Qy	1191	TATTGCTGACCTGGGCTAGCTGTTAAATTTCAACAGTGACACAAATGAAAGTTGACATACC	1250
Db	1141	TATTGCTGACCTGGGCTAGCTGTTAAATTTCAACAGTGATACAAATGAAAGTTGACATACC	1200
Qy	1251	CTTGAAACACAGGGTGGGCAACAGGCGGTACATGGCTCAGAAAGTCTCGACAGAGCCT	1310
Db	1201	CTTGAATACAGGGTGGGCAACAGGCGGTACATGGCTCAGAAAGTCTCGATGAAAGCCT	1260
Qy	1311	GAGTAAAACCAATTTCCAGCCCTACATCATGCTGACATCTACAGCTTTGGTTGATCAT	1370
Db	1261	GAATAAAACCAATTTCCAGCCCTACATCATGCTGACATCTATAGCTTTGGTTGATCAT	1320
Qy	1371	TTGGGAGATGGCCGCTGCTGATTATACAGGAGAAATCGTGGAGGAATATCAATTACCATTA	1430
Db	1321	TTGGGAAATGGCTGCTGTTGATTATACAGGAGAAATCGTGGAGGAATATCAATTACCATTA	1380
Qy	1431	TTACCAACATGGTCCCTAGTGACCCCATCTTTATGAAGACATCGCTGAGGTGCTGTGTGAA	1490
Db	1381	TTACCAACATGGTCCCTAGTGACCCCATCTTTATGAAGACATCGCTGAGGTGCTGTGTGAA	1440
Qy	1491	ACGCTTGGGGCAATCGTCTCTAAACCGCTGGAAACAGTGAATGATGCTTTCGAGCCGTTTT	1550
Db	1441	ACGCTTGGGGCAATCGTCTCTAAACCGCTGGAAACAGTGAATGATGCTTTCGAGCCGTTTT	1500
Qy	1551	GAAGCTGATGTGAGAATGCTGGGCCCAATAATCCAGCATCCAGACTCAGAGCTTTTGAGAAAT	1610

Db 1501 GAAGCTAATGTGCAAGTGTGGCCCATATCCAGCCTCGAGCTCAGACTCAGAGCTTTGAGAA 1560
QY 1611 CAAGAAGACGCTCGCAAGATGGTTGAATCCCAAGATGTAAGAATTTGAC-----AAACAG 1666
Db 1561 CAAGAAGACACTTTGCAAAATGGTTGAATCCCAAGATGTAAGAATTTGACAAATTAACAA 1620
QY 1667 TTTTGAAGAAGATTTAGACTGCAAGAAATTC-----ACCGAGGAAGGTTGGAGTTAGCA 1722
Db 1621 TTTTGAAGGAGAAATTTAGACTGCAAGAAATTCCTTCACCAAGGAATGGGTGGGATTTAGCA 1680
QY 1723 TGGACTAGGATGTCGGCTTGGTTTCAGACTCTCTCTCTACCATCTTCACAGGCTGCTA 1782
Db 1681 TGAATAGAGATGTTGACTTGGTTTCAGACTCTCTCTCTCTA-CATCTTCACAGGCTGCTA 1739
QY 1783 ACAGTAAACCTTTCAGGACTCTGCAAGATGC 1813
Db 1740 ACAGTAAACCTTACCACACTCTACAGAAATAC 1770

RESULT 11

US-08-334-179A-11
; Sequence 11, Application US/08334179A
; Patent No. 6306622
; GENERAL INFORMATION:
; APPLICANT: ROSENBAUM, JAN S.
; APPLICANT: NOHNO, TSUTOMU
; TITLE OF INVENTION: CDNA ENCODING A BMP TYPE II RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE PROCTER AND GAMBLE COMPANY
; STREET: 11810 EAST MIAMI RIVER ROAD
; CITY: ROSS
; STATE: OH
; COUNTRY: US
; ZIP: 45061
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.30, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/334,179A
; FILING DATE: 04-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CORSTANJE, BRAHM J.
; REGISTRATION NUMBER: 34,804
; REFERENCE/DOCKET NUMBER: 5473
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 513-627-2858
; TELEFAX: 513-627-0260
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2402 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(11..1606)
US-08-334-179A-11

Query Match 86.8%; Score 1574.2; DB 3; Length 2402;
Best Local Similarity 94.2%; Pred. No. 0;
Matches 1669; Conservative 0; Mismatches 93; Indels 9; Gaps 3;
QY 51 GAATGGACAATGACTCAGCTATACACTTACATTCAGATTACTGGGAGCCTGTCGTTCAT 110
Db 1 GAATCAGACAATGACTCAGCTATACACTTACATTCAGATTACTGGGAGCCTGTCGTTCAT 60
QY 111 CATTTCTCATGTTCAAGGGCAGAAATCTAGATAGTCTCCATGGTACTGGTATGAAATC 170

Db 61 CATTTCTCATGTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGGCACTGGTATGAAATC 120
QY 171 AGACGTGGACCAAGAAAGACCGGAAATGGAGTACGTTAGCACCAAGAGACACCTTACC 230
Db 121 AGACTTGGACCAAGAAAGACCGGAAATGGAGTACGTTAGCACCAAGAGATACCTTGCC 180
QY 231 TTTCTTAAATGCTATTGCTCAGGACACTGCCAGATGATGCTATTAATAACACATGCAT 290
Db 181 TTTCTTAAAGTCTATTGCTCAGGACACTGCCAGATGATGCTATTAATAACACATGCAT 240
QY 291 AACTAATGSCCATTCCTTTGCCATTATAGAAAGATGATCAGGAGAAACACCGTTAAC 350
Db 241 AACTAATGSCCATTCCTTTGCCATTATAGAAAGATGATCAGGAGAAACACCATTAAC 300
QY 351 TTTCTGGGTGATGAAAGGCTCTGATTTTCAATGCAAGGATTTCAACAAAAGCCCA 410
Db 301 TTTCTGGGTGATGAAAGGCTCTGATTTTCAATGCAAGGATTTCAACAAAAGCCCA 360
QY 411 GCTACGAGGACAATAGAAATGTTGCGACCAAATTTGTGCAACCAATATTTGAGGCTTAC 470
Db 361 GCTACGAGGACAATAGAAATGTTGCGACCAAATTTGTGCAACCAAGTATTTGAGGCTTAC 420
QY 471 ACTGCCCCCTGTCGTTATAGGCCCAATCTTTGATGCGACGCTCCGATGGCTGCTGCT 530
Db 421 ACTGCCCCCTGTCGTTATAGGTCCTTTTGTATGGCAGCATCCGATGGCTGCTGCTGCT 480
QY 531 CATCTCTATGGCTGCTGTTATTTGTCGCCATGATCGCTCTTCTCCAGCTGCTTCTGTACAA 590
Db 481 CATTTCCATGGCTGCTGTTATAGTTGCTATGATCATCTTCTCCAGCTGCTTTTGTATAA 540
QY 591 ACATTACTGTAAGAGTATCTCAAGCAGAGGCTGTTACAAACCGTACTTGGAAACAGATGA 650
Db 541 GCATTAATGTAAGAGTATCTCAAGCAGAGGCTGTTACAAACCGTACTTGGAAACAGATGA 600
QY 651 AGCATTTATTCAGTAGGAGATCACTGAAGACCTGATTGACCACTCACAAGCTCTCG 710
Db 601 AGCATTTATTCAGTAGGAGATCACTGAAGACCTGATTGACCACTCACAAGCTCTCG 660
QY 711 TAGTGGATCTGGATTACCTTTTATGGTTTCAGGAACTATTTGCCAAACAGATTCAGATGT 770
Db 661 GAGTGGATCTGGATTGCTTTTATGGTTTCAGGAACTATTTGCCAAACAGATTCAGATGT 720
QY 771 TCGGACGTTGGTAAAGGCGGATGAGAGAGTATGGATGGGTAAATGCGCTGGTGAAA 830
Db 721 TCGGACGTTGGTAAAGGCGGATGAGAGAGTATGGATGGGTAAATGCGCTGGTGAAA 780
QY 831 AGTGGCTGCTCAAAGTATTTTACCACCTGAAGAGCTAGCTGCTTTAGAGAAACAGAAAT 890
Db 781 AGTGGCTGCTCAAAGTATTTTACCACCTGAAGAGCTAGCTGCTTTAGAGAAACAGAAAT 840
QY 891 CTACGACGCGTGTAAATGCGCTCATGAAAATATATCTTGGTTTATAGCTGCAGACATTAA 950
Db 841 CTACGACGCGTGTAAATGCGCTCATGAAAATATATCTTGGTTTATAGCTGCAGACATTAA 900
QY 951 AGGCACCGGTTCTCGGACTCAGCTCTATTTGATTACTGATTAACATGAGATGGGTCTCT 1010
Db 901 AGGCACCTGGTTCTCGGACTCAGCTCTATTTGATTACTGATTAACATGAGATGGATCTCT 960
QY 1011 CTATGACTTCTCGGAAATGTCACCTCGACACCAAGCCCTACTCAAGTTAGCTTATTC 1070
Db 961 CTATGACTTCTCGGAAATGTCACCTCGACACCAAGCCCTACTCAAGTTAGCTTATTC 1020
QY 1071 TGCTGCCTGCTGTGTCGCCACTCCACACAGAAAATTTATGGCAGCGCAAGCAAGCCTGC 1130
Db 1021 TGCTGCTTGTGCTGTGTCGCCACTCCACACAGAAAATTTATGGTACCCCAAGGAGCCTGC 1080
QY 1131 AATTGCTCATCGAGACCTGAAGAGCAAAAATTCCTTATTAAGAAAAATGGTATGTTGCTG 1190
Db 1081 AATTGCTCATCGAGACCTGAAGAGCAAAAATTCCTTATTAAGAAAAATGGTATGTTGCTG 1140
QY 1191 TATTGCTCACCTGGGCTAGCTGTTTAAATTTCAACAGTGCACAAAATGAAGTTGACATACC 1250

Db 1141 TATTGCTGACCTGGGCGCTAGCTGTTTAAATTCACAGTGATACAAATGAAGTTGACATACC 1200
QY 1251 CTTGAACACCGAGGTGGGCACACGCGGTACATGCTCCAGAAAGTGTGGACGAGAGCCT 1310
Db 1201 CTTGNAATACCGAGGTGGGCACACGCGGTACATGCTCCAGAAAGTGTGGATGAAGCCT 1260
QY 1311 GAGTAAACCAATTTCCAGCCCTACATCATCGCTGACATCTATAGCTTTGGTTTGATCAT 1370
Db 1261 GAATAAACAACCAATTTCCAGCCCTACATCATCGCTGACATCTATAGCTTTGGTTTGATCAT 1320
QY 1371 TTGGGAGATGCGCGTCTGCTATTTACAGGAGGAATCGTGAGGAATATCAATTACCATA 1430
Db 1321 TTGGGAATGCTCGTCTGCTATTTACAGGAGGAATCGTGAGGAATATCAATTACCATA 1380
QY 1431 TTCAACAATGCTGCTAGTGACCCCATCTTATGAAGACATGCTGAGGTGCTGTGTGAA 1490
Db 1381 TTCAACAATGCTGCTAGTGACCCCATCTTATGAAGACATGCTGAGGTGCTGTGTGAA 1440
QY 1491 ACGTTTGGCGCAATCGTCTTAAACCGCTGGAACAGTGATGAATGTCTTCGAGCGGTTTT 1550
Db 1441 ACGTTTGGCGCAATCGTCTTAAACCGCTGGAACAGTGATGAATGTCTTCGAGCGGTTTT 1500
QY 1551 GAAGCTGATGTCAGAAATGCTGGGCGCCATAATCCAGATCCAGACTCACAGCTTTGAGAAT 1610
Db 1501 GAAGCTAATGTCAGAAATGCTGGGCGCCATAATCCAGATCCAGACTCACAGCTTTGAGAAT 1560
QY 1611 CAAGAAGACGCTCGCAAGATGTTGAATCCAGAGTGTAAGATTTTGAC- - - - AAACAG 1666
Db 1561 CAAGAAGACGCTCGCAAGATGTTGAATCCAGAGTGTAAGATTTTGACAAATTAACAA 1620
QY 1667 TTTTGAGAGAAATTTAGACTGCAAGAAATTC- - - - ACCCGAGGAAGGTGGAGTTAGCA 1722
Db 1621 TTTTGAGGAGAAATTTAGACTGCAAGAAATTC- - - - ACCCGAGGAAGGTGGAGTTAGCA 1680
QY 1723 TGGACTAGGATGTCGGTGTGTTTCCAGACTCTCTCTTACCATCTTCCAGGCTGCTA 1782
Db 1681 TGGAAATAGGATGTTGACTTGGTGTTCAGACTCTCTCTTACCATCTTCCAGGCTGCTA 1739
QY 1783 ACAGTAAACCTTCCAGGACTCTGAGAAATGC 1813
Db 1740 ACAGTAAACCTTCCAGGACTCTGAGAAATGC 1770

RESULT 12

US-08-158-735A-1
; Sequence 1, Application US/08158735A
; Patent No. 6248554
; GENERAL INFORMATION:
; APPLICANT: COOK, JONATHAN S.
; APPLICANT: CORREA, PAUL E.
; APPLICANT: KOENIG, BETH B.
; APPLICANT: ROSENBAUM, JAN S.
; APPLICANT: TING, JERRY
; TITLE OF INVENTION: DNA SEQUENCE CODING FOR A BMP RECEPTOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE PROCTER & GAMBLE COMPANY
; STREET: 11810 EAST MIAMI RIVER ROAD
; CITY: ROSS
; STATE: OH
; COUNTRY: USA
; ZIP: 45061
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/158,735A
; FILING DATE: 24-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CORSTANJE, BRAHM J.

; REGISTRATION NUMBER: 34,804
; REFERENCE/DOCKET NUMBER: 5088
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 627-2858
; TELEFAX: (513) 627-0260
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2056 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(291..1790)
; US-08-158-735A-1

Query Match 78.6%; Score 1424.4; DB 3; Length 2056;
Best Local Similarity 90.3%; Pred. No. 0;
Matches 1584; Conservative 0; Mismatches 76; Indels 94; Gaps 2;
QY 39 CAGGACACGTCGCAATTTGGACAAATGACTCAGCTATACACTTACATCAGATTACTCTGGGAGC 98
Db 269 CAGGACGCTGCGAAATCAGCAATGACTCAGCTATACACTTACATCAGATTACTCTGGGAGC 328
QY 99 CTGCTGTTTCATCATTTCTCATGTTCAAGGGCAGAAATCTAGATAGTAGTATGCTCCATGTGAC 158
Db 329 CTGCTGTTTCATCATTTCTCATGTTCAAGGGCAGAAATCTAGATAGTAGTATGCTCCATGGCAC 388
QY 159 TGTATGAAATCAGACGTCGGAACAGAAAGACGCGGAAATGGAAGTGAAGTGAAGTGAAGTGAAG 218
Db 389 TGTATGAAATCAGACGTCGGAACAGAAAGACGCGGAAATGGAAGTGAAGTGAAGTGAAGTGAAG 448
QY 219 GGACACCTTACCTTCTTAAATGCTATTGCTCAGGACACTGCCAGATGACCTATTAA 278
Db 449 GGATACCTTGCCTTCTTAAAGTGTATTGCTCAGGACACTGCCAGATGATGCTATTAA 508
QY 279 TAACACATGATCAATTAATGGCCATTGCTTGGCAATTTAGAAAGAGATGATCAGGGAGA 338
Db 509 TAACACATGATCAATTAATGGCCATTGCTTGGCAATTTAGAAAGAGATGATCAGGGAGA 568
QY 339 AACACGTTAACTTCTGGGTGTATGAAGTATGAAGCTCTGATTTTCAATGCAAGGATTC 398
Db 569 AACCAATTAATCTTCTGGGTGTATGAAGTATGAAGCTCTGATTTTCAATGCAAGGATTC 628
QY 399 ACCAAAGCCCGACTACGACGACCAATAGAAATGCTTCCGACCAATTTGTCGAACCAATA 458
Db 629 ACCAAAGCCCGACTACGACGACCAATAGAAATGCTTCCGACCAATTTGTCGAACCAATA 688
QY 459 TTTGACGCTTACACTGCCCTTGTCTGTTATAGGCCATTTCTTTGATGGCAGCGTCCGATG 518
Db 689 TTTGACGCTTACACTGCCCTTGTCTGTTATAGGTCCGTTCTTTGATGGCAGCATCCGATG 748
QY 519 GTGGCTGTGCTCATCTCTATGGCTGTCTGTATGTCGCCATGATCGTCTTCTCCAGCTG 578
Db 749 GTGGTGTGCTCATTTCCATTCCTGCTGTATGTTGCTATGATCATCTTCTCTCCAGCTG 808
QY 579 CTTCTGTTACAAACATTAAGTATCTCAAGCAGAGTCTGTTACCAACCGTCACTT 638
Db 809 CTTTGTCTAAGCATTTATTGTAAGAGTATCTCAAGCGGGTCTGTTTACCAACCGTCACTT 868
QY 639 GGAACAGGATGAAGCATTTATTTCAGTAGGAGATCACTGAAAGACTGATGATGACCAATC 698
Db 869 GGAACAGGATGAAGCATTTATTTCAGTAGGAGATCACTGAAAGACTGATGATGACCAATC 928
QY 699 ACAAGCTCTGTTAGTGGATCTGGATTAACCTTTATTTGGTTTACGCGAACTATTGCGCAACA 758
Db 929 CCAAGCTCTGGGAGTGGATCTGGATTTGCTTTTATTTGGTTTACGCGAACTATTGCGCAACA 988
QY 759 GATTGATGTTTCCGACGTTGGTAAAGGCGGTATGGAAGTATGATGATGATGATGATGATGATGATG 818
Db 989 GATTGATGTTTCCGACGTTGGTAAAGGCGGTATGGAAGTATGATGATGATGATGATGATGATGATG 1048
QY 819 GCGTGTGAAAAAAGTGGCTGTCAAAGTATTTTTTACCACCTGAAAGAGCTAGCTGGTGTAG 878

Db 1049 GCGTGGTGAAGAGTGGCTGCTCAAGTGTCTTTTACCACCTGAAGAAGCTAGCTGGTTTAG 1108
QY 879 AGAAACAGAAATCTACAGACGGTGTAAATGCTCATGAAATATATCTTGGTTTTATAGC 938
Db 1109 AGAAACAGAAATCTACAGACGGTGTAAATGCTCATGAAATATATCTTGGTTTTATAGC 1168
QY 939 TGCAGACATTAAGGACCGGTTCTTGGACTGAGCTGTATTGATTACTGATTACCATGA 998
Db 1169 TGCAGACATTAAGGACCGGTTCTTGGACTGAGCTGTATTGATTACTGATTACCATGA 1228
QY 999 GAATGGGTCTCTCTATGACTTCTGAAATGTGCACCCCTGGACACAGAGCCCTACTCAA 1058
Db 1229 AATGGATCTCTATGACTTCTGAAATGTGCACCACTAGACACAGAGCCCTACTCAA 1288
QY 1059 GTTAGCTTATTCCTGCTGCTGTGGTCTGTGCCACCTCCACAGAAATTTATGGCAGCA 1118
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QY 1179 TGGTAGTTGCTGTATTGCTGACCTGGCGCTAGCTGTTAAATTCACAGTGACACAATGA 1238
Db 1409 TGGAAAGTTGCTGTATTGCTGACCTGGCGCTAGCTGTTAAATTCACAGTGACACAATGA 1468
QY 1239 AGTTGACATACCTTTGAACACAGGCTGGGACACCGCGGTACATGGCTCCAGAAAGTGT 1298
Db 1469 AGTTGACATACCTTTGAATACAGGCTGGGACCAAGCGGTACATGGCTCCAGAAAGTGT 1528
QY 1299 GGACGAGAGCCTGAGTAAACCAATTTCCAGCCCTACATCATGGCTGACATCTACAGCTT 1358
Db 1529 GGATGAAGCCTGAATTAACCAATTTCCAGCCCTACATCATGGCTGACATCTACAGCTT 1588
QY 1359 TGGTTTGATCATTTGGAGATGCGCGTCTGCTATTACAGAGGAATCGTGAGGAATA 1418
Db 1589 TGGTTTGATCATTTGGGAATGCGCTGCTGTTGTTATACAGAGGAATCGTGAGGAATA 1648
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QY 1479 CGTGTGTGAAACGCTTGGGCAATCGTCTTACCCGCTGGAACAGTGATGA 1533
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Db 1769 TTGGAGCAAGTCCCTGTAAAGTGATGAGTGAGTGGCGGAGTTACTCTGTGCTCACCAC 1828
QY 1534 -----TGTCTTCGAGCCGTTTTGAAGCTGATGTCAAGATG 1568
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Db 1889 TTGGGCCCCAATATCCAGCCCTCCAGACTCAAGCTTTGAGAAATCAAGAAACACCTTGCAAA 1948
QY 1629 GATGGTTGAATCCAGGATGAAGATTTTGAC ---AAACAGTTTTTGAGAAAGATTTTAG 1684
Db 1949 AATGGTTGAATCCAGATGTAAGATTTTGACAAATTTTGAAGGAGATTTTAG 2008
QY 1685 ACTGCAAGAAATTC 1698
Db 2009 ACTGCAAGAAATTC 2022

RESULT 13
US-08-481-337A-5
; Sequence 5, Application US/08481337A
; Patent No. 5863738
; GENERAL INFORMATION:

APPLICANT: TEN DIJKE, Peter
APPLICANT: HELDIN, Carl-Henrik
APPLICANT: MIYAZONO, Kohel
APPLICANT: SAMPATH, Kuber T.
TITLE OF INVENTION: Morphogenic Protein-Specific Cell
TITLE OF INVENTION: Surface Receptors and Uses Therefor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,337A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, Thomas C.
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: CRP-097CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2932 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 310..1905
OTHER INFORMATION: /product= "Human ALK3"
US-08-481-337A-5

Query Match 76.5%; Score 1387; DB 2; Length 2932;
Best Local Similarity 87.8%; Pred. No. 0;
Matches 1561; Conservative 0; Mismatches 205; Indels 11; Gaps 4;
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Db 288 CAGGAACAATTAACAATTGAACAATGACTCAGCTATACATTTACATCAGATTTATTGGGAGC 347
QY 99 CTGTCTGTTTCATCAATTTCTCATGTTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGGTAC 158
Db 348 CTATTTGTTTCATCAATTTCTCGTGTTCAGGACAGAAATCTGGATAGTATGCTTTTCATGGCAC 407
QY 159 TGGTATGAATCAGACGTGGACCAAGAGCGGAAAAATGGAGTGACGTTAGCACCAGA 218
Db 408 TGGGATGAATCAGACTCCGACCAAGAAAAAGTCAGAAAAATGGAGTAACCTTAGCACCAGA 467
QY 219 GGACACCTTTACCTTTCTTAAATGTTGCTCAGGACACTGCCAGATGACGCTATTAA 278
Db 468 GGATACCTTTGCTTTTAAAGTGTATGCTCAGGGCACTGTCAGATGATGCTATTAA 527
QY 279 TAAACATGCATTAACCTTCTGGGTGATGAAGTATGAAGGCTCTGATTTTCAATGAAGATTTC 398
Db 528 TAAACATGCATTAACCTTCTGGGTGATGAAGTATGAAGGCTCTGATTTTCAATGAAGATTTC 647
QY 339 AACACAGTTAACTTCTGGGTGATGAAGTATGAAGGCTCTGATTTTCAATGAAGATTTC 398
Db 588 AACACAGTTAACTTCTGGGTGATGAAGTATGAAGGCTCTGATTTTCAATGAAGATTTC 647
QY 399 ACCAAAGCCAGCTACGAGCAATAGAATGTTGTCGAGCAATTTTGTGCAACCAATA 458

Db 648 TCCAAAAGCCAGCTACGCCGGAACAATAGAAATGTTGTCGACCAAAATTTATGTAACCAAGTA 707
Qy 459 TTTGCAGCTACACTGCCCTGTCGTTATAGGCCCAATCTCTTGATGCGAGCGTCGATG 518
Db 708 TTTGCAACCACTGCGCCCTGTTGTCATAGGTCGCTTTTGTATGGCAGCATTCGATG 767
Qy 519 GCTGGCTGTCTCATCTCTATGCGTGTCTGTATTTGTCGCCATGATCTCTTCTCCAGCTG 578
Db 768 GCTGGTTTGTCTATTTCTATGGCTGTCTGCATAATTTGCTATGATCATCTTCTCCAGCTG 827
Qy 579 CTCTCTGTATACAACTTACTGTAAGATATCTCAAGCAGAGCTGTTTACAACTGATCTT 638
Db 828 CTCTTGTATACAACTTATGCAAGAGCATCTCAAGCAGAGCTGTTTACAACTGATCTT 887
Qy 639 GGAACAGGATGAAGCATTTATTCAGTAGGAGATCACTCAAGACCTGATTGACAGATC 698
Db 888 GGAACAGGATGAAGCATTTATTCAGTTGGAGATCACTAAAGACCTTATTGACCAATC 947
Qy 699 ACAAGCTCTGGTAGTGATCTCGAATTTACCTTTATGTTTACGCGAATCTATTCGCAACA 758
Db 948 ACAAGTTCTGGTAGTGGCTGTGACTACTTTTATTTGTTTACGCGAATCTATTCGCAACA 1007
Qy 759 GATTCAGATGGTTCGGCAGGTTGGTAGGCGCGGTATGGAGAGATGATGGTGAATG 818
Db 1008 GATTCAGATGGTTCGGCAGGTTGGTAGGCGCGGTATGGAGAGATGATGGTGAATG 1067
Qy 819 GCGTGGTGAAGAGTGGCTGTCAAGTATTTTACCACCTGAAGAGCTAGCTGTTTACG 878
Db 1068 GCGTGGCAGAAAGTGGCGGTGAAGATTTCTTTACCACTGAAGAGCCAGCTGGTTTACG 1127
Qy 879 AGAAACAGAAATCTTACCAGACGGTGTGTTAATGCGTCAATGAAATATATCTGTTTATAGC 938
Db 1128 AGAAACAGAAATCTTACCAGACGGTGTGTTAATGCGCCTGAAATATCTGTTTATAGC 1187
Qy 939 TGCAAGATTAAGGACCGGTTCTCGGACTAGCTGATTTGATTTACTGATTTACCATGA 998
Db 1188 GGCAGACATTAAGGATACAGGTTCTGGACTAGCTCTATTTGATTTACTGATTTACCATGA 1247
Qy 999 GAATGGTCTCTCTATGACTTCTGAAATGTGCGCCCTGACACAGGAGCCCTACTCAA 1058
Db 1248 AATGATCTCTCTATGACTTCTGAAATGTGCTACACTGGACAGAGCCCTGCTTAA 1307
Qy 1059 GTTAGCTTATTTCTGCTGCTGTGCTGTGCTGCCACCTCCACACAGAAATTTATGGCAGCA 1118
Db 1308 ATTTGGCTTATTTAGCTGCTGTGCTGTGCTGCCACCTCCACACAGAAATTTATGGCAGCA 1367
Qy 1119 AGCAAGCTGCAATTTGCTCATCGAGACCTGGAAGAGCAAAAACATCTTATTAAGAAAAA 1178
Db 1368 AGGAAAGCCGCAATTTGCTCATCGAGACCTTAAAGAGCAAAAACATCTCATCAAGAAAAA 1427
Qy 1179 TGGTAGTTGCTGTATTTGCTGACCTGGGCTAGCTGTTAAATCAACAGTGACACAATGA 1238
Db 1428 TGGAGTTGCTGTATTTGCTGACCTGGGCTAGCTGTTAAATCAACAGTGACACAATGA 1487
Qy 1239 AGTTGATACATCCCTTGAACACAGGTTGGGCGCAGGCGGTACATGGCTCCAGAGTGT 1298
Db 1488 AGTTGATGCTTGTGAATACAGGTTGGGCGCAGGCGGTACATGGCTCCGAGTGT 1547
Qy 1299 GGAAGAGCTGAGTTAAACCAATTTCCAGCCCTACATGCTGCTGATCTTACAGCTT 1358
Db 1548 GGACGAAGCTTGAACCAAAACCACTTCCAGCCCTACATGCTGCTGATCTTACAGCTT 1607
Qy 1359 TGGTTTGTATTTGGAGATGCGGCTGCTGCTGTTATTCAGAGGAGTATGTTGGAGGAATA 1418
Db 1608 CGGCTTANTATTTGGAGATGCTGCTGCTGTTATTCAGAGGAGTATGTTGGAGGAATA 1667
Qy 1419 TCAATTAACCATATTACAACATGTTGCTGTAGTGACCCATCTTATGAAGACATGCTGAGGT 1478
Db 1668 CCAATTTGCCATATTACAACATGTTACCGAGTGTGCTCATACAGAGATATGCTGAGGT 1727
Qy 1479 CGTGTGTGAACGCTTGGGCGCAATGCTCTCTAAACCGCTGGAACAGTGATGATGCT 1538
Db 1728 TGTGTGTGTAACAGCTTTGGGCGCAATTTGTTCTAATCGTGTGAACAGTGATGATGCT 1787

Qy 1539 TCAGAGCGTTTGAAGCTGATGTGCAATGCTGGGCCCAATATCCAGCATCCAGACTCAC 1598
Db 1788 ACAGAGCAGTTTTGAAGCTATATGTGCAATGCTGGGCCCAATATCCAGCTCCAGACTCAC 1847
Qy 1599 AGCTTTGAGAATCAAGAAGACGCTCCCAAGATGTTGAATCCCAAGATGTAAGAATTTG 1658
Db 1848 AGCATTTGAGAAATTAAGAAGACGCTTCCCAAGATGTTGAATCCCAAGATGTAAGAATCTG 1907
Qy 1659 A-----CAACAGTTTTGAGAAGAAATTTAGACTGCAAGAA-----ATTCAACCCGAGGAAG 1709
Db 1908 ATGTTTAAACCAATCGGAGGAGAACTCTAGACTGCAAGAACTGTTTTTATCCCATGGCATG 1967
Qy 1710 GGTGGAGTTAGCATGACT-AGGATGTCGCTTGGTTTCCAGACTCTCTCTC- TACCA 1767
Db 1968 GGTGGAAATAGAGTGAATAGGATGTTAACTTGGTTCTCAGACTCTTCTTCTACTACGT 2027
Qy 1768 CTTACAGGCTGCTAACAGTAAACCTTTCCAGACTCT 1804
Db 2028 GTTACAGGCTGCTAATATTAACCTTTTCAGTACTCT 2064

RESULT 14

US-09-382-256-5
; Sequence 5, Application US/09382256A
; Patent No. 6207814
; GENERAL INFORMATION:
; APPLICANT: MIYAZONO, Kohei
; TEN DIJKE, Petra
; FRANZEN, Petra
; YAMASHITA, Hidetoshi
; HEUDIN, Carl-Henrik
; TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS
; HAVING SERINE THREONINE KINASE DOMAINS,
; AND THEIR USE
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/382,256A
; FILING DATE: 24-Aug-1999
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: No. 6207814ember 17, 1993
; APPLICATION NUMBER: GB 9224057.1
; FILING DATE: No. 6207814ember 17, 1992
; APPLICATION NUMBER: GB 9304677.9
; FILING DATE: March 8, 1993
; APPLICATION NUMBER: GB 9304680.3
; FILING DATE: March 8, 1993
; APPLICATION NUMBER: 9311047.6
; FILING DATE: May 28, 1993
; APPLICATION NUMBER: 9313763.6
; FILING DATE: July 2, 1993
; APPLICATION NUMBER: 9316099.2
; FILING DATE: August 3, 1993
; APPLICATION NUMBER: 321344.5
; FILING DATE: October 15, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6207814man D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5298.1

RESULT 15

US-09-395-115-5
; Sequence 5, Application US/09395115
; Patent No. 6271365
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohsei; Dijke, Peter Ten;
; APPLICANTS: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
; TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/395,115
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,265
; FILING DATE: 30-October-1995
; APPLICATION NUMBER: PCI/GB93/02367
; FILING DATE: 17-No. 6271365ember-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9224057.1
; FILING DATE: 17-No. 6271365ember-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304677.9
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304680.3
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9311047.6
; FILING DATE: 28-May-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9313763.6
; FILING DATE: 2-July-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9336099.2
; FILING DATE: 3-August-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9321344.5
; FILING DATE: 15-October-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohlei, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2932 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 310..1905

US-09-395-115-5

Query Match 76.5%; Score 1387; DB 3; Length 2932;
Best Local Similarity 87.8%; Pred. No. 0;
Matches 1561; Conservative 0; Mismatches 205; Indels 11; Gaps 4;
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Db 288 CAGGAAACATTACAATTGAACATGACTCAGCTATACATTTACATCAGATTATTGGGAGC 347
Qy 99 CTCTCTGTTTCATCATTTCTCATGTTCAAGGGCAGAATCTAGATAGTAGTATGCTCCATGTAC 158
Db 348 CTATTTGTTTCATCATTTCTCGTCTCAAGGACAGAATCTGGATAGTAGTCTTCATGGCAC 407
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Db 408 TGGGATGAAATCAGACTCCGACCCAGAAAAGTGAAGATGAGTAGTGAGTCAGCTTAGCACCA 467
Qy 219 GGACACCTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCAGATGACGCTATTAA 278
Db 468 GGATACCTTGGCTTTTAAAGTGCTATTGCTCAGGGCACTGTCCAGATGATGCTATTAA 527
Qy 279 TAACACATGCATAAATAATGGCCATTGCTTTGCCATTATAGAAAGAGATGATCAGGAGAG 338
Db 528 TAACACATGCATAAATAATGGCACTTTGCTTGCATCATAGAAAGAGATGATCAGGAGAG 587
Qy 339 AACCACGTTAACTTCTGGGGTATGAAGTATGAAGCTCTGATTTTCAATGCAAGGATTC 398
Db 588 AACCACATTAAGTTTCAAGGGTATGAAGTATGAAGTATGAAGTATGAAGTATGAAGTATGA 647
Qy 399 ACCAAAAGCCAGCTACGAGGAGCAATAGAATGCTTGGGACCAATTTTGGCAACCAATA 458
Db 648 TCCAAAAGCCAGCTACGAGGAGCAATAGAATGCTTGGGACCAATTTTGGCAACCAATA 707
Qy 459 TTTGAGCCTACACTGCCCCCTGTGCTTATAGGCCCATTTCTTTGATGGCAGCTCCGATG 518
Db 708 TTTGCAACCCACACTGCCCCCTGTGCTCATAGTCCGCTTTTGTGATGGCAGCATTCGATG 767
Qy 519 GCTGGCTGTCTCATCTCTATGGCTGTCTGTATTGTCGCCATGATGCTTCTTCCAGCTG 578
Db 768 GCTGGTTTGTCTCATTTCTATGGCTGTCTGCATTAATTGCTATGATCATCTTCTTCCAGCTG 827
Qy 579 CTTTCTGTTACAAACATTACTGTAAGAGATATCTCAAGCAGAGGTCGTTTACAACCGTGACTT 638
Db 828 CTTTGTGTACAAACATTATTGCAAGAGCATCTCAAGCAGAGCTGCTGTATACATCGTATTT 887
Qy 639 GGAAACAGGATGAAGCATTTATTTCAGTAGGAGATCACTGAAAGACCTGATGACCAAGTC 698
Db 888 GGAAACAGGATGAAGCATTTATTCCAGTTGGAGATCACTTAAAGACCTTTATTGACCCAGTC 947
Qy 699 ACAAGCTCTGCTAGTGGATCTGGATTACCTTTATTTGTTTACGCGAAGTATTTGCCAACA 758
Db 948 ACAAGTTTCTGCTAGTGGGTCCTGGACTACCTTTATTTGTTTACGCGAAGTATTTGCCAACA 1007
Qy 759 GATTTCAGATGTTTCGCGAGCTTGGTAAGGCGCGGTATGAGAGATGATGATGGTGGTAAATG 818
Db 1008 GATTTCAGATGTTTCGCGCAAGTTGGTAAGGCGCGATATGAGAGATGATGATGGGCAATG 1067
Qy 819 GCGTGGTGAAGAAAGTGGCTGTCAAAAGTATTTTTTACCAGTGAAGAGTACGTGGTTTAG 878
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Qy 879 AGAAAACAGAAATCTACGAGCGGTGTTAATGGCTCATGAAATATATCTTGGTTTATAGC 938
Db 1128 AGAAAACAGAAATCTACCAAACTGTGCTAATGGCCCATGAAAACATATCTTGGTTTATAGC 1187
Qy 939 TGCAGACATTAAAGGACCGGTTCTCGGACTCAGCTGATTTGATTACTGATTACCATCA 998
Db 1188 GGCAGACATTAAAGGTACAGGTTCTGGACTCAGCTCTATTTGATTACTGATTACCATGA 1247
Qy 999 GAATGGGTCTCTCTATGACTTCTCCGAAATGTCCACCCCTGGACACAGAGCCCTACTCAA 1058
Db 1248 AAATGGATCTCTCTATGACTTCTCCGAAATGTCTACACTGGACACAGAGCCCTGCTTAA 1307

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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14485.394 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1750.4	96.5	3003	9	US-10-868-497-90
5	1750.4	96.5	3167	6	US-10-463-190-119
6	1750.4	96.5	3167	6	US-10-463-190-120
7	1750.4	96.5	3167	9	US-10-868-497-88
8	1750.4	96.5	3167	9	US-10-868-497-89
9	1581.4	87.2	2070	3	US-09-903-068-13
10	1581.4	87.2	2070	9	US-10-739-413-13
11	1574.2	86.8	2402	3	US-09-742-153-11
12	1424.4	78.6	2056	7	US-10-641-319-3
13	1387	76.5	2932	3	US-09-903-068-5
14	1387	76.5	2932	3	US-09-982-543A-7
15	1387	76.5	2932	6	US-10-286-152A-37
16	1387	76.5	2932	6	US-10-463-190-116
17	1387	76.5	2932	9	US-10-739-413-5
18	1387	76.5	2932	9	US-10-868-497-85
19	1387	76.5	2932	9	US-10-492-380-37
20	1387	76.5	2932	9	US-10-450-763-22861
21	1387	76.5	2932	10	US-11-098-889-5
22	1374.6	75.8	2623	5	US-10-153-217-1
23	1343	74.1	1599	9	US-10-745-237-307

24	1258.8	69.4	2730	9	US-10-450-763-22868	Sequence 22868, A
25	1104	60.9	1743	8	US-10-128-558-48	Sequence 48, Appl
26	978.2	54.0	1185	6	US-10-029-386-20369	Sequence 20369, A
27	918	50.6	1929	8	US-10-128-558-49	Sequence 49, Appl
28	810.4	44.7	1695	9	US-10-450-763-22867	Sequence 22867, A
29	773.8	42.7	2659	8	US-10-487-556-21	Sequence 21, Appl
30	716	39.5	1952	3	US-09-903-068-17	Sequence 17, Appl
31	716	39.5	1952	3	US-09-982-543A-7	Sequence 7, Appl
32	716	39.5	1952	9	US-10-739-413-17	Sequence 17, Appl
33	716	39.5	1952	10	US-11-098-889-7	Sequence 7, Appl
34	707.6	39.0	1575	6	US-10-463-190-117	Sequence 117, App
35	707.6	39.0	1575	9	US-10-868-497-86	Sequence 86, Appl
36	707.6	39.0	2032	5	US-10-044-716-13	GENERAL INFORMATI
37	707.6	39.0	2032	6	US-10-286-152A-39	Sequence 39, Appl
38	707.6	39.0	2032	6	US-10-139-814-13	Sequence 13, Appl
39	707.6	39.0	2032	6	US-10-172-118-570	Sequence 570, App
40	707.6	39.0	2032	6	US-10-295-027-67	Sequence 67, Appl
41	707.6	39.0	2032	6	US-10-295-027-788	Sequence 788, App
42	707.6	39.0	2032	6	US-10-295-027-836	Sequence 836, App
43	707.6	39.0	2032	6	US-10-295-027-880	Sequence 880, App
44	707.6	39.0	2032	6	US-10-173-999-63	Sequence 63, Appl
45	707.6	39.0	2032	6	US-10-463-190-118	Sequence 118, App

ALIGNMENTS

RESULT 1
US-09-874-628-1
; Sequence 1, Application US/09874628
; Patent No. US2002013133A1
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; THIES, R. Scott
; YAMAJI, No. US2002013133A1oru
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute Inc.- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/874,628
; FILING DATE: 05-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,934
; FILING DATE: 17-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, Steven R
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 876 1170
; TELEFAX: 617 876 5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: CPK1-23a

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;
; NAME/KEY: CDS
; LOCATION: 61...1656
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-874-628-1

Query Match      100.0%; Score 1813; DB 3; Length 1813;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGTGGATCCCCCGGCTGCAGGAATTTCTGCGCGCCGAGGACACGTCGCAATTTGGACA 60
DB 1 CTAGTGGATCCCCCGGCTGCAGGAATTTCTGCGCGCCGAGGACACGTCGCAATTTGGACA 60

QY 61 ATGACTCAGCTATACACTTACATCAGATTAATCTGGGAGCGTGTCTGTTCAATTTCTCAT 120
DB 61 ATGACTCAGCTATACACTTACATCAGATTAATCTGGGAGCGTGTCTGTTCAATTTCTCAT 120

QY 121 GTTCAAGGCGAGAATCTAGATAGTATGCTCCATGCTGCTGGTATGAAATCAGCGTGGAC 180
DB 121 GTTCAAGGCGAGAATCTAGATAGTATGCTCCATGCTGCTGGTATGAAATCAGCGTGGAC 180

QY 181 CAGAAAGCCGAAAAATGGAGTACGTTAGCACGAGGACACCTTACCTTTTCTTAAAA 240
DB 181 CAGAAAGCCGAAAAATGGAGTACGTTAGCACGAGGACACCTTACCTTTTCTTAAAA 240

QY 241 TGCTATTGCTCAGGACACTGCCCGAGATGACGCTATTAATAACATGATTAATGGC 300
DB 241 TGCTATTGCTCAGGACACTGCCCGAGATGACGCTATTAATAACATGATTAATGGC 300

QY 301 CATTGCTTTGCCATTATAGAGAAGATGATCAGGGAGAGAACACAGTTAACTTCTGGGTG 360
DB 301 CATTGCTTTGCCATTATAGAGAAGATGATCAGGGAGAGAACACAGTTAACTTCTGGGTG 360

QY 361 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCAAAAGCCAGCTACGCAGG 420
DB 361 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCAAAAGCCAGCTACGCAGG 420

QY 421 ACAATAGAAATGTTGTCGACACCAATTTGTGCAACCAATATTTGCAAGCTTACACTG 480
DB 421 ACAATAGAAATGTTGTCGACACCAATTTGTGCAACCAATATTTGCAAGCTTACACTG 480

QY 481 GTGCTTATAGGCGCATCTTTGATGCGACGCTCCGATGCGTGGCTGCTCATCTCTATG 540
DB 481 GTGCTTATAGGCGCATCTTTGATGCGACGCTCCGATGCGTGGCTGCTCATCTCTATG 540

QY 541 GCTGCTGTATTGTCGCCATGATCGTCTTCCAGCTGCTTCTGTTACAAACATTTACTGT 600
DB 541 GCTGCTGTATTGTCGCCATGATCGTCTTCCAGCTGCTTCTGTTACAAACATTTACTGT 600

QY 601 AAGAGTATCTCAGCAGAGGCTGTTTACAAACCGTGATCTTGGAAACAGGATGAAGCATTTAT 660
DB 601 AAGAGTATCTCAGCAGAGGCTGTTTACAAACCGTGATCTTGGAAACAGGATGAAGCATTTAT 660

QY 661 CCAGTAGGAGAACTCACTGAAAGACCTGATTTGACACAGTACAAAGCTCTGGTAGTGGATCT 720
DB 661 CCAGTAGGAGAACTCACTGAAAGACCTGATTTGACACAGTACAAAGCTCTGGTAGTGGATCT 720

QY 721 GGATTTACCTTTATGGTTTCAGCGAACTATTGCAAAACAGATTTAGATGGTTTCGGCAGGTT 780
DB 721 GGATTTACCTTTATGGTTTCAGCGAACTATTGCAAAACAGATTTAGATGGTTTCGGCAGGTT 780

QY 781 GGTAAGGCGCGGTATGGAGAGATATGGATGGGTAAATGCGGTGGTGGAAAAAGTGGCTGTC 840
DB 781 GGTAAGGCGCGGTATGGAGAGATATGGATGGGTAAATGCGGTGGTGGAAAAAGTGGCTGTC 840

QY 841 AAAGTATTTTACCACCTGAGAACTAGCTGGTTTACAGAAACAGAAATCTACACAGC 900
DB 841 AAAGTATTTTACCACCTGAGAACTAGCTGGTTTACAGAAACAGAAATCTACACAGC 900

QY 901 GTGTTAATGCGCTCATGAAAAATATCTTGGTTTTATAGCTGCAGACATTTAAAGGCCACCGGT 960
DB 901 GTGTTAATGCGCTCATGAAAAATATCTTGGTTTTATAGCTGCAGACATTTAAAGGCCACCGGT 960
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QY 961 TCCTGGACTCAGCTGTATTGATTTACTGATTTACCATGAGAAATGGTCTCTCTATGACTTC 1020
DB 961 TCCTGGACTCAGCTGTATTGATTTACTGATTTACCATGAGAAATGGTCTCTCTATGACTTC 1020

QY 1021 CTGAAATGTGCCACCCCTGGACACAGAGCCCTACTCAAGTTAGCTTATTTCTGCTCCCTGT 1080
DB 1021 CTGAAATGTGCCACCCCTGGACACAGAGCCCTACTCAAGTTAGCTTATTTCTGCTCCCTGT 1080

QY 1081 GGTCTGTGCCACCTCCACACAGAAATTTATGGCAGCGCAAGCCCTGCAATTTGCTCAT 1140
DB 1081 GGTCTGTGCCACCTCCACACAGAAATTTATGGCAGCGCAAGCCCTGCAATTTGCTCAT 1140

QY 1141 CGAGACCTGAAGACGAAAAAATCATCTTTATTAAGAAAAATGGTAGTTGCTGATTTGCTGAC 1200
DB 1141 CGAGACCTGAAGACGAAAAAATCATCTTTATTAAGAAAAATGGTAGTTGCTGATTTGCTGAC 1200

QY 1201 CTGGGCTTAGCTGTTTAAATTCACACAGTGACACAAATGAAGTTGACATACCCCTTGAACACC 1260
DB 1201 CTGGGCTTAGCTGTTTAAATTCACACAGTGACACAAATGAAGTTGACATACCCCTTGAACACC 1260

QY 1261 AGGTGGGCACACGCGGTACATGGCTCCAGAAGTGTCTGGACGAGAGCTTGAGTAAAAAC 1320
DB 1261 AGGTGGGCACACGCGGTACATGGCTCCAGAAGTGTCTGGACGAGAGCTTGAGTAAAAAC 1320

QY 1321 CATTTCAGCCCTACATCATGCTGACATCTACAGCTTTTGGTTTGAATCATTTGGAGATG 1380
DB 1321 CATTTCAGCCCTACATCATGCTGACATCTACAGCTTTTGGTTTGAATCATTTGGAGATG 1380

QY 1381 GCCCGTCTGCTGTTTACAGGAGGAATCGTGAGGAATATCAATTAACCATTTACAAATG 1440
DB 1381 GCCCGTCTGCTGTTTACAGGAGGAATCGTGAGGAATATCAATTAACCATTTACAAATG 1440

QY 1441 GTGCTTAGTGACCATCTTATGAAGACATGCGTCAGGTCTGTGTGTGTAACCGTTTGGG 1500
DB 1441 GTGCTTAGTGACCATCTTATGAAGACATGCGTCAGGTCTGTGTGTGTAACCGTTTGGG 1500

QY 1501 CCAATGCTCTTAACCGCTGGAACAGTGTGAAATGCTTTCGAGCGGTTTTGAAGCTGATG 1560
DB 1501 CCAATGCTCTTAACCGCTGGAACAGTGTGAAATGCTTTCGAGCGGTTTTGAAGCTGATG 1560

QY 1561 TCAGAAATGCTGGGCCCCATAATCCAGCATCCAGACTCCAGCTTTGAGAAATCAAGAAAGC 1620
DB 1561 TCAGAAATGCTGGGCCCCATAATCCAGCATCCAGACTCCAGCTTTGAGAAATCAAGAAAGC 1620

QY 1621 CTCGAAAGATGGTTGAATCCAGGATGTAAGATTTGACAAACAGTTTTGAGAAAGAAAT 1680
DB 1621 CTCGAAAGATGGTTGAATCCAGGATGTAAGATTTGACAAACAGTTTTGAGAAAGAAAT 1680

QY 1681 TTAGACTGCAAGAAATTCACCCGAGGAAGGTGGAGTTAGCATGGACTAGGATGTCGGCT 1740
DB 1681 TTAGACTGCAAGAAATTCACCCGAGGAAGGTGGAGTTAGCATGGACTAGGATGTCGGCT 1740

QY 1741 TGGTTTCCAGACTCTCTCTCTACCATCTTCACAGGCTGCTAACAGTAAACCTTTTCAGGA 1800
DB 1741 TGGTTTCCAGACTCTCTCTCTACCATCTTCACAGGCTGCTAACAGTAAACCTTTTCAGGA 1800

QY 1801 CTCTGCAGAAATGC 1813
DB 1801 CTCTGCAGAAATGC 1813
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RESULT 2
US-10-600-645-1
; Sequence 1, Application US/10600645
; Publication No. US20040142417A1
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; CELESTE, Anthony J.
; THIES, R. Scott
; YAMAJI, Noboru
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19

Db	1432	GGAGGAATATCAATTAACCATATTACACATGGTGCCTAGTGACCCATCTTTATGAAGACAT	1491
Qy	1470	CGGTGAGTCTGTGTGTGAAACGCTTGCAGCCCAATCGTCTCTAAACCGCTGGACAGTGA	1529
Db	1492	CGGTGAGTCTGTGTGTGAAACGCTTGCAGCCCAATCGTCTCTAAACCGCTGGAAACAGTGA	1551
Qy	1530	TGAATGTCTTCGAGCCGCTTTTGAAGCTGTATGTCAGAAATGCTGGGCCCAATAATCCAGCATC	1589
Db	1552	TGAATGTCTTCGAGCCGCTTTTGAAGCTGTATGTCAGAAATGCTGGGCCCAATAATCCAGCATC	1611
Qy	1590	CAGACTCACAGCTTTGAGAAATCAAGAAGACGCTCGCAAGATGTTGAATCCCAAGGATGT	1649
Db	1612	CAGACTCACAGCTTTGAGAAATCAAGAAGACGCTCGCAAGATGTTGAATCCCAAGGATGT	1671
Qy	1650	AAAGATTGTCAAAACAGTTTTTGAGAAAGAAATTTAGACTGCAAGAAATTTCAACCCGAGGAAG	1709
Db	1672	AAAGATTGTCAAAACAGTTTTTGAGAAAGAAATTTAGACTGCAAGAAATTTCAACCCGAGGAAG	1731
Qy	1710	GGTGGAGTTAGCATGGACTAGGATGTCTGGCTTGGTTTTCCAGACTCTCTCTCTACCATCT	1769
Db	1732	GGTGGAGTTAGCATGGACTAGGATGTCTGGCTTGGTTTTCCAGACTCTCTCTCTCTA-CACT	1790
Qy	1770	TCACAGSCTGCTAAACAGTAACCTTTTCAGGACTCTGCAGAAATGC	1813
Db	1791	TCACAGSCTGCTAAACAGTAAA-CTTTTCAGGACTCTGCAGAAATGC	1833

RESULT 4
US-10-868-497-90
; Sequence 90, Application US/10868497
; Publication No. US20050106683A1
; GENERAL INFORMATION:
; APPLICANT: Winkler, David G.
; APPLICANT: Shi, Jiye
; APPLICANT: Lacham, John
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR SCLEROSTIN AND
; FILE REFERENCE: 60117-128
; CURRENT APPLICATION NUMBER: US/10/868,497
; CURRENT FILING DATE: 2004-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 3003
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-868-497-90

Query Match	96.5%	Score 1750.4	DB 9	Length 3003
Best Local Similarity	99.6%	Pred. No. 0		
Matches 1776	Conservative	0	Mismatches	6
			Indels	2
			Gaps	2

Qy	30	TGGCGCGCCGAGACAGCTGCGAATTTGGACAAATGACTCAGCTATACACTTACATCAGATT	89
Db	52	TGGCGCGGACAGGACAGCTGCGAATTTGGACAAATGACTCAGCTATACACTTACATCAGATT	111
Qy	90	ACTGGGAGCTGCTGTTTCATCATTTCTCATGTTCAAGGGCAGAAATCTAGATAGTATGCT	149
Db	112	ACTGGGAGCTGCTGTTTCATCATTTCTCATGTTCAAGGGCAGAAATCTAGATAGTATGCT	171
Qy	150	CCATGTTACTGGTATGAAATCAGACGTGGACACAGAGAGAGCCGGAATTTGGAGTGACGTT	209
Db	172	CCATGTTACTGGTATGAAATCAGACGTGGACACAGAGAGAGCCGGAATTTGGAGTGACGTT	231
Qy	210	AGCACCAGAGGACACCTTTACCTTTTAAATGCTATTGCTCAGGACACTGCGCCAGATGA	269
Db	232	AGCACCAGAGGACACCTTTACCTTTTAAATGCTATTGCTCAGGACACTGCGCCAGATGA	291
Qy	270	CGCTATTATAACACATGCATACTAATGGCCCATGCTTTGCCATTATAGAAGAAATGA	329
Db	292	CGCTATTATAACACATGCATACTAATGGCCCATGCTTTGCCATTATAGAAGAAATGA	351

Qy	330	TCAGGGAGAAAACCAACGTTAACTTTCTGGTGTATGAAGTATGAAGGCTCTGATTTTCAATG	389
Db	352	TCAGGGAGAAAACCAACGTTAACTTTCTGGTGTATGAAGTATGAAGGCTCTGATTTTCAATG	411
Qy	390	CAAGGATTCACAAAAGCCCCAGCTACGACGAGCAATAGAAATGTTGTCGGACCAATTTGTCG	449
Db	412	CAAGGATTCACAAAAGCCCCAGCTACGACGAGCAATAGAAATGTTGTCGGACCAATTTGTCG	471
Qy	450	CAACCAATATTTTCAGCCTACACTGCCCCCTGTGTTATAGGCCCATCTTTTGTATGTCGACG	509
Db	472	CAACCAATATTTTCAGCCTACACTGCCCCCTGTGTTATAGGCCCATCTTTTGTATGTCGACG	531
Qy	510	CGTCCGATGGCTGGCTGTCTCATCTATGCGCTGTCTGTATTTGTGCCCATGATCGCTT	569
Db	532	CGTCCGATGGCTGGCTGTCTCATCTATGCGCTGTCTGTATTTGTGCCCATGATCGCTT	591
Qy	570	CTCCAGCTGCTTCTGTTTACAAACATTTACTGTAAGAGTATCTCAAGCAGAGGTCGTTTACAA	629
Db	592	CTCCAGCTGCTTCTGTTTACAAACATTTACTGTAAGAGTATCTCAAGCAGAGGTCGTTTACAA	651
Qy	630	CCGTGACTTGGAAACAGGATGAAGCATTTTATTCAGTAGGAGAAATCACTGAAGACCTGAT	689
Db	652	CCGTGACTTGGAAACAGGATGAAGCATTTTATTCAGTAGGAGAAATCACTGAAGACCTGAT	711
Qy	690	TGACCAAGTCAACAAAGCTCTGGTAGTGGATCTGGATTACCTTTATTTGGTTTTCAGGCAAT	749
Db	712	TGACCAAGTCAACAAAGCTCTGGTAGTGGATCTGGATTACCTTTATTTGGTTTTCAGGCAAT	771
Qy	750	TGCCAAACAGATTCAGATGGTTTCGGCAGGTTGGTAAGGCCGGTATGGAGAAATGATGAT	809
Db	772	TGCCAAACAGATTCAGATGGTTTCGGCAGGTTGGTAAGGCCGGTATGGAGAAATGATGAT	831
Qy	810	GGGTAATGCGGTGGTGAAGAAAGTGGCTGTCAAAGTATTTTACCACCTCAAGAAAGCTAG	869
Db	832	GGGTAATGCGGTGGTGAAGAAAGTGGCTGTCAAAGTATTTTACCACCTCAAGAAAGCTAG	891
Qy	870	CTGGTTTAGAGAAAACAGAAATCTTACCAGACGGTGTAAATGCGTCATGAAATATACTTGS	929
Db	892	CTGGTTTAGAGAAAACAGAAATCTTACCAGACGGTGTAAATGCGTCATGAAATATACTTGS	951
Qy	930	TTTTATAGTGCAGACATTTAAAGGCCACCGGTTCTCGGACTCAGCTGTATTTGATTAATGTA	989
Db	952	TTTTATAGTGCAGACATTTAAAGGCCACCGGTTCTCGGACTCAGCTGTATTTGATTAATGTA	1011
Qy	990	TTACCATGAGAAATGGGTCTCTCTATGACTTCTCTGAAATGTGCCACCTGGACACACAGAGC	1049
Db	1012	TTACCATGAGAAATGGGTCTCTCTATGACTTCTCTGAAATGTGCCACCTGGACACACAGAGC	1071
Qy	1050	CCTACTCAAGTTAGCTTTATTTCTGCTGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG	1109
Db	1072	CCTACTCAAGTTAGCTTTATTTCTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1131
Qy	1110	TGGCAGCGAAGCAAGCCTGCAATTTGCTCATCGAGACCTGAAAGAGCAAAAACATCCTTAT	1169
Db	1132	TGGCAGCGAAGCAAGCCTGCAATTTGCTCATCGAGACCTGAAAGAGCAAAAACATCCTTAT	1191
Qy	1170	TAAAGAAAATGCTAGTGTGCTGTATTTGCTGACCTGGCCCTAGCTGTTAAATTTCAACAGTGA	1229
Db	1192	TAAAGAAAATGCTAGTGTGCTGTATTTGCTGACCTGGCCCTAGCTGTTAAATTTCAACAGTGA	1251
Qy	1230	CACAAATGAAGTTGACATACCTTTGAAACACAGGGTGGGCACCCAGCGGTACATGGCTCC	1289
Db	1252	CACAAATGAAGTTGACATACCTTTGAAACACAGGGTGGGCACCCAGCGGTACATGGCTCC	1311
Qy	1290	AGAAGTGTGGACGAGAGCCTGAGTAAACCAATTTTCCAGCCCTACATCATGGCTGACAT	1349
Db	1312	AGAAGTGTGGACGAGAGCCTGAGTAAACCAATTTTCCAGCCCTACATCATGGCTGACAT	1371
Qy	1350	CTACAGCTTTGGTTTGTATCATTTGGGAGATGGCCCGTCCCTGTATTTACAGGAGGAATCGT	1409
Db	1372	CTACAGCTTTGGTTTGTATCATTTGGGAGATGGCCCGTCCCTGTATTTACAGGAGGAATCGT	1431
Qy	1410	GGAGGAATATCAATTTACCATAATTACAAATGCTGCTAGTGACCCATCTTATGAAGACAT	1469

Db 1432 GGAGGAATATCAATTACCATATTTACAAATGGTGGCTAGTGACCCATCTTATGAAGACAT 1491
QY 1470 GCGTGAGGTCGTGTGTGTGAACCGTTGCGGCAATCGTCTTAACCGCTGGAACAGTGA 1529
Db 1492 GCGTGAGGTCGTGTGTGTGAACCGTTGCGGCAATCGTCTTAACCGCTGGAACAGTGA 1551
QY 1530 TGAATGCTTCGAGCCGTTTGAAGCTGATGTGAGAAATCGTGGGCCCATTAATCCAGCATC 1589
Db 1552 TGAATGCTTCGAGCCGTTTGAAGCTGATGTGAGAAATCGTGGGCCCATTAATCCAGCATC 1611
QY 1590 CAGACTCACAGCTTTGAGAAATCAAGAAGACGCTCGCAAGATGGTTGAATCCAGGATGT 1649
Db 1612 CAGACTCACAGCTTTGAGAAATCAAGAAGACGCTCGCAAGATGGTTGAATCCAGGATGT 1671
QY 1650 AAGATTTCGACAAACAGTTTTCGAGAAAGAAATTTAGACTGCAAGAAATTCACCCGAGGAAG 1709
Db 1672 AAGATTTCGACAAACAGTTTTCGAGAAAGAAATTTAGACTGCAAGAAATTCACCCGAGGAAG 1731
QY 1710 GGTGGAGTTAGCATGGACTAGGATGTGCGCTTGGTTCCAGACTCTCTCTTACCATCT 1769
Db 1732 GGTGGAGTTAGCATGGACTAGGATGTGCGCTTGGTTCCAGACTCTCTCTTACCATCT 1790
QY 1770 TCACAGGCTGCTAACAGTAGTAACCTTTTCAGGACTCTGCAGAAATGC 1813
Db 1791 TCACAGGCTGCTAACAGTAGTAA-CTTTCAGGACTCTGCAGAAATGC 1833

RESULT 5

US-10-463-190-119
; Sequence 119, Application US/10463190
; Publication No. US20040009535A1
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary E.
; APPLICANT: Galas, David J.
; APPLICANT: Kovacevich, Brian
; APPLICANT: Mulligan, John T.
; APPLICANT: Paepfer, Bryan W.
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Winkler, David G.
; TITLE OF INVENTION: COMPOSITIONS AND MEHTODS FOR
; FILE REFERENCE: 240083 508C2
; CURRENT FILING DATE: 2003-06-16
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 119
; LENGTH: 3167
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-463-190-119

Query Match 96.5%; Score 1750.4; DB 6; Length 3167;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

QY 30 TCGGCGCCGAGGACACGTCGCAATTTGGAATGACTCAGCTATACACTTACATCAGATT 89
Db 195 TGGCCCGGACGACACGTCGCAATTTGGAATGACTCAGCTATACACTTACATCAGATT 254
QY 90 ACTGGAGCCTCTGTTTCATCATTTCTCATGTTCAAGGGCAGAAATCTAGATAGTATGCT 149
Db 255 ACTGGAGCCTCTGTTTCATCATTTCTCATGTTCAAGGGCAGAAATCTAGATAGTATGCT 314
QY 150 CCATGCTACTGTTATGAATCAGCTGGACAGAAAGACCGGAAATTTGAGTGCAGCTT 209
Db 315 CCATGCTACTGTTATGAATCAGCTGGACAGAAAGACCGGAAATTTGAGTGCAGCTT 374
QY 210 AGCACAGAGGACACCTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCAGATGA 269
Db 375 AGCACAGAGGACACCTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCAGATGA 434

QY 270 CGCTATTATAACACATGCATAAATAAGGCCATTTCCTTCCATTATATAGAAGACATGA 329
Db 435 CGCTATTATAACACATGCATAAATAAGGCCATTTCCTTCCATTATATAGAAGACATGA 494
QY 330 TCAGGAGGAAAAACACGTTAACTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATG 389
Db 495 TCAGGAGGAAAAACACGTTAACTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATG 554
QY 390 CAAAGATTTCACAAAGCCGACTACGAGGACAAATAGAAATTTGTGCGGACCAATTTTGTG 449
Db 555 CAAAGATTTCACAAAGCCGACTACGAGGACAAATAGAAATTTGTGCGGACCAATTTTGTG 614
QY 450 CAAACAAATATTGACGCTACACTGCCCTGTCTGTATAGGCCCATTTCTTTGATGGCAG 509
Db 615 CAAACAAATATTGACGCTACACTGCCCTGTCTGTATAGGCCCATTTCTTTGATGGCAG 674
QY 510 GGTCCGATGGCTGGCTGTCTCATCTATGGCTGTCTGTATTTGCGCCATGATCGTCTT 569
Db 675 GGTCCGATGGCTGGCTGTCTCATCTATGGCTGTCTGTATTTGCGCCATGATCGTCTT 734
QY 570 CTCAGCTGCTTCTGTTACAAACATTACTGTAAGATATCTCAAGAGAGGCTGTTACAA 629
Db 735 CTCAGCTGCTTCTGTTACAAACATTACTGTAAGATATCTCAAGAGAGGCTGTTACAA 794
QY 630 CCGTGACTTGGAAACAGGATGAAGCAATTTATCCAGTAGGAGAAATCACTGAAGAGACTGAT 689
Db 795 CCGTGACTTGGAAACAGGATGAAGCAATTTATCCAGTAGGAGAAATCACTGAAGAGACTGAT 854
QY 690 TGACCAGTCAAAAGCTCTGGTAGTGGATCTGGATTACCTTTATTTGGTTTCAGCGAACTAT 749
Db 855 TGACCAGTCAAAAGCTCTGGTAGTGGATCTGGATTACCTTTATTTGGTTTCAGCGAACTAT 914
QY 750 TGCCAAAACAGATTTCAGATGGTTTCGCAAGTTGGTAAAGGCCGGTATGAGAAATATGAT 809
Db 915 TGCCAAAACAGATTTCAGATGGTTTCGCAAGTTGGTAAAGGCCGGTATGAGAAATATGAT 974
QY 810 GGGTAAATGGCGTGGTGAAGAAAGTGGCTCAAAAGTATTTTACCACTGAAGAGAGCTAG 869
Db 975 GGGTAAATGGCGTGGTGAAGAAAGTGGCTCAAAAGTATTTTACCACTGAAGAGAGCTAG 1034
QY 870 CTGGTTTAGAGAAAAACAGAAATCTACAGACGGTGTAAATGCGTCAATGAAATATATCTGG 929
Db 1035 CTGGTTTAGAGAAAAACAGAAATCTACAGACGGTGTAAATGCGTCAATGAAATATATCTGG 1094
QY 930 TTTTATAGCTGACAGACATTAAGGACCCGGTTCTGGAACCTCAGCTGATTTGATTACTGA 989
Db 1095 TTTTATAGCTGACAGACATTAAGGACCCGGTTCTGGAACCTCAGCTGATTTGATTACTGA 1154
QY 990 TTACCATGAGAAATGGGTCTCTATGACTTCTGAAATGTGCCACCTGGACACGAGAC 1049
Db 1155 TTACCATGAGAAATGGGTCTCTATGACTTCTGAAATGTGCCACCTGGACACGAGAC 1214
QY 1050 CCTACTCAAGTTAGCTTATTTCTGCTGCTGGTGTGTCGCCACCTCCACAGAAATTTA 1109
Db 1215 CCTACTCAAGTTAGCTTATTTCTGCTGCTGGTGTGTCGCCACCTCCACAGAAATTTA 1274
QY 1110 TGGCAGCAAGGACGCTGCAATTTGCTCATCGAGACCTGGAAGACAAACATCCTTAT 1169
Db 1275 TGGCAGCAAGGACGCTGCAATTTGCTCATCGAGACCTGGAAGACAAACATCCTTAT 1334
QY 1170 TAAGAAAAATGGTAGTGTCTGATTTGCTGACTGGCCCTAGCTGTTAAATTCACAGTGA 1229
Db 1335 TAAGAAAAATGGTAGTGTCTGATTTGCTGACTGGCCCTAGCTGTTAAATTCACAGTGA 1394
QY 1230 CACAAATGAAGTTGACATACCTTTGAAACACAGGCTGGGACACGAGCGGTACATGGCTCC 1289
Db 1395 CACAAATGAAGTTGACATACCTTTGAAACACAGGCTGGGACACGAGCGGTACATGGCTCC 1454
QY 1290 AGAAGTGTGACGAGAGCCTGAGTAAACCAATTTCCAGCCCTACATCATGGCTGACAT 1349
Db 1455 AGAAGTGTGACGAGAGCCTGAGTAAACCAATTTCCAGCCCTACATCATGGCTGACAT 1514
QY 1350 CTACAGCTTTGGTTTGATCAATTTGGAGATGGCCCGTCTGCTGTTATTACAGGAGGAATCGT 1409

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Db 1515 CTACAGCTTTGGTTTGATCATTTGGGAGATGGCCCGTGGCTGTATTACAGAGGAATCGT 1574
Qy 1410 GGAGGAATATCAATACCATATTACATCGTCCCTAGTAGTACCCATCTTTATGAAGACAT 1469
Db 1575 GGAGGAATATCAATACCATATTACATCGTCCCTAGTAGTACCCATCTTTATGAAGACAT 1634
Qy 1470 GCGTAGGTCGTGTGTGTGAACCGCTTGGCCCAATCGTCTCTAACCGCTGGAAACAGTGA 1529
Db 1635 GCGTAGGTCGTGTGTGTGAACCGCTTGGCCCAATCGTCTCTAACCGCTGGAAACAGTGA 1694
Qy 1530 TGAATGCTTCGAGCCGCTTTGAAGCTGTAGATGTGAGATGTGAGATGTGAGATGTGAGATGT 1589
Db 1695 TGAATGCTTCGAGCCGCTTTGAAGCTGTAGATGTGAGATGTGAGATGTGAGATGTGAGATGT 1754
Qy 1590 CAGACTCACAGCTTTGAGAACTCAAGAGAGCGCTCGCAAGAGATGTTCAATCCCAAGGATGT 1649
Db 1755 CAGACTCACAGCTTTGAGAACTCAAGAGAGCGCTCGCAAGAGATGTTCAATCCCAAGGATGT 1814
Qy 1650 AAGAAATTTGACAAACAGCTTTTGAGAAAGAAATTTAGACTGCAAGAAATTTCAACCCGAGGAAG 1709
Db 1815 AAGAAATTTGACAAACAGCTTTTGAGAAAGAAATTTAGACTGCAAGAAATTTCAACCCGAGGAAG 1874
Qy 1710 GGTGGAGTTAGCATGGACTAGGATGTGGCTTGGTTTCCAGACTCTCTCTCTACCATCT 1769
Db 1875 GGTGGAGTTAGCATGGACTAGGATGTGGCTTGGTTTCCAGACTCTCTCTCTCTA-CATCT 1933
Qy 1770 TCAGAGCTCTACACAGTAAACCTTTTCAGGACTCTGCAGAAATGC 1813
Db 1934 TCAGAGCTCTACACAGTAAACCTTTTCAGGACTCTGCAGAAATGC 1976

RESULT 6
US-10-463-190-120
; Sequence 120, Application US/10463190
; Publication No. US20040009535A1
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary E.
; APPLICANT: Galas, David J.
; APPLICANT: Kovacevich, Brian
; APPLICANT: Mulligan, John T.
; APPLICANT: Paepel, Bryan W.
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Winkler, David G.
; TITLE OF INVENTION: COMPOSITIONS AND MEHTODS FOR
; FILE REFERENCE: INCREASING BONE MINERALIZATION
; CURRENT FILING DATE: 2003-06-16
; CURRENT APPLICATION NUMBER: US/10/463,190
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 120
; LENGTH: 3167
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-463-190-120
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Query Match 96.5%; Score 1750.4; DB 6; Length 3167;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

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Qy 30 TGGCGCCGCGCAGACAGCTGGCAATTTGGCAATGACTCAGCTATACACTTACATCAGATT 89
Db 195 TGGCCCGGACAGACAGCTGGCAATTTGGCAATGACTCAGCTATACACTTACATCAGATT 254
Qy 90 ACTGGGAGCCTGTCTGTTCATCATTTCTCATGTTTCAAGGGCAGAACTAGATAGTATGCT 149
Db 255 ACTGGGAGCCTGTCTGTTCATCATTTCTCATGTTTCAAGGGCAGAACTAGATAGTATGCT 314
Qy 150 CCAATGTACTGTGTATGAATACAGCTGGACAGAGAGCGGAAATGGAGTACGTT 209
Db 315 CCAATGTACTGTGTATGAATACAGCTGGACAGAGAGCGGAAATGGAGTACGTT 374
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Qy 210 AGCACACAGGAGACACCTTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCAGATGA 269
Db 375 AGCACACAGGAGACACCTTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCAGATGA 434
Qy 270 CGCTATTAAATACACATGCATTAATATGCCCATTGCTTTGCCATTTATAGAAGAATGA 329
Db 435 CGCTATTAAATACACATGCATTAATATGCCCATTGCTTTGCCATTTATAGAAGAATGA 494
Qy 330 TCAGGAGAGAAACACAGCTTTAACTTTCTGGGTGTATGAAGTATGAAGGCTCTCATTTCAATG 389
Db 495 TCAGGAGAGAAACACAGCTTTAACTTTCTGGGTGTATGAAGTATGAAGGCTCTCATTTCAATG 554
Qy 390 CAAGGATTCACAAAAGCCAGCTACGCGAGCAATAGAAATGTTGTCGGACCAATTTGTC 449
Db 555 CAAGGATTCACAAAAGCCAGCTACGCGAGCAATAGAAATGTTGTCGGACCAATTTGTC 614
Qy 450 CAACCAATATTTGCGAGCTACACTGCCCCCTGCTGTTATAGGCCCATTTCTTTGATGGCAG 509
Db 615 CAACCAATATTTGCGAGCTACACTGCCCCCTGCTGTTATAGGCCCATTTCTTTGATGGCAG 674
Qy 510 CGTCCGATGGCTGGCTGCTCATCTATGGCTGCTGTATGTCGCCATGATCGTCTT 569
Db 675 CGTCCGATGGCTGGCTGCTCATCTATGGCTGCTGTATGTCGCCATGATCGTCTT 734
Qy 570 CTCAGCTGCTTCTGTTTCAAAACATTTACTGTAAGAGTATCTCAAGCAGAGGTCGTTACAA 629
Db 735 CTCAGCTGCTTCTGTTTCAAAACATTTACTGTAAGAGTATCTCAAGCAGAGGTCGTTACAA 794
Qy 630 CGGTGACTTTGGAAACAGGATGAAGCATTTATTCAGTAGGAGATCACTGAAAGACCTGAT 689
Db 795 CGGTGACTTTGGAAACAGGATGAAGCATTTATTCAGTAGGAGATCACTGAAAGACCTGAT 854
Qy 690 TGACCACTCACAAAGCTCTGGTAGTGATCTGATTTACCTTTATTTGGTTCAGCGCAACTAT 749
Db 855 TGACCACTCACAAAGCTCTGGTAGTGATCTGATTTACCTTTATTTGGTTCAGCGCAACTAT 914
Qy 750 TGCCAAACAGATTCAGATGGTTTCGGCAGGTTGGTAAGGGCCGGTATGGAGAAATGATGGAT 809
Db 915 TGCCAAACAGATTCAGATGGTTTCGGCAGGTTGGTAAGGGCCGGTATGGAGAAATGATGGAT 974
Qy 810 GGGTAAATGGCGTGTGAAAGAGTGGCTGTCAAAGTATTTTTCACCTGAAAGAGCTAG 869
Db 975 GGGTAAATGGCGTGTGAAAGAGTGGCTGTCAAAGTATTTTTCACCTGAAAGAGCTAG 1034
Qy 870 CTGGTTTAGAGAAACAGAAATCTACAGAGCGGTGTTAAATGCGTCATGAAATATACTGG 929
Db 1035 CTGGTTTAGAGAAACAGAAATCTACAGAGCGGTGTTAAATGCGTCATGAAATATACTGG 1094
Qy 930 TTTTATAGCTGCAGACATTTAAAGGCCACCGGTTCTCGGACTCAGCTGTATTGATTACTGA 989
Db 1095 TTTTATAGCTGCAGACATTTAAAGGCCACCGGTTCTCGGACTCAGCTGTATTGATTACTGA 1154
Qy 990 TTAACATGAAATGGGTCTCTCTATGACTTCCCTGAAATGTGCCACCTGAGACACCAGAGC 1049
Db 1155 TTAACATGAAATGGGTCTCTCTATGACTTCCCTGAAATGTGCCACCTGAGACACCAGAGC 1214
Qy 1050 CCTACTCAAGTTAGCTTTATTTCTGCGCTGTGGTCTGTGCCACCTCCACAGAAATTTTA 1109
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Db 1275 TGGCAGCGAAGGCAAGCCCTGCAATTTGCTCATCGAGACCTGAGAGCAAAAACATCTTAT 1334
Qy 1170 TAAGAAAAATGGTAGTTGCTGATTTGCTGACCTGGCCCTAGCTGTTTAAATTTCAACAGTGA 1229
Db 1335 TAAGAAAAATGGTAGTTGCTGATTTGCTGACCTGGCCCTAGCTGTTTAAATTTCAACAGTGA 1394
Qy 1230 CAACAATGAAGTTGACATACCTTTGAAACACAGGGTGGGCAACAGCGGTGATCATGCTCC 1289
Db 1395 CAACAATGAAGTTGACATACCTTTGAAACACAGGGTGGGCAACAGCGGTGATCATGCTCC 1454
Qy 1290 AGAAGTGTGGACGAGAGCTTGAGTAAACCAATTTCCAGCCCTACATCATGGCTGACAT 1349
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Db 1455 AGAAGTCTGGACGAGCGCTGATTAACCAATTTCCAGCCCTACATCATCGCTGACAT 1514
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Db 1515 CTACAGCTTTGGTTGATCATTTGGGAGATGGCCCGTCTGCTGTATTTACAGGAGGAATCGT 1574
QY 1410 GGAGGAATATCAATTACCATATTAACAATGCTGCTAGTGACCCATCTTATGAAGACAT 1469
Db 1575 GGAGGAATATCAATTACCATATTAACAATGCTGCTAGTGACCCATCTTATGAAGACAT 1634
QY 1470 GGCTGAGGTCTGCTGTGTGTAACCGCTTGGCGCAATTCGTCTTAACCGCTGGAAACAGTGA 1529
Db 1635 GCGTGAGGTCTGCTGTGTGTAACCGCTTGGCGCAATTCGTCTTAACCGCTGGAAACAGTGA 1694
QY 1530 TGAATGCTTTCAGCGCTTTTGAAGCTGATGTGAGAAATGCTGGGCCCATTAATCCAGCATC 1589
Db 1695 TGAATGCTTTCAGCGCTTTTGAAGCTGATGTGAGAAATGCTGGGCCCATTAATCCAGCATC 1754
QY 1590 CAGACTCACAGCTTTGAGAAATCAAGAGACGCTCGCAAGATGGTTGAAATCCAGGATGT 1649
Db 1755 CAGACTCACAGCTTTGAGAAATCAAGAGACGCTCGCAAGATGGTTGAAATCCAGGATGT 1814
QY 1650 AAGAGTTTGCACAAACAGTTTTCAGAAAGAAATTTAGACTGCAAGAAATTCACCCGAGGAAG 1709
Db 1815 AAGAGTTTGCACAAACAGTTTTCAGAAAGAAATTTAGACTGCAAGAAATTCACCCGAGGAAG 1874
QY 1710 GGTGGAGTTAGCATGACATAGGATGTGCGCTTGGTTTCAGACTCTCTCTCTACCATCT 1769
Db 1875 GGTGGAGTTAGCATGACATAGGATGTGCGCTTGGTTTCAGACTCTCTCTCTA-CATCT 1933
QY 1770 TCACAGGCTGCTAACAGTAACTTTCAGGACTCTGCAGAAATGC 1813
Db 1934 TCACAGGCTGCTAACAGTAAA-CTTTCAGGACTCTGCAGAAATGC 1976

RESULT 7

US-10-868-497-88
; Sequence 88, Application US/10868497
; Publication No. US20050106683A1
; GENERAL INFORMATION:
; APPLICANT: Winkler, David G.
; APPLICANT: Shi, Jiye
; APPLICANT: Latham, John
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR SCLEROSTIN AND
; TITLE OF INVENTION: METHODS FOR INCREASING BONE MINERALIZATION
; FILE REFERENCE: 60117-128
; CURRENT APPLICATION NUMBER: US/10/868,497
; CURRENT FILING DATE: 2004-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 3167
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-868-497-88

Query Match 96.5%; Score 1750.4; DB 9; Length 3167;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

QY 30 TGGGGCCGCGAGACACGTCGCAATTTGGACAATGACTAGCTATACACTTACATCAGATT 89
Db 195 TGGCCCGGAGACACGTCGCAATTTGGACAATGACTAGCTATACACTTACATCAGATT 254
QY 90 ACTGGAGCGTGTCTTTCATCATTTCTCATGTTCAAGGGCAGAACTAGATAGTATGCT 149
Db 255 ACTGGAGCGTGTCTTTCATCATTTCTCATGTTCAAGGGCAGAACTAGATAGTATGCT 314
QY 150 CCATGCTACTGTGTATGAATTCAGACGTGCAACAGAGAAAGCCGGAATTTGGAGTGCAGTT 209
Db 315 CCATGCTACTGTGTATGAATTCAGACGTGCAACAGAGAAAGCCGGAATTTGGAGTGCAGTT 374

QY 210 AGCACGAGGACACCTTTACCTTTCTTAAATATGCTATTGCTCAGGACACTGCCCATGCA 269
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QY 270 CGCTATTAAACACATGCATAAATGCGCATTTGCTTGGCCATTATAGAAAGAGATGA 329
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QY 330 TCAGGGAGAAACACGCTTAACTTCTGGGTGTATGAAGTATGAAGCTCTGATTTTCAATG 389
Db 495 TCAGGGAGAAACACGCTTAACTTCTGGGTGTATGAAGTATGAAGCTCTGATTTTCAATG 554
QY 390 CAAGGATTTCACCAAAAGCCAGCTACGAGAGACAAATAGAAATGCTTCGAGACCAATTTG 449
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QY 450 CAACCAATATTTCAGAGCCTACACTGCCCCCTGTCTGTATAGGCCCAATCTTTGATGGCAG 509
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QY 510 GCTCCGATGGCTGGCTGTCTCATCTCTATGGCTGTCTGTATTTGTCGCCATGATCGTCTT 569
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QY 570 CTCCAGCTGCTTCTGTTTACAAACATTTACTGTAAGAGTATCTCAAGCAGAGGTCGTTACAA 629
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QY 630 CCGTGACTTGGAAACAGGATGAAGCAATTTATTCAGTAGGAGAAATCACTGAAAAGACTGAT 689
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QY 690 TGACAGGTCAAAAGCTCTGGTAGTGGATCTGGATTTACCTTTATTTGGTTTCAGCGAACTAT 749
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QY 750 TGCCAAACAGATTTCAGATGGTTTCGGCAGGTTGGTAAGGCCGGTATGAGAAAGTATGGAT 809
Db 915 TGCCAAACAGATTTCAGATGGTTTCGGCAGGTTGGTAAGGCCGGTATGAGAAAGTATGGAT 974
QY 810 GGGTAAATGGCGTGGTGAAAAAGTGGCTGTCAAAGTATTTTTTACCACCTGAAGAAAGCTAG 869
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QY 1110 TGGCAGCGCAAGCGCTGCAATTTGCTCATCTGAGACCTGGAAGACCAAAACATCCTTAT 1169
Db 1275 TGGCAGCGCAAGCGCTGCAATTTGCTCATCTGAGACCTGGAAGACCAAAACATCCTTAT 1334
QY 1170 TAAGAAAAATGGTAGTTGCTGTATTGCTGACCTGGGCCCTTAGCTGTTTAAATTCACACAGTGA 1229
Db 1335 TAAGAAAAATGGTAGTTGCTGTATTGCTGACCTGGGCCCTTAGCTGTTTAAATTCACACAGTGA 1394
QY 1230 CACAAATGAAGTTGATACATACCTTGAACACACAGGTTGGGCACACGCGGTACATGGCTCC 1289
Db 1395 CACAAATGAAGTTGATACATACCTTGAACACACAGGTTGGGCACACGCGGTACATGGCTCC 1454
QY 1290 AGAAGTGTGGACGAGAGCCTGAGTAAAAAACCTTTTCCAGCCCTACATCATGGCTGACAT 1349

Db	1455	AGAA	TGCT	TGAC	GAGAC	GC	TGAG	TAAAAA	CCAT	TTCCAG	CCCT	TACAT	CA	TG	GGCT	TG	CAT	1514		
Qy	1350	CTAC	AGCT	TTG	GGT	TTG	ATCAT	TTT	GGG	GAGAT	GGCC	CGT	CGCT	GTAT	TAC	CAGG	AGGAAT	CGT	1409	
Db	1515	CTAC	AGCT	TTG	GGT	TTG	ATCAT	TTT	GGG	GAGAT	GGCC	CGT	CGCT	GTAT	TAC	CAGG	AGGAAT	CGT	1574	
Qy	1410	GGAG	GAAT	ATCA	ATTTAC	CAATAT	TACA	ATG	TGGT	GCCT	TAGT	GAC	CCCAT	CTCT	TAT	TGA	AGACAT		1469	
Db	1575	GGAG	GAAT	ATCA	ATTTAC	CAATAT	TACA	ATG	TGGT	GCCT	TAGT	GAC	CCCAT	CTCT	TAT	TGA	AGACAT		1634	
Qy	1470	CGCT	GAGT	CGT	GTG	TG	AAAC	CGTT	TG	CGGC	CAAT	CGT	CTCT	CAAC	CGCT	TG	GAAC	ACAT	GA	1529
Db	1635	CGCT	GAGT	CGT	GTG	TG	AAAC	CGTT	TG	CGGC	CAAT	CGT	CTCT	CAAC	CGCT	TG	GAAC	ACAT	GA	1694
Qy	1530	TGAAT	TGCT	CT	CGAC	CGG	TTTT	TGA	AGCT	TGAT	GT	CAGA	AT	TGCT	TGG	GCCCAT	TAAT	CCAG	CAT	1589
Db	1695	TGAAT	TGCT	CT	CGAC	CGG	TTTT	TGA	AGCT	TGAT	GT	CAGA	AT	TGCT	TGG	GCCCAT	TAAT	CCAG	CAT	1754
Qy	1590	CAGAC	T	CAC	AGCT	TTG	AGAAT	CA	AGA	AGAC	GCCT	CG	AAAG	ATG	TTG	AAAT	CCCA	GAG	TGT	1649
Db	1755	CAGAC	T	CAC	AGCT	TTG	AGAAT	CA	AGA	AGAC	GCCT	CG	AAAG	ATG	TTG	AAAT	CCCA	GAG	TGT	1814
Qy	1650	AAAG	ATTTG	ACAA	ACAG	TTTT	TG	AGAA	AGAA	TTT	TAG	ACT	GC	CAAG	AAAT	T	CAC	CCG	AGAG	1709
Db	1815	AAAG	ATTTG	ACAA	ACAG	TTTT	TG	AGAA	AGAA	TTT	TAG	ACT	GC	CAAG	AAAT	T	CAC	CCG	AGAG	1874
Qy	1710	GGT	GGAG	T	TAG	CAT	GG	ACT	TG	GGCT	TG	TTTT	CC	AG	CT	CTCT	CT	CT	CT	1769
Db	1875	GGT	GGAG	T	TAG	CAT	GG	ACT	TG	GGCT	TG	TTTT	CC	AG	CT	CTCT	CT	CT	CT	1933
Qy	1770	TCAC	AGG	TGCT	TAAC	AGT	TAAC	CTTT	TG	AG	CT	CT	CC	AG	CT	CT	CC	AG	ATGC	1813
Db	1934	TCAC	AGG	TGCT	TAAC	AGT	TAAC	CTTT	TG	AG	CT	CT	CC	AG	CT	CT	CC	AG	ATGC	1976

RESULTS

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RESULTS 8
US-10-868-497-89
; Sequence 89, Application US/10868497
; Publication No. US20050106683A1
; GENERAL INFORMATION:
; APPLICANT: Winkler, David G.
; APPLICANT: Shi, Jiye
; APPLICANT: Latham, John
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR SCLEROSTIN AND
; TITLE OF INVENTION: METHODS FOR INCREASING BONE MINERALIZATION
; FILE REFERENCE: 60117-128
; CURRENT APPLICATION NUMBER: US/10/868,497
; CURRENT FILING DATE: 2004-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 3167
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-868-497-89

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Query Match	96.5%	Score 1750.4;	DB 9;	Length 3167;
Best Local Similarity	99.6%	Pred. No. 0;		
Matches 1776;	Conservative	0;	Mismatches	6; Indels 2; Gaps 2;

Qy	30	TGCGGCCGCCAGGACACGTCGGAAATCGACAATGACTACGCTATACACTTACATCAGATT	89
Db	195	TGCGCCGACAGGACACGTCGGAAATCGACAATGACTACGCTATACACTTACATCAGATT	254
Qy	90	ACTGGGAGCCTGCTGTTTCATCTTCTCATGTTCAAGGGCAGAACTCAGATGATGCT	149
Db	255	ACTGGGAGCCTGCTGTTTCATCTTCTCATGTTCAAGGGCAGAACTCAGATGATGCT	314
Qy	150	CCATGTTACTGGTATGAAATCAGACGCTGGACCGAAGAACCGCGAAATCGAGTGACGTT	209
db	315	CCATGTTACTGGTATGAAATCAGACGCTGGACCGAAGAACCGCGAAATCGAGTGACGTT	374

Db 1455 AGAAGTCTGGACGAGCTGAGTAAACCAATTTCCAGCCCTACATCATCGCTGCAT 1514
QY 1350 CTACAGCTTTGGTTTGGATCATTTGGGAGATGGCCCGCTCGCTGTATTTACAGGAGGAATCGT 1409
Db 1515 CTACAGCTTTGGTTTGGATCATTTGGGAGATGGCCCGCTCGCTGTATTTACAGGAGGAATCGT 1574
QY 1410 GGAGGAATATCAATTAACCATATTAACAATGGTGGCTAGTGACCCATCTTTATGAAGACAT 1469
Db 1575 GGAGGAATATCAATTAACCATATTAACAATGGTGGCTAGTGACCCATCTTTATGAAGACAT 1634
QY 1470 GCGTGAAGTCTGTGTGTAAGACGCTTGGGGCAATCGTCTCTAACCGCTGGAAACAGTGA 1529
Db 1635 GCGTGAAGTCTGTGTGTAAGACGCTTGGGGCAATCGTCTCTAACCGCTGGAAACAGTGA 1694
QY 1530 TGAATGCTTCGAGCGGTTTGAAGCTGTATGTGAGAAATGCTGGGCCCATTAATCCAGCATC 1589
Db 1695 TGAATGCTTCGAGCGGTTTGAAGCTGTATGTGAGAAATGCTGGGCCCATTAATCCAGCATC 1754
QY 1590 CAGACTCAGAGCTTTGAGAAATCAAGNAGAGCGTCCGAAAGATGGTTGAATCCAGCATG 1649
Db 1755 CAGACTCAGAGCTTTGAGAAATCAAGNAGAGCGTCCGAAAGATGGTTGAATCCAGCATG 1814
QY 1650 AAGATTTTGCACAAACAGTTTTCGAGAAAGAAATTTAGACTCGAAGAAATTCACCCGAGGAAG 1709
Db 1815 AAGATTTTGCACAAACAGTTTTCGAGAAAGAAATTTAGACTCGAAGAAATTCACCCGAGGAAG 1874
QY 1710 GTGGAGTTAGCATGAGCTAGGATGTGCGGCTTGGTTTCAGAGCTCTCTCTCTACCATCT 1769
Db 1875 GTGGAGTTAGCATGAGCTAGGATGTGCGGCTTGGTTTCAGAGCTCTCTCTCTA-CATCT 1933
QY 1770 TCACAGGCTGCTAACAGTAAACCTTTTCAGGACTCTGCAGAAATGC 1813
Db 1934 TCACAGGCTGCTAACAGTAAAC-CTTTTCAGGACTCTGCAGAAATGC 1976

RESULT 9
US-09-903-068-13
; Sequence 13, Application US/09903068
; Patent No. US20020123139A1
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
; Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
; Having Serine Threonine Kinase Domains And Their Use
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/903,068
; FILING DATE: 11-Jul-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/679,187
; FILING DATE: <Unknown>
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: 17-No. US20020123139A1ember-1993
; APPLICATION NUMBER: 9224057.1
; FILING DATE: 17-No. US20020123139A1ember-1992
; APPLICATION NUMBER: 9304677.9
; FILING DATE: 8-March-1993
; APPLICATION NUMBER: 9304680.3
; FILING DATE: 8-March-1993
; APPLICATION NUMBER: 9311047.6
; FILING DATE: 28-May-1993

APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
APPLICATION NUMBER: 9136099.2
FILING DATE: 3-August-1993
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kohlel, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2070 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Mouse
FEATURE:
NAME/KEY: CDS
LOCATION: 217..1812
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-903-068-13

Query Match 87.2%; Score 1581.4; DB 3; Length 2070;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 1678; Conservative 0; Mismatches 96; Indels 9; Gaps 3;

QY 39 CAGGACAGTGGCAATTCGACATCAGTATACATCAGATTCATCAGATTCGAGC 98
Db 195 CAGGACGCTGGCAATTCGACATCAGTATACATCAGATTCATCAGATTCGAGC 254
QY 99 CTGCTGTTTCATCATTTCTCATGTTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGGTAC 158
Db 255 CTGCTGTTTCATCATTTCTCATGTTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGGC 314
QY 159 TGGTATGAATCAGAGTGGACCAAGAACGCGGAAATGGAGTGCCTTAGCACCAGA 218
Db 315 TGGTATGAATCAGAGTGGACCAAGAACGCGGAAATGGAGTGCCTTAGCACCAGA 374
QY 219 GGACACCTTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCCCAGATGACGCTATTAA 278
Db 375 GGATACCTTGGCTTTCTTAAAGTGTCTATTGCTCAGGACACTGCCCCAGATGATGCTATTAA 434
QY 279 TAACATGCATACATAATAGCCATTTGCTTTGCCATTATAGAAGAGATGATCAGGAGA 338
Db 435 TAACATGCATACATAATAGCCATTTGCTTTGCCATTATAGAAGAGATGATCAGGAGA 494
QY 339 AACGAGTTAACTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATGAAGATTC 398
Db 495 AACGAGTTAACTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATGAAGATTC 554
QY 399 ACCAAAGCCAGCTACGACGACAAATAGAATGTTGTCGGACCAATTTGTGCAACCAATA 458
Db 555 ACCAAAGCCAGCTACGACGACAAATAGAATGTTGTCGGACCAATTTGTGCAACCAATA 614
QY 459 TTTGAGGCTACACTGCCCCCTGTCTGTTATAGGCCCATTTCTTTGATGGCAGCGTCCGATG 518
Db 615 TTTGAGGCTACACTGCCCCCTGTCTGTTATAGGTCGGTTCTTTGATGGCAGCATCCGATG 674
QY 519 GCTGCTGTGCTCATCTCTATGGCTGTCTGTATTTGTCGCATGATGCTCTTCTCCAGCTG 578
Db 675 GCTGCTGTGCTCATCTCTATGGCTGTCTGTATTTGCTATGATCATCTCTTCTCCAGCTG 734
QY 579 CTTCTGTTTACAAACATTACTGTAAAGATATCTCAAGACGAGGCTCGTTTACAACCGTAC 638

Db 735 CTTTTGCTATAAGCATTTATTTGTAAGAGTATCTCAAGCAGGGGTGTTTACAAACCGTGATTT 794
Qy 639 GGAACAGGATGAACCATTTATTTCCAGTAGGAGATCACTGAAAGACCTGATTGACAGATC 698
Db 795 GGAACAGATGAACCATTTATTTCCAGTAGGAGATCACTGAAAGACCTGATTGACCAATC 854
Qy 699 ACAAGCTCTGGTAGTGGATCTGGATTA CTTTATGTTTACGGAACTATTGCGCAACA 758
Db 855 CCAAAGCTCTGGAGTGGATCTGGATTCGCTTTTATTGGTTTACGGAACTATTGCGCAACA 914
Qy 759 GATTTCAGATGGTTCCGAGGTGGTAAGGCGCGGTATGGAAGAGTATGGATGGTAAATG 818
Db 915 GATTTCAGATGGTTCCGAGGTGGTAAGGCGCGGTATGGAAGAGTATGGATGGTAAATG 974
Qy 819 GCGTGGTGAAGAAAGTGGCTGTCAAAGTATTTTACCACCTGAAGAACTAGCTGGTTTAG 878
Db 975 GCGTGGTGAAGAAAGTGGCTGTCAAAGTATTTTACCACCTGAAGAACTAGCTGGTTTAG 1034
Qy 879 AGAAACAGAAATCTTACAGACCGTGTAAATGCGTCAATGAAATATATCTTGGTTTTATAGC 938
Db 1035 AGAAACAGAAATCTTACAGACCGTGTAAATGCGTCAATGAAATATATCTTGGTTTTATAGC 1094
Qy 939 TGCAGACATTTAAGGACCGGTTCTCGACTCAGCTGATTTGATTACTGATTTACCATGA 998
Db 1095 TGCAGACATTTAAGGACCGGTTCTCGACTCAGCTGATTTGATTACTGATTTACCATGA 1154
Qy 999 GAATGGGTCTCTATCACTTCTGAAATGTGCCACCTCGACACAGAGCCCTACTCAA 1058
Db 1155 AAATGGATCTCTATGACTTCTGAAATGTGCCACCTAGACACAGAGCCCTACTCAA 1214
Qy 1059 GTTAGCTTATTTCTGCTGCTGTGTGTCGCCACCTCCACACAGAAATTTATGGCAGCA 1118
Db 1215 GTTAGCTTATTTCTGCTGCTGTGTGTCGCCACCTCCACACAGAAATTTATGGTACCCA 1274
Qy 1119 AGGCAAGCTTGAATGCTCATGAGACCTGAAGAGCAAAATCTCTTATTAAAGAAA 1178
Db 1275 AGGCAAGCTTGAATGCTCATGAGACCTGAAGAGCAAAATCTCTTATTAAAGAAA 1334
Qy 1179 TGTGAGTTGCTGATTTGCTGACCTGGCCCTAGCTGTTAAATTTCAACAGTGACACAATGA 1238
Db 1335 TGAAGTTGCTGATTTGCTGACCTGGCCCTAGCTGTTAAATTTCAACAGTGATACAATGA 1394
Qy 1239 AGTTGACATACCTTTGAACACCGGTGGCCACAGCGGTACATGGCTCCAGAAAGTCT 1298
Db 1395 AGTTGACATACCTTTGAATACCGGTGGCCACCAAGCGGTACATGGCTCCAGAAAGTCT 1454
Qy 1299 GGAAGAGCTGAGTTAAACCAATTTCCAGCCCTACATCATGGCTGACATCTACAGCTT 1358
Db 1455 GGATGAAGCTTGAATAAACCAATTTCCAGCCCTACATCATGGCTGACATCTATAGCTT 1514
Qy 1359 TGGTTTGATCATTTGGAGATGCGCGTCTGTTTACAGGAGGAATCGTGGAGGAATA 1418
Db 1515 TGGTTTGATCATTTGGAGATGCGCGTCTGTTTACAGGAGGAATCGTGGAGGAATA 1574
Qy 1419 TCAATTACCATATTACAACATGGTGGCTAGTGACCCATCTTATGAAGACATGCGTGAGGT 1478
Db 1575 TCAATTACCATATTACAACATGGTGGCTAGTGACCCATCTATGAGACATGCGTGAGGT 1634
Qy 1479 CGTGTGTGAACCGCTTGGCCCAATCGTCTCTAACCGCTGAAACAGTGATGAATGTCT 1538
Db 1635 TGTGTGTGTGAACCGCTTGGCCCAATCGTGTCTTAACCGCTGAAACAGCGATGAATGTCT 1694
Qy 1539 TCGAGCGTTTTGAAAGTGTGCAAGTCTGGGCCCAATTAATCCAGATCCAGATCCAC 1598
Db 1695 TCGAGCGTTTTGAAAGTGTGCAAGTCTGGGCCCAATTAATCCAGATCCAGATCCAC 1754
Qy 1599 AGCTTTGAGAAATCAAGAAAGCTGCAAGATGTTGAAATCCAGATGTAAGATTTG 1658
Db 1755 AGCTTTGAGAAATCAAGAAAGCTGCAAGATGTTGAAATCCAGATGTAAGATTTG 1814
Qy 1659 AC----AAACAGTTTTGAGAAAGATTTAGATGCAAGAAATTC----ACCCGAGGAAG 1710
Db 1815 ACAATTAACAAATTTTGAGGAGAAATTTAGACTGCAAGAAATCTTCTTCAACCAAGGAATGG 1874

Qy 1711 GTGAGGTAGCATGGACTAGGATGTCGGCTTGGTTTCCAGACTCTCTCTCTACCATCTT 1770
Db 1875 GTGGATTAGCATGGAAATAGGATGTTGACTTGGTTTCCAGACTCTTCTCTCTA-CATCTT 1933
Qy 1771 CACAGGCTGCTAAACAGTAAACCTTTCCAGGACTCTGCAGAAATGC 1813
Db 1934 CACAGGCTGCTAAACAGTAAACCTTTACGCTACTCTACAGAAATAC 1976

RESULT 10

US-10-739-413-13
; Sequence 13, Application US/10739413
; Publication No. US20050048607A1
; GENERAL INFORMATION:
; APPLICANT: MIYAZONO, Kohei
; APPLICANT: INAMURA, Takeshe
; APPLICANT: DEN DIJKE, Peter
; TITLE OF INVENTION: PROTEINS HAVING SERINE/THREONINE KINASE DOMAINS, CORRESPONDING
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND THEIR USE
; FILE REFERENCE: LUD 5539.1 CIP
; CURRENT APPLICATION NUMBER: US/10/739,413
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US/09/267,963
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/GB93/02367
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: US 09/039,177
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-739-413-13

Query Match 87.2%; Score 1581.4; DB 9; Length 2070;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 1678; Conservative 0; Mismatches 96; Indels 9; Gaps 3;

Qy 39 CAGGACACGCTGGCAATTGGACAATGACTCAGCTTATACACTTACATCAGATTTACTGGAGC 98
Db 195 CAGGACGCTGGCAATCAGACAATGACTCAGCTTATACACTTACATCAGATTTACTGGAGC 254
Qy 99 CTGCTGTTTCATCATTTCTCATGTTTCAAGGGCAGAAATCTAGATAGTATGCTTCATGGTAC 158
Db 255 CTGCTGTTTCATCATTTCTCATGTTTCAAGGGCAGAAATCTAGATAGTATGCTTCATGGC 314
Qy 159 TGGTATGAATCAGACGTCGACACAGAGAAAGCCGAAATGGAGTGACGTTAGCACACAGA 218
Db 315 TGGTATGAATCAGACGTCGACACAGAGAAAGCCGAAATGGAGTGACGTTAGCACACAGA 374
Qy 219 GGACACCTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCAGATGACGCTATTAA 278
Db 375 GGATACCTTGGCTTTCTTAAAGTGCTATTGCTCAGGACACTGCCAGATGATGCTATTAA 434
Qy 279 TAAACATGCAATACTAATGCGCATTTGCTTGCATATTAGAAAGATGATCAGGGAGA 338
Db 435 TAAACATGCAATACTAATGCGCATTTGCTTGCATATTAGAAAGATGATCAGGGAGA 494
Qy 339 AACCAAGTTAACTTCTGGGTGATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTC 398
Db 495 AACCAATTAACCTTCTGGGTGATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTC 554
Qy 399 ACCAAAAGCCAGCTACGAGGACCAATAGAATGTTGTCGAGACCAATTTGTGCAACCAATA 458
Db 555 ACCGAAAGCCAGCTACGAGGACCAATAGAATGTTGTCGAGACCAATTTGTGCAACCAATA 614
Qy 459 TTTGAGCCCTACACTGCCCCCTGTCGTTATAGCCCAATCTTTTGTATGGCAGGCTCCGATG 518
Db 615 TTTGAGCCCTACACTGCCCCCTGTCGTTATAGCCCAATCTTTTGTATGGCAGGATCCGATG 674

QY 519 GCTGGCTGCTCATCTCTATGGCTGCTGATTTGTCGCATGATGCTCTCTCCAGCTG 578
DB 675 GCTGGTTGCTCATTTCCATGCTGCTGTATGATTTGCTATGATCATCTCTCCAGCTG 734
QY 579 CTTCTGTTTAAACAATTAAGAGTATCTCAAGCAGAGGTCGTTTACAACCGTGACTT 638
DB 735 CTTTGTCTATAAGCATTATTGTAAGAGTATCTCAAGCAGGGTCTGTACAACCGTGATT 794
QY 639 GGAACAGGATGAAGCATTATTCCAGTAGAGAACTCACTGAAAGACCTGATGACAGTC 698
DB 795 GGAACAGGATGAAGCATTATTCCAGTAGAGAACTCACTGAAAGACCTGATGACAGTC 854
QY 699 ACAAGCTCTGCTAGTGGATCTGGATTACCTTTATTGGTTACGGAACCTATTGCCAAACA 758
DB 855 CCAAGCTCTGGAGTGGATCTGGATTGCTTTATTGGTTACGGAACCTATTGCCAAACA 914
QY 759 GATTGAGATGGTTCCGACGGTTGGTAAGGCGCGTATGGAGAAGTATGGATGGGTAATG 818
DB 915 GATTGAGATGGTTCCGACGGTTGGTAAGGCGCGTATGGAGAAGTATGGATGGGTAATG 974
QY 819 GCGTGTGAAAAGTGGCTGTCAAAGTATTTTACCCTGAAAGAGCTAGCTGGTTTATG 878
DB 975 GCGTGTGAAAAGTGGCTGTCAAAGTATTTTACCCTGAAAGAGCTAGCTGGTTTATG 1034
QY 879 AGAAACAGAAATCTACACAGCGTGTAAATGGCTCATGAAATATACCTGTTTATAGC 938
DB 1035 AGAAACAGAAATCTACACAGCGTGTAAATGGCTCATGAAATATACCTGTTTATAGC 1094
QY 939 TGCAGACATTAAAGGCACCGGTTCTGGACTCAGCTGTATTTGATTACTGATTACCATGA 998
DB 1095 TGCAGACATTAAAGGCACCGGTTCTGGACTCAGCTGTATTTGATTACTGATTACCATGA 1154
QY 999 GAATGGGTCTCTATGACTTCTGAAATGTCGACCCCTGGACACAGAGCCCTACTCAA 1058
DB 1155 AAATGGATCTCTATGACTTCTGAAATGTCGACACCTAGACACAGAGCCCTACTCAA 1214
QY 1059 GTTAGCTTATCTGCTGCTGTGTCTGTCGCCACCTCCACACAGAAATTTATGGACGCA 1118
DB 1215 GTTAGCTTATCTGCTGCTGTGTCTGTCGCCACCTCCACACAGAAATTTATGGTACCCA 1274
QY 1119 AGGCAAGCCTGCAATTTGCTCATCGAGACCTGAAGAGCAAAAACATCTTTATTAAGAAAA 1178
DB 1275 AGGCAAGCCTGCAATTTGCTCATCGAGACCTGAAGAGCAAAAACATCTTTATTAAGAAAA 1334
QY 1179 TGTGATGCTGTATTTGCTGACCTGGGCTTACTGTTTAAATTCACAGTGAACAAATGA 1238
DB 1335 TGGAGTTGCTGTATTTGCTGACCTGGGCTTACTGTTTAAATTCACAGTGAACAAATGA 1394
QY 1239 AGTTGACATACCTTGAACACAGAGGTGGGACCCAGCGGTACATGGCTCCAGAAAGTCT 1298
DB 1395 AGTTGACATACCTTGAATACAGAGGTGGGACCCAGCGGTACATGGCTCCAGAAAGTCT 1454
QY 1299 GGACAGAGCCTGAGTAAACCAATTTCCAGCCCTACATCATGGCTGACATCTACAGCTT 1358
DB 1455 GATGAAACCTGATATAAAACCAATTTCCAGCCCTACATCATGGCTGACATCTAGCTT 1514
QY 1359 TGGTTTGATCATTTGGAGATGGCCGCTGCTGTATTTACAGAGGAAATGTCGGAGAAATA 1418
DB 1515 TGGTTTGATCATTTGGAAATGGCTGCTGCTGTTGTTTACAGAGGAAATCGTGGAGAAATA 1574
QY 1419 TCAATTTACCATATTACAACATGGTGCCTAGTCACCATCTTATGAAGACATGCGTGAGT 1478
DB 1575 TCAATTTACCATATTACAACATGGTGCCTAGTACCCATCTTATGAGGACATGCGTGAGT 1634
QY 1479 CGTGTGTGAAACGCTTCGGGCCAATCGCTCTCTAACCGCTGGAACAGTGATGAATGCT 1538
DB 1635 TGTGTGTGAAACGCTTCGGGCCAATCGTGTCTAACCGCTGGAACAGTGATGAATGCT 1694
QY 1539 TCGAGCCGTTTGAAGCTGATGTAGAAATGCTGGGCCCAATAATCCAGCAATCCAGACTCAC 1598
DB 1695 TCGAGCAGTTTGAAGCTAATGTAGAAATGTTGGGCCCAATAATCCAGCCTCCAGACTCAC 1754
QY 1599 AGCTTTGAGAATCAAGAACACGCTCCGCAAGAGTGGTTGAATCCAGGATGTAAGATTG 1658

DB 1755 AGCTTTGAGATCAAGAAGACACTTGCAGAAATGGTTGATCCAGGATGTAAGATTG 1814
QY 1659 AC---AAACAGTTTTGAGAAAGAAATTTAGACTGCAAGAAATTC-----ACCCGAGGAAG 1710
DB 1815 ACAATTAACAATTTTGAGGGAGAAATTTAGACTGCAAGAACTTCTTCACCCCAAGGAATGG 1874
QY 1711 GTGGAGTTAGCTAGCACTAGGATGCGGCTTGGTTTCCAGACTCTCTCTCTACCATCTT 1770
DB 1875 GTGGAGTTAGCATGGAATAGGATGTTGACTTGGTTTCCAGACTCTCTCTCTA-CATCTT 1933
QY 1771 CACAGCTGCTAAACAGTAAACCTTTCCAGACTCTCTCAGAATGC 1813
DB 1934 CACAGCTGCTAAACAGTAAACCTTACCCTACTCTTACAGAATAC 1976

RESULT 11
US-09-742-153-11
; Sequence 11, Application US/09742153
; Publication No. US20030096296A1
; GENERAL INFORMATION:
; APPLICANT: Rosenbaum, Jan S
; TITLE OF INVENTION: The Use of a BMP Protein Receptor
; ; Complex for Screening Bone Metabolism Actives and Cells
; ; Co-Transfected with a Type II BMP Receptor and a Type I
; ; BMP Receptor
; ;
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Procter & Gamble Company
; STREET: 11810 East Miami River Road
; CITY: Ross
; STATE: OH
; COUNTRY: USA
; ZIP: 45061
; ;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/742,153
; FILING DATE: 20-Dec-2000
; CLASSIFICATION: <unknown>
; ;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,467
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hersko, Bart S.
; REGISTRATION NUMBER: 32,572
; REFERENCE/DOCKET NUMBER: 5474R
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 627-0633
; TELEFAX: (513) 627-0260
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2402 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-742-153-11

Query Match 86.8%; Score 1574.2; DB 3; Length 2402;
Best Local Similarity 94.2%; Pred. No. 0;
Matches 1669; Conservative 0; Mismatches 93; Indels 9; Gaps 3;
QY 51 GAATTGGCAATGACTCAGCTATACACTTACATCAGATTACTGGAGGCTGCTGTTCTAT 110
DB 1 GAATCAGACAATGACTCAGCTATACACTTACATCAGATTACTGGAGGCTGCTGTTCTAT 60
QY 111 CATTTCTCATGTTCAAGGGCAGAACTCTAGATAGTATGCTCCATGGTACTGGTATGAAATC 170

Db	61	CA	TTTCTCATGTTCAAGGGCAGAAATCTAGATAGTAGTATGCTCCATGGCACTGGTATGAAATC	120
Qy	171	AG	ACGTGGACCAAGAAAGACCGGAAAAATGGAGTGAACGTTAGCACACAGAGGACACCTTACC	230
Db	121	AG	ACTTGGACCAAGAAAGCCAGAAAAATGGAGTGAACGTTAGCACACAGAGGATACCTTGCC	180
Qy	231	TTTCTTAAATTCGCTATTGCTCAGGACACTGCCCCAGATCAGCGTATTATTAACATGAT	290	
Db	181	TTTCTTAAAGTGTATTGCTCAGGACACTGCCCCAGATGATGCTATTATTAACACATGAT	240	
Qy	291	AAC	TAAATGGCCATTCGCTTTGCCATTATAGAAGACATGATCAGGGAGAGAAACCAAGTTAAC	350
Db	241	AAC	TAAATGGCCATTCGCTTTGCCATTATAGAAGACATGATCAGGGAGAGAAACCAATTAA	300
Qy	351	TTT	CGGGTATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCAAAAGCCCA	410
Db	301	TTT	CGGGTATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCGAAAGCCCA	360
Qy	411	GCT	ACGACGAGGACAATAGAAATGTTGTCGGACCAATTTGTGCAACCAATATTTGCGACGCTAC	470
Db	361	GCT	ACGACGAGGACAATAGAAATGTTGTCGGACCAATTTGTGCAACCAATATTTGCGACGCTAC	420
Qy	471	ACT	GCCCCCTGTCGTTATAGGCCCACTCTTTGATGGCAGCGCTCCGATGGCTGGCTGCT	530
Db	421	ACT	GCCCCCTGTCGTTATAGGGTCCGTTCTTTGATGGCAGCAATCGATGGCTGGTGTGCT	480
Qy	531	CAT	CTCTATGGCTGCTCTGTTATGTGCCCATGATCGTCTTCTCCAGCTGCTTCTGTATCAA	590
Db	481	CAT	TTCCATGGCTGCTGTATAGTTGCTATGATCATCTTCTCCAGCTGCTTCTGTATCAA	540
Qy	591	AC	ATTACTGTAAAGAGTATCTCAAGCAGAGGTGCTTACAAACCGTGACTTTGGAAACAGGATGA	650
Db	541	GCA	TATTGTAAAGAGTATCTCAAGCAGGGGTGCTTACAAACCGTGACTTTGGAAACAGGATGA	600
Qy	651	AG	CATTATTCCAGCTAGAGAAATCACTGAAAGACCTGATTACACAGCTCACAAGCTCTGG	710
Db	601	AG	CATTATTCCAGTAGAGAAATCATTTGAAAGACCTGATTACACAGCTCCCAAGCTCTGG	660
Qy	711	TAG	TGGATCTGGATTACCTTTATTTGGTTTCAGCGAACTATTGCCAAAACAGATTTCAGATGGT	770
Db	661	GAG	TGGATCTGGATTGCTTTATTTGGTTTCAGCGAACTATTGCCAAAACAGATTTCAGATGGT	720
Qy	771	TCG	CAGGTTGGTAAGGCCGGTATGGAGAAAGTATGGATGGGTAAATGGCGTGGTGAAAA	830
Db	721	TCG	CAGGTTGGTAAGGCCCGCTATGGAGAAAGTATGGATGGGTAAATGGCGTGGTGAAAA	780
Qy	831	AGT	GGCTGTCAAAGTATTTTTTACCAGTGAAGAGCTAGCTGGTTTAGAGAAAACAGAAAT	890
Db	781	AGT	GGCTGTCAAAGTATTTTTTACCAGTGAAGAGCTAGCTGGTTTAGAGAAAACAGAAAT	840
Qy	891	CTA	CCAGACGGTGTAAATGCGTCAATGAAAAATATACTTGGTTTTATAGCTGCAGACATAA	950
Db	841	CTA	CCAGACGGTGTAAATGCGTCAATGAAAAATATACTTGGTTTTATAGCTGCAGACATAA	900
Qy	951	AGG	CAACCGGTTCTCGACTCAGCTGTATTTGATTACTGATTACCATCAGAAATGGGCTCTCT	1010
Db	901	AGG	CACTGGTTCTCGACTCAGCTGTATTTGATTACTGATTACCATCAGAAATGGGATCTCT	960
Qy	1011	CTA	TGACTTCTGAAATGTCGCCCTCGGACACAGAGCCCTACTCAAGTTAGCTTATTC	1070
Db	961	CTA	TGACTTCTGAAATGTCGCCCTCGGACACAGAGCCCTACTCAAGTTAGCTTATTC	1020
Qy	1071	TG	CTGCTGTGCTGTGTCACCTCCACACAGAAATTTATGGCACGCAAGCGACGCTGC	1130
Db	1021	TG	CTGCTGTGCTGTGTCACCTCCACACAGAAATTTATGGTATCCCAAGGGAAGCGCTGC	1080
Qy	1131	AA	TGTCTCATCGAGACCTGAAGACGCAAAAAACATCCTTATTAAAGAAAAATGGTAGTTCGT	1190
Db	1081	AA	TGTCTCATCGAGACCTGAAGACGCAAAAAACATCCTTATTAAAGAAAAATGGTAGTTCGT	1140
Qy	1191	TAT	TGTGACCTCGGCTAGCTGTTAAATTTCAACAGTGACACAAATGAAGTTGACATACC	1250
Db	1141	TAT	TGTGACCTCGGCTAGCTGTTAAATTTCAACAGTGACACAAATGAAGTTGACATACC	1200

QY	1251	CTTGAAACAC	CAGGCTGGGCAC	CCAGGCGGTA	CATGGCTCC	AGAAAGT	GTGCA	CAGAGCCT	13110
DB	1201	CTTGAATAC	CAAGGCTGGGCAC	CCAGGCGGTA	CATGGCTCC	AGAAAGT	GTGCA	GAAGCCT	12660
QY	1311	GAGTAAAAA	CCATTTTC	CAGCCCTAC	ATCATCGGCT	GCATCAT	CACAGCT	TTTGGTTTGATCAT	13700
DB	1261	GAATAAAAA	CCATTTTC	CAGCCCTAC	ATCATCGGCT	GCATCAT	CTATAGCT	TTTGGTTTGATCAT	13200
QY	1371	TTGGGAGAT	GGCCCGT	CGCTGTAT	TTACAGGAG	GAATCGT	GGAGGAAT	TATCAAT	14300
DB	1321	TTGGGAAAT	GGCTCGT	CGTTGTTAT	TACAGGAG	GAATCGT	GGAGGAAT	TATCAAT	13800
QY	1431	TTACAA	CATGCTAGT	GACCCATCT	TATGAAG	ACATCGCT	GTGAGGT	CGTGTGTGA	14900
DB	1381	TTACAA	CATGCTG	CCCACTAGT	ACCCATCTT	ATGAGG	ACATCGCT	GTGAGGT	14400
QY	1491	ACGCTT	CGGCCAAT	CGTCTTA	ACCGCT	GGAAACAGT	GAATGCT	CTTCGAGCCGCTTT	15500
DB	1441	ACGCTT	CGGCCAAT	CGTGTCTTA	ACCGCT	GGAAACAGG	ATGAATGCT	CTTCGAGCAGT	15000
QY	1551	GAAGCT	GATGT	CAGAAAT	GTCTGGG	CCCATTA	TCCAGCA	CTCCAGACT	16100
DB	1501	GAAGCT	TAATGT	CAGAAAT	GTCTGGG	CCCATTA	TCCAGCT	CTCCAGACT	15600
QY	1611	CAAGA	ACACGCT	CGCAAA	AGATGGT	TGAATCC	CAAGAT	GTAAAGAT	16660
DB	1561	CAAGA	ACACACT	TTGC	AAAAATGGT	TGAATCC	CAAGAT	GTAAAGAT	16200
QY	1667	TTTTT	GAAAGAA	TTT	TAGACT	GC	CAAGAAATTC	---ACCGGAG	17220
DB	1621	TTTTT	GAGGAGAA	TTT	TAGACT	GC	CAAGAAATTC	---ACCGGAG	16800
QY	1723	TGGACT	AGGAT	GTGCGG	CTTGGTT	TTCCAG	ACTCTCT	CTCTACC	17820
DB	1681	TGGAA	TAGGAT	GTGACT	TTGGTT	TTCCAG	ACTCTCT	CTCTACC	17390
QY	1783	ACAGT	AAACCTTT	CAGGAC	CTCTCG	AGAA	TGC		18130
DB	1740	ACAGT	AAACCTTT	ACCG	CACCTCT	CAGAA	TATC		17700

RESULT 12

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US-10-641-319-3
; Sequence 3, Application US/10641319
; Publication No. US20040143863A1
; GENERAL INFORMATION:
; APPLICANT: Li, Linheng
; APPLICANT: Zhang, Jwang
; TITLE OF INVENTION: Hematopoietic Stem Cell Niche Cells
; FILE REFERENCE: 64928
; CURRENT APPLICATION NUMBER: US/10/641,319
; CURRENT FILING DATE: 2003-08-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 2056
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-641-319-3

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Query Match	78.6%	Score 1424.4	DB 7	Length 2056
Best Local Similarity	90.3%	Pred. No. 0		
Matches 1584	Conservative	0	Mismatches	76
			Indels	94
			Gaps	2

QY	39	CAGGACACGTCGGCAATTTGGACAATGACTCAGCTATACACTTACATCAGATTACTGGAGC	98
DB	269	CAGGACGCTGCGCAATTCAGACAATGACTCAGCTATACACTTACATCAGATTACTGGAGC	328
QY	99	CTGTCTGTTTCATCATTTCTCATGTTTCAAGGGCAGAACTCAGATAGTAGTCTCCATGGTAC	158
DB	329	CTGTCTGTTTCATCATTTCTCATGTTTCAAGGGCAGAACTCAGATAGTAGTCTCCATGGGAC	388

Qy	159	TGGTATGAATACAGACGTGGACAGAGAAGCCGGAAAAATGGAGTGAAGTATAGCACGAGA	218
Db	389	TGGTATGAATACAGACTTGGACCAAGAAGAAGCCAGAAAAATGGAGTGAAGTATAGCACGAGA	448
Qy	219	GGACACCTTACCTTCTTAAATGCTATTCGTCTAGGACACTGCCACAGATGATGATGCTATTA	278
Db	449	GGATACCTTGGCTTCTTAAAGTGCTATTCGTCTAGGACACTGCCACAGATGATGCTATTA	508
Qy	279	TAAACATGCAATAACTAATGGCCATTCGTTTGGCCATTATAGAAGAAAGATGATCAGGAGGA	338
Db	509	TAAACATGCAATAACTAATGGCCATTCGTTTGGCCATTATAGAAGAAAGATGATCAGGAGGA	568
Qy	339	AACACAGTTTAACCTCTGGGTGTGAAGATATGAAGGCTCTGATTTTCAATGCAAGGATTC	398
Db	569	AACACATTTAACTTCTGGGTGTGAAGATATGAAGGCTCTGATTTTCAATGCAAGGATTC	628
Qy	399	ACCAAGGCCAGCTACGCAGGACCAATAGATGTTGTCGACCAAAATTTGTGCACCAATTA	458
Db	629	ACCAAGGCCAGCTACGCAGGACCAATAGATGTTGTCGACCAAAATTTGTGCACCAATTA	688
Qy	459	TTTGCAGCTACACTGCCCTCGTTTATAGGCCCATTTCTTGATGCGCAGCGTCCGATG	518
Db	689	TTTGCAGCTACACTGCCCTCGTTTATAGGCCCATTTCTTGATGCGCAGCATCCGATG	748
Qy	519	GCTGGCTGTGCTCATCTATPGCTGTCTGTATTTGTGCGCATGATGCTTTCTCCAGCTG	578
Db	749	GCTGGTGTGCTCATTTCCATGGCTGTCTGTATAGTTGCTATGATCATCTTCTCCAGCTG	808
Qy	579	CTTCTGTTTACAAACATTACTGTAGAGTACTCAAGCAGAGGTCGTTTACAACCGTGACTT	638
Db	809	CTTCTGCTATGAAGCATTTATTCAGTAGAGATCTCAAGCAGGCGTGTATCAACCGTGATTT	868
Qy	639	GGAAACAGGATGAAGCATTTATTCAGTAGAGAAATCACTGAAGACCTGATGACCAAGTC	698
Db	869	GGAAACAGATGAAGCATTTATTCAGTAGAGAAATCACTGAAGACCTGATGACCAAGTC	928
Qy	699	ACAAAGCTCTGGTATGATGGAATCCTGTTATGTTTACGCGAACTATGCCAAACA	758
Db	929	CCAAAGCTCTGGAGTGGATCTGATTTGCCCTTTATTTGTTTCAAGCAACTATTTGCCAAACA	988
Qy	759	GATTCAGATGGTTCCGACAGGTTGTTAAGGCCGCTATGGAAGAGTATGGAATGGTAAATG	818
Db	989	GATTCAGATGGTTCCGACAGGTTGTTAAGGCCGCTATGGAAGAGTATGGAATGGTAAATG	1048
Qy	819	CGCTGGTGAAGAGTGGCTGTCAGAAATATTTTTTACCACCTGAAGAGCTAGCTGGTTTAC	878
Db	1049	CGCTGGTGAAGAGTGGCTGTCAGAAATATTTTTTACCACCTGAAGAGCTAGCTGGTTTAC	1108
Qy	879	AGAAACAGAAATCTACACAGCGGTGTTAATGCGTCATGAAATATATCTTGGTTTTATAGC	938
Db	1109	AGAAACAGAAATCTACACAGCGGTGTTAATGCGTCATGAAATATATCTTGGTTTTATAGC	1168
Qy	939	TGCAGACATTTAAGGACACCGGTTCTCGACTCAGCTGTATTTGATTTACTGATTTACATGA	998
Db	1169	TGCAGACATTTAAGGACACCGGTTCTCGACTCAGCTGTATTTGATTTACTGATTTACATGA	1228
Qy	999	GAATGGGTCTCTATGACTTTCCTGAAATGTGCCACCTCGACACACAGAGCCCTACTCAA	1058
Db	1229	AAATGGATCTCTATGACTTTCCTGAAATGTGCCACCTAGACACACAGAGCCCTACTCAA	1328
Qy	1059	GTTAGCTTATTTCTGCTGCCTGTGCTGTGCCACCTCCACACAGAAATTTTATGGCAGCA	1118
Db	1289	GTTAGCTTATTTCTGCTGCCTGTGCTGTGCCACCTCCACACAGAAATTTTATGGTACCCA	1348
Qy	1119	AGGCAAGCTGCAATTCGCTCATCGAGACCTTGAGAGCAAAAACATCTTATTTAAGAAAAA	1178
Db	1349	AGGCAAGCTGCAATTCGCTCATCGAGACCTTGAGAGCAAAAACATCTTATTTAAGAAAAA	1408
Qy	1179	TGGTAGTTCGTATTCGTCACCTGGCCCTAGCTGTTAAATTCAAACAGTCACCAATGA	1238
Db	1409	TGGAAGTTCGTATTCGTCACCTGGCCCTAGCTGTTAAATTCAAACAGTCACCAATGA	1468
Qy	1239	AGTTGACATACCCCTTGAACACACCGGTTGGGACCCAGCGCGGTACATGCTCCAGAAAGTCT	1298

Db	1469	AGTTGACATACCTTGAATACCAAGGTGGGCAACCAAGCGGTACATGGCTCCAGAAGTGCT	1528
Qy	1299	GGACGAGAGCCTCAGATAAAACCATTTCCAGCCCTACATCATGGCTGACATCTTACAGCTT	1358
Db	1529	GGATGAAGGCTCGAATAAAACCATTTCCAGCCCTACATCATGGCTGACATCTTATAGCTT	1588
Qy	1359	TGCTTTGATCATTTGGAGATGGCCGTCCTCTATTTCAGAGAGGAATCGTGAGGAATA	1418
Db	1589	TGCTTTGATCATTTGGGAATGGCTCGTCTGTATTACAGAGGGAATCGTGAGGAATA	1648
Qy	1419	TCAATTACCATATTACAACATGGTGGCTAGTGACCCATCTTATGAAGACATGCGTGAGGT	1478
Db	1649	TCAATTACCATATTACAACATGGTGGCCAGTGACCCATCCTATGAGGACATGCGTGAGGT	1708
Qy	1479	CGTGTGTGTAACCGTTGGGGCAATCGTCTCTAACCGCTGGAACAGTGATGAA-----	1533
Db	1709	TGTGTGTGTAACCGTTGGGGCAATCGTGTCTTAACCGCTGGAACAGCGATGAAGTAAG	1768
Qy	1534	-----TGCTTTTCGAGCGCTTTTGAAGCTGATGCGGAGTTACTCTGTGCTCACCACAC	1593
Db	1769	TTGGAGCAAGTCCCTGTAAAGTGATGAGTGAGTGCGGAGTTACTCTGTGCTCACCACAC	1828
Qy	1534	-----TGCTTTTCGAGCGCTTTTGAAGCTGATGCGGAGTTACTCTGTGCTCACCACATG	1568
Db	1829	TCGTGTTGCAATTAATTTCTCTTAGTGTCTTCGAGCAGTTTTGAAGCTAATGTCAGAATG	1888
Qy	1569	CTGGGCCATAATCCAGCATCCAGATCCAGATCTTCAGAGTTTGAAGTCAAGAAGACGCTGCAGAA	1628
Db	1989	TTGGGCCATAATCCAGCCTCCAGATCCAGATCTTCAGAGTTTGAAGTCAAGAAGACATTCGAAA	1948
Qy	1629	GATGGTTGAATCCAGAGTGAAGATTTGAC-----AAACAGTTTTGAGAAAGAAATTTAG	1684
Db	1949	AATGGTTGAATCCAGGATGAAGATTTGACAAATTAACAAATTTTGAAGGGGAAATTTAG	2008
Qy	1685	ACTGCAAGAAATTC	1698
Db	2009	ACTGCAAGAACTTC	2022

RESULT 13

US-09-903-068-5
 ; Sequence 5, Application US/09903068
 ; Patent No. US20020123139A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
 ; Franzen, Petra; Yamashita, Hidetoshi; Helden, Carl-Henrik
 ; TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Felfe & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York City
 ; STATE: New York
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
 ; COMPUTER: IBM
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: Wordperfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/903,068
 ; FILING DATE: 11-Jul-2001
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/679,187
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: PCT/GB93/02367
 ; FILING DATE: 17-No. US20020123139A1ember-1993
 ; APPLICATION NUMBER: 9224057.1
 ; FILING DATE: 17-No. US20020123139A1ember-1992
 ; APPLICATION NUMBER: 9304677.9
 ; FILING DATE: 8-March-1993

APPLICATION NUMBER: 9304680.3
FILING DATE: 8-March-1993
APPLICATION NUMBER: 9311047.6
FILING DATE: 28-May-1993
APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
APPLICATION NUMBER: 9136099.2
FILING DATE: 3-August-1993
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2932 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 310..1905
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-903-068-5

Query Match 76.5%; Score 1387; DB 3; Length 2932;
Best Local Similarity 87.8%; Pred. No. 0;
Matches 1561; Conservative 0; Mismatches 205; Indels 11; Gaps 4;

QY 39 CAGGACGTCGCAATGGCAATGACTCAGCTATACACTATACAGATTACTGGAGC 98
DB 288 CAGGAACAATTAACAATGAACAATGACTCAGCTATACACTATACAGATTATGGAGC 347
QY 99 CTGCTGTTTCATCATTTCTCATGTTCAAGGGCAGAACTAGATAGTATGCTCCATGGTAC 158
DB 348 CTATTTGTTTCATCATTTCTCGTGTTCAGGACAGAACTCGGATAGTATGCTTCATGGCAC 407
QY 159 TGTGTATGAATCAGACGTGGACAGAGAAAGCGGAAATGGAGTACGCTTAGCACCA 218
DB 408 TGGGATGAATCAGACTCCGACAGAAAGAGTCAAGAAATGGAGTAACTTAGCACCA 467
QY 219 GGACACCTTACCTTTCTTAATGCTATTGCTCAGGACACTGCCAGATGACGCTATTAA 278
DB 468 GGATACCTTGCCCTTTTAAAGTGTATTGCTCAGGGCACTGTCCAGATGATGCTATTAA 527
QY 279 TAACACATGATTAACATAAGCCATTGCTTTGCCATTATAGAAGAAAGATGATCAGGAGA 338
DB 528 TAACACATGATTAACATAAGCACTTTGCTTGCATCATAGAAGAAAGATGATCAGGAGA 587
QY 339 AACCACTTAACCTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTC 398
DB 588 AACCACTTAAGCTTCAGGGTGTATGAATATGAAGATCTGATTTTTCAGTGCAGAAATTC 647
QY 399 ACCAAAGCCAGCTACGAGGACAAATAGAAATGTTGTCGACCAATTTGTCNAACCAATA 458
DB 648 TCCAAAGCCAGCTACGCGGACAAATAGAAATGTTGTCGACCAATTTATGTAACCAATA 707
QY 459 TTTCAGGCTTACACTGCCCCCTGCTGTTATAGGCCCAATTTTTCAGTGGCAGGCTCCGATG 518
DB 708 TTTCAGAACCACTGCCCCCTGCTGTTATAGTCCGTTTTCAGTGGCAGGATTCGATG 767
QY 519 GCTGGCTGTCTCATCTCTATGCTGTCTGTATTTGTGCCATGATCGTCTTCTCCAGCTG 578

DB 768 GCTGGTTTTGCTCATTTCTATGGCTGTCTGCAATAATTGCTATGATCATCTTCTCCAGCTG 827
QY 579 CTTCTGTTACAACACATTACTGTAAGAGTATCTCAAGCAGAGGTCGTTACAAACGTCGATTT 638
DB 828 CTTTCTGTTACAACACATTACTGTAAGAGTATCTCAAGCAGAGGTCGTTACAAACGTCGATTT 887
QY 639 GGAAACAGGATGAAGCAATTTATTCAGTAGGAGAAATCACTGAAAGACCTGATTTACCAAGTC 698
DB 888 GGAACAGGATGAAGCAATTTATTCAGTAGGAGAAATCACTGAAAGACCTTATTCACCAAGTC 947
QY 699 ACAAGCTCTGTTAGTGGATCTGGATATCTTTATTTGGTTTTCAGGAACTATTTGCCAAACA 758
DB 948 ACAAGCTCTGTTAGTGGGTCCTGACTACCTTTATTTGGTTTTCAGGAACTATTTGCCAAACA 1007
QY 759 GATTACAGATGTTTCGGCAGGTTGGTAAGGCGGATGGAGAGTATGGATGGTAAATG 818
DB 1008 GATTACAGATGTTTCGGCAGGTTGGTAAGGCGGATGGAGAGTATGGATGGTAAATG 1067
QY 819 GCCTGCTGAAAAAGTGGCTGTCAAAGTATTTTTTACCACCTGAAGAAAGTACGTGGTTTAG 878
DB 1068 GCGTGGCGAAAAAGTGGCGGTGAAAGTATTTTACCACCTGAAGAAAGTACGTGGTTTAG 1127
QY 879 AGAAACAGAAATCTACCAGACGGTGTAAATGCGTCTATGAAATATATATCTGGTTTTATAGC 938
DB 1128 AGAAACAGAAATCTACCAGAACTGTCTAATGCGCCATGAAACATATCTGGTTTTATAGC 1187
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DB 1188 GGCAGACATTTAAAGGTACAGGTTCTCGGACTCAGCTCTATTTGATTTACTGATTACCATGA 1247
QY 999 GAATGGGTCTCTCTATGACTTCTCTGAAATGTGCCACCTGGACACAGAGCCCTACTCAA 1058
DB 1248 AATGGATCTCTATGACTTCTCTGAAATGTCTACACTGGACACAGAGCCCTGCTTAA 1307
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DB 1308 ATTGGCTTATTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1367
QY 1119 AGGCAAGCTCGAATTTGCTCATCGAGACCTGAAGAGCAAAACATCTTTATTAAGAAAA 1178
DB 1368 AGGAAGCCCGCAATTTGCTCATCGAGACCTTAAGAGCAAAACATCTTTATTAAGAAAA 1427
QY 1179 TGTGATGTTGCTGTTATTTGCTGACTGCGGCTAGCTGTTAAATTTCAACAGTGACACAAATGA 1238
DB 1428 TGGGAGTGTCTGCAATTTGCTGACTGCGGCTTCTGCTGTTAAATTTCAACAGTGACACAAATGA 1487
QY 1239 AGTTGACATACCTTTGAAACACAGAGGTGGGCAACAGGCGGTATCATGGCTCCAGAGTGTCT 1298
DB 1488 AGTTGATGTGCTCTTGAATACAGAGGTGGGCAACAGGCTATCATGGCTCCGAGTGTCT 1547
QY 1299 GGACGAGAGCTGAGTTAAACCAATTTCCAGCCCTACATCATGGCTGACATCTACAGCTT 1358
DB 1548 GGACGAGAGCTGAGTTAAACCAATTTCCAGCCCTACATCATGGCTGACATCTACAGCTT 1607
QY 1359 TGTGTTGATCATTTGGGAGATGGCCCGTCTGCTGTTATTAAGAGGAATCGTGAGGAATA 1418
DB 1608 CGGCTTAATCATTTGGGAGATGGCTGCTGCTGTTATTAAGAGGAATCGTGAGGAATA 1667
QY 1419 TCAATTAACATATTAACATCGTGTAGTACCCATCTTTATGAAGAATGCGTGGTGGT 1478
DB 1668 CCAATGCTCATTAACATCGTGTAGTACCCATCTCGTGTATTAAGAGGAATGCGTGGTGGT 1727
QY 1479 CGTGTGTGAAACGCTTGGGCGCAATCGTCTTAACCGCTGGAACAGTGAATGCTCT 1538
DB 1728 TGTGTGTGCAACGCTTGGGCGCAATCGTCTTAACCGCTGGAACAGTGAATGCTCT 1787
QY 1539 TCGAGCCGCTTTTGAAGCTGATGTGAGAAATGCTGGGCCCAATAATCCAGCACTCCAGCTCAC 1598
DB 1788 ACGAGCAGTTTGAAGCTAATGTGAGAAATGCTGGGCCCAATAATCCAGCTCCAGCTCAC 1847
QY 1599 AGCTTTGAGAAATCAAGAGACGCTCGCAAGATGTTGTAATCCAGGATGTAAGATTTG 1658
DB 1848 AGCATTTGAGAAATTAAGAGACGCTTGGCCAAAGATGTTGTAATCCCAAGATGTAAGATTTG 1907

QY 1539 TCAGCGCTTTTGAAGCTGATGTGAGAAATCTGGGCCATAAATCCAGACTCCAGACTCAC 1598
Db 1788 ACCGAGCAGTTTGAAGCTAATGTGAGAAATCTGGGCCACAATCCAGCTCCAGACTCAC 1847
QY 1599 AGCTTTGAGAAATCAAGAGACGCTCGCAAGATGGTTGAATCCAGAGATGAAGATTG 1658
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QY 1659 A----CAAAACAGTTTGAAGAAAGAAATTTAGACTGCAAGAA-----ATTCAACCCGAGGAAG 1709
Db 1908 ATGTTAAACCATCGGAGGAGAACTCTAGACTGCAAGAAATCTGTTTATCCCATGGCATG 1967
QY 1710 GGTGGAGTTAGCATGGACT-AGGATGTGGCTTTGGTTTCCAGACTCTCTCTC- TACCAT 1767
Db 1968 GGTGGAATTAGAGTGGAATAAGGATGTTAACTTTGGTTCTCAGACTCTCTTCTTCACTACGT 2027
QY 1768 CTTTCAGAGCTGTACAGTAAGTAACCTTTACGAGACTCT 1804
Db 2028 GTTCACAGGCTGCTAATATTAAACCTTTTCAGTACTCT 2064

RESULT 15
US-10-286-152A-37
; Sequence 37, Application US/10286152A
; Publication No. US20030134308A1
; GENERAL INFORMATION:
; APPLICANT: Alcon Research, Ltd.
; APPLICANT: Clark, Abbot F.
; TITLE OF INVENTION: Bone Morphogenic Proteins (BMP), BMP Receptors and BMP Binding Peptides
; TITLE OF INVENTION: and Their Use in the Diagnosis and Treatment of Glaucoma
; FILE REFERENCE: 2312 US
; CURRENT APPLICATION NUMBER: US/10/286,152A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 2932
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-286-152A-37

Query Match 76.5%; Score 1387; DB 6; Length 2932;
Best Local Similarity 87.8%; Pred. No. 0;
Matches 1561; Conservative 0; Mismatches 205; Indels 11; Gaps 4;

QY 39 CAGGACAGCTGCGAAATGGCAATGACTAGCTATACACTTACATCAGATTACTGGAGC 98
Db 288 CAGGAAACATTACAATTTGAACAATGACTAGCTATACATTTACATCAGATTACTGGAGC 347
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Db 348 CTATTTGTTTCATCTTCTGTTTCAAGGACAGAAATCTGGATAGTATGCTTCATGGCAC 407
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QY 219 GGNACCTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCAGATGAGCTATTAA 278
Db 468 GGATACCTTGGCTTTTAAAGTGCTATTGCTCAGGGCACTGTCCAGATGATGCTATTAA 527
QY 279 TAACACATGCATAACTTAATGGCCATTGCTTGCATTTAGAGAGAGATGATCAGGGAGA 338
Db 528 TAACACATGCATAACTTAATGGACATTTGCTTTGCCATCATAGAAGAGATGACAGGGAGA 587
QY 339 AACACGTTAACTTCTGGGTGATGAAGTATGAAGCTCTGATTTTCAATGCAAGGATTC 398
Db 588 AACACATTAAGCTTCAGGGTGTATGAATATGAAGATCTGATTTTCACTGCAAGATTC 647
QY 399 ACCAAAGCCAGCTACGAGGAGCAATAGAAATGTTGTCGGACCAATTTGTGCAACCAATA 458
Db 648 TCCAAAGCCAGCTACGCGGAGCAATAGAAATGTTGTCGGACCAATTTATGTAAACCAATA 707

QY 459 TTTGAGCCTACACTGCCCCCTGCTGTTATAGCCCAATCTTTGATGGCAGCGTCCGATG 518
Db 708 TTTGCAACCCACACTGCCCCCTGTTGTCATAGGTCCGTTTGTGATGGCAGCATTCGATG 767
QY 519 GCTGGCTGTGCTCATCTCTATGGCTGTCTGTATGTGCGCATGATCGTCTTCTCCAGCTG 578
Db 768 GCTGGTTTGTCTCATTTCTATGGCTGTCTGCATAATTTGCTATGATCATCTTCTCCAGCTG 827
QY 579 CTTCTGTTTCAACACATTTACTGTAAAGAGTATCTCAAGCAGAGGTCGTTTACAACCGTGACTT 638
Db 828 CTTTGTGTTTCAACACATTTATTGCAAGAGCATCTCAAGCAGACGTCGTTTACAAATCGTATTT 887
QY 639 GGAACAGGATGAAGCATTTTATTCAGTAGGAGAAATCACTGAAAGAGCTGATTTACCAAGTC 698
Db 888 GGAACAGGATGAAGCATTTTATTCAGTTGAGAAATCACTTAAAGAGCTTATTGACCAAGTC 947
QY 699 ACAAGCTCTGTGTAGTGGATCTGGATTAATCTTTATTTGGTTTACGCAACTATTTCGCAAAACA 758
Db 948 ACAAGTTCTGTGTAGTGGCTGTGACTTATTTGGTTTACGCAACTATTTCGCAAAACA 1007
QY 759 GATTTCAGATGTTTCGCGCAGGTTGGTAAAGGCCGATATGAGAGAGTATGGATGGTAAATG 818
Db 1008 GATTTCAGATGTTTCGCGCAAGTTGGTAAAGGCCGATATGAGAGAGTATGGATGGCAATG 1067
QY 819 GCGTGTGAAAAAGTGGCTGTCAAAGTATTTTTTACCACCTGAAAGAGCTAGCTGGTTTAC 878
Db 1068 GCGTGGCAAAAAGTGGCGGTGAAAGTATTTTACCACCTGAAAGAGCTAGCTGGTTTAC 1127
QY 879 AGAAACAGAAATCTACAGACGGTGTAAATGCGTCTATGAAATATATCTTGGTTTATATAGC 938
Db 1128 AGAAACAGAAATCTACCAACTGTGTAATGCGCCATGAAACATATCTTGGTTTATATAGC 1187
QY 939 TGCAGACATTAAGCAGCCGCTTCTGGACTGAGCTGATTTGATTTACTGATTACCATGA 998
Db 1188 GGCAGACATTAAGAGGTACAGGTTCTGGACTGAGCTGATTTGATTTACTGATTACCATGA 1247
QY 999 GAATGGGCTCTCTATGACTTCTGAAATGTGCAACCTGGACACCCAGACCCCTACTCAA 1058
Db 1248 AATGGATCTCTATGACTTCTGNAATGTGCTACACTGGACACCCAGACCCCTGCTTAA 1307
QY 1059 GTTAGCTTATCTGTGCTGCTGTGCTGTGCGACCTTCCACAGAAATTTATGGCAGCA 1118
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QY 1119 AGCAAGCTCTCAATTTGCTCATGAGACCTGAGACCAAAACATCTTATTAAGAAATA 1178
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Db 1488 AGTTGATGTGCTTGAATATCCAGGGTGGGCAACCAACGCTACATGGCTCCGAAAGTCT 1547
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QY 1359 TGGTTTGTATCATTTGGGAGATGGCCGCTGCTGTATTACAGAGGAATCGTGAGGAAATA 1418
Db 1608 CGGCTTAATCATTTGGGAGATGGCTGCTGTGTTGATACAGAGGGGATCGTGGAAAGATA 1667
QY 1419 TCAATTACCATATTACAACATGGTGCCTTAGTACCCTCTTATGAAGACATCGCTGAGGT 1478
Db 1668 CCAATTGGCATATTACAACATGGTACCGAGTGTATCGTCTATACGAAGATATGCGTGAAGT 1727
QY 1479 CGTGTGTGAACCGTTGCGGCCAATCGTCTCTAACCGCTGGAACAGTGAATGTCT 1538
Db 1728 TGTGTGTGTAACCGTTTGGGCCAATTTGTGTCTAATCGGTGGAAACAGTGAATGTCT 1787
QY 1539 TCGAGCCGTTTTTGAAGCTGATGTGAGAAATGCTGGGCCCAATAATCCAGCATCCAGACTCAC 1598

Db	1788	ACGAGCAGTTTTGAAGCTAATGTGAGAAATGCTGGGCCCAATCCAGCCTCCAGACTCAC	1847
Qy	1599	AGCTTTGAGAAATCAAGAACGCTCGCAAGATGGTTGAATCCAGGATGTAAAGATTGG	1658
Db	1848	AGCATTGAGAAATTAAGAACGCTTGCCAAAGATGGTTGAATCCCAAGATGTAAAAATCTG	1907
Qy	1659	A----CAACAGTTTTGAGAAAGAAATTTAGACTGCAAGAA-----ATTCAACCCGAGGAAG	1709
Db	1908	ATGGTTAAACCATCGGAGGAGAAACTCTAGACTGCAAGAACTGTTTTTACCCCATGGCATG	1967
Qy	1710	GGTGGAGTTAGCATGGACT-AGGATGTCGGCTTGGTTTCCAGACTCTCTCCTC-TACCAT	1767
Db	1968	GGTGGAAATTAGAGTGGAAATAAGGATGTTAACTTGGTTCTCAGACTCTTCTTCACTACGT	2027
Qy	1768	CTTCACAGGCTGCTAACAGATAAACCTTTCAGGACTCT	1804
Db	2028	GTTACACAGGCTGCTAATATTAAACCTTTCAGTACTCT	2064

Search completed: December 9, 2005, 19:34:45
Job time : 1042 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 17:16:24 ; Search time 167 Seconds
(without alignments)
4058.673 Million cell updates/sec

Title: US-10-600-645-1

Perfect score: 1813

Sequence: 1 CTAGTGGATCCCGGGCTG.....TTCCAGGACTCTGCAGAAATGC 1813

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications NA New:*
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 - 2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
 - 3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
 - 4: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
 - 5: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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 - 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
 - 10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	154.4	8.5	2090	6	US-10-420-192-7
2	55.8	3.1	2197	6	US-10-750-185-35470
3	45.4	2.5	1481	6	US-10-750-185-39254
4	38	2.1	840	6	US-10-750-185-53450
5	36.6	2.0	193363	7	US-11-112-908-32
6	36.4	2.0	94905	7	US-11-117-187-208
7	36.4	2.0	1082144	7	US-11-117-187-211
8	35.6	2.0	82596	7	US-11-117-187-207
9	35.6	2.0	94905	7	US-11-117-187-208
10	35.6	2.0	1082144	7	US-11-117-187-211
11	35.2	1.9	1342	6	US-10-750-185-29585
12	35.2	1.9	40349	7	US-11-117-187-184
13	34.8	1.9	72600	7	US-11-117-187-206
14	33.8	1.9	150038	7	US-11-121-086-23
15	33.6	1.9	1843	6	US-10-750-185-57651
16	33.4	1.8	127340	7	US-11-112-908-35
17	33	1.8	1108	6	US-10-750-185-55126
18	32.8	1.8	2554	8	US-11-132-285-1
19	32.8	1.8	3334	8	US-11-132-285-39
20	32.8	1.8	3501	6	US-10-131-826A-37
21	32.6	1.8	2577	6	US-10-750-185-29680
22	32.6	1.8	3073	7	US-11-113-424-11
23	32.4	1.8	1464	6	US-10-750-185-64192

24	32.4	1.8	162289	7	US-11-121-086-20	Sequence 20, Appl
25	32.2	1.8	1120	6	US-10-750-185-26173	Sequence 26173, A
26	32.2	1.8	2105	7	US-11-054-385-11	Sequence 11, Appl
C 27	32	1.8	1544	6	US-10-750-185-48490	Sequence 48490, A
C 28	32	1.8	50959	7	US-11-117-187-210	Sequence 210, App
C 29	32	1.8	79122	7	US-11-117-187-200	Sequence 200, App
C 30	32	1.8	187745	7	US-11-121-086-83	Sequence 83, Appl
C 31	31.8	1.8	2291	6	US-10-750-185-39137	Sequence 39137, A
C 32	31.8	1.8	94618	7	US-11-117-187-191	Sequence 191, App
C 33	31.6	1.7	2819	8	US-11-112-944-13	Sequence 13, Appl
C 34	31.6	1.7	67088	7	US-11-117-187-186	Sequence 186, App
C 35	31.6	1.7	83391	7	US-11-117-187-189	Sequence 189, App
C 36	31.6	1.7	90336	7	US-11-117-187-195	Sequence 195, App
C 37	31.4	1.7	1514	6	US-10-750-185-55434	Sequence 55434, A
C 38	31.4	1.7	85682	7	US-11-117-187-205	Sequence 205, App
C 39	31.4	1.7	189252	7	US-11-121-086-54	Sequence 54, Appl
40	31.4	1.7	611587	7	US-11-117-187-209	Sequence 209, App
41	31.2	1.7	827	6	US-10-750-185-40032	Sequence 40032, A
C 42	31.2	1.7	1210	6	US-10-750-185-52435	Sequence 52435, A
C 43	31.2	1.7	3546	6	US-10-793-626-4326	Sequence 4326, Ap
C 44	31	1.7	1701	6	US-10-750-185-44445	Sequence 44445, A
C 45	31	1.7	1884	6	US-10-750-185-58049	Sequence 58049, A

ALIGNMENTS

RESULT 1

US-10-420-192-7
; Sequence 7, Application US/10420192
; Publication No. US20050260579A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Herbert Y.
; APPLICANT: Wang, Xiao-Fan
; APPLICANT: Weinberg, Robert A.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded Products and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 0399.1086-022
; CURRENT APPLICATION NUMBER: US/10/420,192
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US 09/584,929
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 08/446,936
; PRIOR FILING DATE: 1995-05-23
; PRIOR APPLICATION NUMBER: US 08/311,703
; PRIOR FILING DATE: 1994-09-23
; PRIOR APPLICATION NUMBER: US 07/786,063
; PRIOR FILING DATE: 1991-10-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2090
; TYPE: DNA
; ORGANISM: genomic
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (336)...(2038)
US-10-420-192-7

Query Match	8.5%;	Score 154.4;	DB 6;	Length 2090;
Best Local Similarity	50.8%;	Pred. No. 2.4e-40;		
Matches	396;	Conservative	0;	Mismatches 381; Indels 3; Gaps 1;
QY	825	TGAAAAGTGGCTGTCAAAAGTATTTTTTACCACTGAAGAAGCTAGCTGGTTTAGAGAAC	884	
Db	1148	TGAGACAGTGGCAGTCAAGATCTTCCCTATGAGGAGTATGCCCTCTTGAAGACACAGAA	1207	
QY	885	AGAAATCTACACAGACGGTGTAAATGCGTCATGAATAATATCTGGTTTATAGCTCAGA	944	
Db	1208	GGACATCTTCTCAGACATCAATCTGAAGCATGAGACATACCTCCAGTCTCCTGACGGCTGA	1267	
QY	945	CATTAAGGCACCGGTTCTGGGACTCAGCTGTATTGATTACTGATTACCATGAGATGG	1004	

Db	1268	GGAGCGAAGACGAGTTGGGGAACAATACTGGCTGATCAGCGCTTCCACGCCAAGG	1327
Qy	1005	GTCTCTATGACTTCTGAAATGTGCCACCTGGACACGAGACCCCTACTCAAGTTAGC	1064
Db	1328	CAACCTACAGAGTACCTGACCGGCATGTCACTAGCTGGGAGACCTGCGAAGCTGG	1387
Qy	1065	TTATTCTGCTGCTGTGGTCTGTGCGCACTCCACACAG---AAATTATGGCAGCAAGG	1121
Db	1388	CAGCTCCCTCGCCGGGGATTGCTCACTCCACAGTGATCACACTCCATGTGGGAGCC	1447
Qy	1122	CAAGCCTGCAATTGCTCATCGAGACCTGAAGAGCAAAAACATCCTTATTAAAGAAAATGG	1181
Db	1448	CAAGATGCCCATCTGCACAGGGACCTCAAGAGCTCCAATATCTCTGTGAAGAACGACCT	1507
Qy	1182	TAGTTGCTGTATTGCTGACCTGGGCCCTAGCTGTTTAAATTCAACAGTGACACAAATGAAGT	1241
Db	1508	AACCTGTGCTGTGTGACTTTTGGGCTTTCCTCGCTCGAGCCCTACTCTGTCTGTGGA	1567
Qy	1242	TGACATACCCCTTTGAACACCGAGGTGGCACCGCGGTACATGCTCCAGAGTGCTGGA	1301
Db	1568	TGACTGGCTAAACAGTGGCGAGTGGAACTGCAAGATACATGGCTCCAGAGTCTTAGA	1627
Qy	1302	CGAGAGCCTGAGTAAAAACCAATTTCCAGCCCTACATCATGGCTGACATCTACAGCTTTGG	1361
Db	1628	ATCCAGGATGAATTTGGAGAATGTGTAGTCCCTTCAAGCAGACCCGATGCTACTCCATGGC	1687
Qy	1362	TTTGATCATTTGGGAGATGGCCCTCGCTGTATTACAGGAGGAATCTGTGAGGAATATCA	1421
Db	1688	TCTGGTGCTCTGGGAATGACATCTCGCTGTAACTGAGTGGGAGAGTAAAGATTATGA	1747
Qy	1422	ATTAACCATATTAACAATGTGTGCTTGTGACCCCATCTTATTGAAGACATGCGTGAGGTCTG	1481
Db	1748	GCCTCCATTTTGGTTTCCAAAGTGTGCGGGAGACCCCTGTGTGTGAAAGCATGAAGACACGT	1807
Qy	1482	GTGTGTGAACCGCTTGGCGGCAATCGTCTTAACCGCTGGAAACAGTGCATGAATGCTCTCG	1541
Db	1808	GTTGAGAGATCGAGGGCGAACCAAGAAATTCAGAGTCTTGCTCAACCAACAGGGCATCCA	1867
Qy	1542	AGCCGTTTTGAAGCTGATGTGAGAAATGCTGGGCCCAATAATCCAGCATCCAGATCCACAGC	1601
Db	1868	GATGGTGTGTGACACGTTTGAAGTGTGTGGGACACGACCCAGAGGCCCGTCTTCACAGC	1927

RESULT 2

RESULT 2	Query Match	2.5%	Score 45.4;	DB 6;	Length 1481;
US-10-750-185-35470/c	Best Local Similarity	65.0%;	Pred. NO. 0.00023;		
; Sequence 35470, Application US10750185	Matches	67;	Conservative	0;	Mismatches 36;
; Publication No. US20050260603A1				Indels	0;
				Gaps	0;

[illegible]

RESULT 3

```

US-10-750-185-39254/c
; Sequence 39254, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFIELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 39254
; LENGTH: 1481
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-39254

```

QY	292	ACTAATGGCCATTCGCTTTGCCATTATAGAAAGATGATCAGGAGAGAAA	CCACGCTTAACT	351
DB	406	ACAGATGGATATTGTTTTACGATGATAGAAAGATGACTCTGGGATGCCCGTGGTCACT		347
QY	352	TCTGGGTGTATGAAGTAGTGAAGGCTCTGATTTTCAATGCAAGG		394
DB	346	TCTGGATGTTCTAGGACTAGAAGGCTCAGATTTTCAGTGTGGG		304

RESULT 4

```

RESDU1 4
US-10-750-185-53450
; Sequence 53450, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31

```

Query Match 3.1%; Score 55.8; DB 6; Length 2197;
Best Local Similarity 56.1%; Pred. No. 1.1e-07;
Matches 105; Conservative 0; Mismatches 82; Indels 0; Gaps 0;


```
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53450
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Bovine 1986680986810
US-10-750-185-53450

Query Match      2.1%; Score 38; DB 6; Length 840;
Best Local Similarity 53.3%; Pred. No. 0.044;
Matches 80; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 884 CAGAAATCTACAGACGGTGTAAATCGCTCATGAATAATATATCTGGTTTATAGCTGCAG 943
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  490 CATAAATTTATTATTCATTTTGTGATAATTAATGAAGTAAACATGAGATTATAGATAAAA 549

QY 944 ACATTAAGGACCGGTTCTCGACTCAGCTGTATTTGATTACTGATTACCATGAGAATG 1003
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  550 ACTTCTAAATTTCTCAATTTTTTTAGGCGCTTCACTCAATTTACTACAAACATAAAATC 609

QY 1004 GGTCTCTATGACTTCTGAAATGTGCCA 1033
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  610 CTGCTCTTGATTTTAAAGGAAATTTGTCA 639

RESULT 5
US-11-112-908-32
; Sequence 32, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32
; LENGTH: 193363
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-32

Query Match      2.0%; Score 36.6; DB 7; Length 193363;
Best Local Similarity 54.0%; Pred. No. 5.7;
Matches 75; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1317 AAACATATTCAGCCCTACATCATGCGTGCATCTACAGCTTTGGTTTGATCATTTGGGA 1376
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  11115 AGACTTTTGGCTTCTCGACAGTAGTCATTTCTCTAAAGGCGAGCAATTCATTTATCTGA 111174

QY 1377 GATGGCCGTCGCTGTATTACAGAGGAATCGTGAGGATATATCAATTACCATATTACAA 1436
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  111175 AATGGTTAGTCTTTGATAAATTTTAATGAATCTCTGGAAACCTCTATTATCTCTCCAA 111234

QY 1437 CATGGTGCCTTAGTGACCCA 1455
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  111235 GATGCTGCCCTTAARACCA 111253

RESULT 6
US-11-117-187-208
```

```
; Sequence 208, Application US/11117187
; Publication No. US20050266560A1
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; APPLICANT: COPENHAVER, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD:309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/09/531,120
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 208
; LENGTH: 94905
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-208

Query Match      2.0%; Score 36.4; DB 7; Length 94905;
Best Local Similarity 57.4%; Pred. No. 4;
Matches 85; Conservative 0; Mismatches 61; Indels 2; Gaps 1;

QY 1588 TCCAGACTCACAGCTTTGAGAATCAAGACACGCTCGCAAGATGGTTGATCCAGAT 1647
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  10482 TACACCATCAAGCTTTGAGAAGCAATAAGAAAGCTTGGTTAGTGTGTTGGAGTCAAAAT 10541

QY 1648 GTAAAGATTTGACAAACAGTTTTGAG--AAAGAATTTAGACTGCAAGAAATTCACCCGAG 1705
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  10542 GAGTAGATGTCATTTATATGATTGAGTATAGAACTAGAACCGCAACCAATTCCTCAAAG 10601

QY 1706 GAAGGTGGAGTTAGCATGGACTAGGAT 1733
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  10602 CTAAGTAGTAGTATTTCTCTGTTAGAGAT 10629

RESULT 7
US-11-117-187-211/c
; Sequence 211, Application US/11117187
; Publication No. US20050266560A1
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; APPLICANT: COPENHAVER, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD:309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/09/531,120
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 211
; LENGTH: 1082144
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-211

Query Match      2.0%; Score 36.4; DB 7; Length 1082144;
Best Local Similarity 57.4%; Pred. No. 21;
Matches 85; Conservative 0; Mismatches 61; Indels 2; Gaps 1;

QY 1588 TCCAGACTCACAGCTTTGAGAATCAAGACACGCTCGCAAGATGGTTGATCCAGAT 1647
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  1071663 TACACCATCAAGCTTTGAGAAGCAATAAGAACTAGAACTGTTGTTGGAGTCAAAAT 1071604

QY 1648 GTAAAGATTTGACAAACAGTTTTGAG--AAAGAATTTAGACTGCAAGAAATTCACCCGAG 1705
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  1071603 GAGTAGATGTCATTTATATGATTGAGTATAGAACTAGAACCGCAACCAATTCCTCAAAG 1071544
```

QY 1706 GAAGGTGGAGTTAGCATGGACTAGGAT 1733
DB 1071543 CTAAGTAGTATTTCCTCTGTTAGAGAT 1071516

RESULT 8

US-11-117-187-207/c
; Sequence 207, Application US/11117187
; Publication No. US20050266560A1
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; APPLICANT: COPENHAVER, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD:309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/09/531,120
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 207
; LENGTH: 82596
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-207

Query Match 2.0%; Score 35.6; DB 7; Length 82596;
Best Local Similarity 57.6%; Pred. No. 6.7; Mismatches 0; Indels 2; Gaps 1;
Matches 83; Conservative 0;
QY 1590 CAGACTCACAGCTTTGAGAATCAAGAAGACGCTCGCAAAAGATGGTTGAATCCAGGATGT 1649
DB 20705 CACCATCAAGCTTTGAGAAGCAATAAGAAGCTATGTCAGCTTTTGGAGTCAAAATATGA 20646
QY 1650 AAGATTTGACAAACAGTTTTCAG--AAAGAAATTTAGACTGCAAGAAATTCACCCGAGGA 1707
DB 20645 CTAGATGTCATGTGGATGATTGAGTATAGAACTAAACCGCAACTGGTTCCCAAGGGCT 20586
QY 1708 AGGGTGGAGTTAGCATGGACTAGG 1731
DB 20585 AAAGTAGTGTAGAGATACAAAG 20562

RESULT 9

US-11-117-187-208/c
; Sequence 208, Application US/11117187
; Publication No. US20050266560A1
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; APPLICANT: COPENHAVER, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD:309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/09/531,120
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 208
; LENGTH: 94905
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-208

Query Match 2.0%; Score 35.6; DB 7; Length 94905;
Best Local Similarity 57.6%; Pred. No. 7.4; Mismatches 0; Indels 2; Gaps 1;
Matches 83; Conservative 0;
QY 1590 CAGACTCACAGCTTTGAGAATCAAGAAGACGCTCGCAAAAGATGGTTGAATCCAGGATGT 1649

DB 91513 CACCATCAAGCTTTGAGAAGCAATAAGAAGCTATGTGAGCTTTTGGAGTCAAAATATGA 91454
QY 1650 AAAGATTTGACAAACAGTTTTTCAG--AAAGAAATTTAGACTGCAAGAAATTCACCCGAGGA 1707
DB 91453 CTAGATGTCATGTGGATGATTGAGTATAAGAAGCTAAACCGCAACTGGTTCCCAAGGGCT 91394
QY 1708 AGGGTGGAGTTAGCATGGACTAGG 1731
DB 91393 AAAGTAGTGTTAGAAGATACAAAG 91370

RESULT 10

US-11-117-187-211
; Sequence 211, Application US/11117187
; Publication No. US20050266560A1
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; APPLICANT: COPENHAVER, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD:309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/09/531,120
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 211
; LENGTH: 1082144
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-211

Query Match 2.0%; Score 35.6; DB 7; Length 1082144;
Best Local Similarity 57.6%; Pred. No. 38; Mismatches 0; Indels 2; Gaps 1;
Matches 83; Conservative 0;
QY 1590 CAGACTCACAGCTTTGAGAATCAAGAAGACGCTCGCAAAAGATGGTTGAATCCAGGATGT 1649
DB 987951 CACCATCAAGCTTTGAGAAGCAATAAGAAGCTATGTCAGCTTTTGGAGTCAAAATATGA 988010
QY 1650 AAAGATTTGACAAACAGTTTTTCAG--AAAGAAATTTAGACTGCAAGAAATTCACCCGAGGA 1707
DB 988011 CTAGATGTCATGTGGATGATTGAGTATAAGAAGCTAAACCGCAACTGGTTCCCAAGGGCT 988070
QY 1708 AGGGTGGAGTTAGCATGGACTAGG 1731
DB 988071 AAAGTAGTGTTAGAAGATACAAAG 988094

RESULT 11

US-10-750-185-29585/c
; Sequence 29585, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29585

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OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 13:31:58 ; Search time 5033 Seconds
(without alignments)
16853.761 Million cell updates/sec

Title: US-10-600-645-1
Perfect score: 1813
Sequence: 1 CTAGTGGATCCCCGGGCTG.....TTCAGGACTCTGAGAATGC 1813

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2:	gb_est2:*
3:	gb_est3:*
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5:	gb_est5:*
6:	gb_est6:*
7:	gb_est7:*
8:	gb_est8:*
9:	gb_est9:*
10:	gb_est10:*
11:	gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1389.6	76.6	1521	10 AY411158	Mus muscu
2	1274.6	70.3	1532	10 AY411156	Homo sapi
3	1002.2	55.3	1532	10 AY411157	Pan trogl
4	774.6	42.7	1121	3 BM473726	AGENCOURT
5	736	40.6	874	1 AU124197	AU124197
6	734	40.5	915	7 CV558493	UI-M-HZO-
7	728.6	40.2	842	8 CX204646	MNS07540
8	717.2	39.6	1911	4 AK086130	Mus muscu
9	715.6	39.5	779	7 CK638737	UI-M-HO-
10	710	39.2	1509	10 AY418115	Mus muscu
11	707.6	39.0	783	6 CF744610	UI-M-GVO-
12	705	38.9	826	8 DR156725	HESC2 69
13	703.8	38.8	763	7 CV557698	UI-M-HZO-
14	702	38.7	1509	10 AY418113	Homo sapi
15	682.6	37.7	769	6 CD351417	UI-M-GIO-
16	672.8	37.1	1509	10 AY418114	Pan trogl
17	668.4	36.9	909	5 BU152346	AGENCOURT
18	667.2	36.8	804	7 CN530503	UI-M-HO-
19	666.6	36.8	772	7 CN460181	UI-M-HO-
20	664.8	36.7	717	7 CO045435	UI-M-HO-
21	664.8	36.7	775	6 CD352514	UI-M-GIO-
22	662.2	36.5	807	1 AU124052	AU124052

ALIGNMENTS

RESULT 1	AY411158	1521 bp	DNA	linear	GSS 16-DEC-2003
LOCUS	Mus musculus BMPRIA gene, VIRTUAL TRANSCRIPT, partial sequence,				
DEFINITION	genomic survey sequence.				
ACCESSION	AY411158				
VERSION	AY411158.1	GI:39767126			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	1 (bases 1 to 1521)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, P., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Inferred nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1521)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, P., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.				
FEATURES	Location/Qualifiers				
source	1..1521				
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	/mol_type="genomic DNA"				
	/db_xref="taxon:10090"				
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	/gene="BMPRIA"				
	/locus_tag="HCM4130"				
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ORIGIN					
Query Match	76.6%	Score	1389.6	DB 10	Length 1521
Best Local Similarity	94.8%	Pred. No. 0			
Matches 1452	Conservative	0	Mismatches	69	Indels 11
					Gaps 1

QY	1208	TAGCTGTTAAATTTCAACAGTGACACAAATGAAGTTGACATACCTTTGAACACACAGGGTGG	1267
Db	1081	TAGCTGTTAAATTTCAACAGTGATACAAATGAAGTTGACATACCTTTGAATACACAGGGTGG	1140
QY	1268	GCACACAGCGGTACATGGCTCCAGAAAGTCTCGACAGAGCGCTGAGTAAAAACCATTTCC	1327
Db	1141	GCACCAAGCGGTACATGGCTCCAGAAAGTCTCGATGAAAGCGCTGAATAAAAAACCATTTCC	1200
QY	1328	AGCCCTTACATCATGCTGACATCTACAGCTTTTGGTTTGTATCATTTGGGAGATGGCCCGTC	1387
Db	1201	AGCCCTTACATCATGCTGCTGACATCTATAGCTTTTGGTTTGTATCATTTGGGAAATGGCTCGTC	1260
QY	1388	GCTGTATTACAGGAGGAATCGTGGAGGAATATCAATTACCATATTACACATGGTGCCTA	1447
Db	1261	GTT-----GGAAATCGTGGAGGAATATCAATTACCATATTACACATGGTGCCTA	1309
QY	1448	GTGACCCATCTTATGAAGACATGCGTGAGGTGCTGTGTGTGAACCGCTTGGCGCCAATCG	1507
Db	1310	GTGACCCATCTTATGAAGACATGCGTGAGGTGCTGTGTGTGAACCGCTTGGCGCCAATCG	1369
QY	1508	TCTCTAAACCGCTGGAAACAGTGATGAATGCTCTTCGAGCCGTTTGAAGCTGATGTCAGAAT	1567
Db	1370	TGCTCTAACCGCTGGAAACAGCGATGAATGCTCTTCGAGCAGTTTGAAGCTAATGTCAGAAT	1429
QY	1568	GCTGGGCCCATTAATCCAGCATCCAGACTCAGACTTTCAGAAATCAAGAGAGCGCTCGCAA	1627
Db	1430	GTTGGGCCCATTAATCCAGCTCCAGACTCAGACTTTCAGAAATCAAGAGAGACTTTGCCA	1489
QY	1628	AGATGGTTGAATCCCGAGGATGTAAAGATTGTA	1659
Db	1490	AAATGGTTGAATCCCGAGGATGTAAAGATTGTA	1521
RESULT 2			
LOCUS	AY411156	1532 bp	DNA linear GSS 16-DEC-2003
DEFINITION	Homo sapiens BMRP1A gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.		
ACCESSION	AY411156		
VERSION	AY411156.1	GI:39767124	
KEYWORDS	GSS.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 1532)		
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.		
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios		
JOURNAL	Science	302 (5652),	1960-1963 (2003)
PUBMED	14671302		
REFERENCE	2 (bases 1 to 1532)		
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.		
FEATURES	Location/Qualifiers		
source	1..1532		
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	<1..>1532		
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	/locus_tag="HCM4130"		

Query Match				70.3%;	Score 1274.6;	DB 10;	Length 1532;
Best Local Similarity				89.2%;	Prod. No. 0;		
Matches 1367;				Conservative	0;	Mismatches 165;	Indels 0;
							Gaps 0;
Qy	128	GGCAGAAATCTAGATAGTATGCTCCATGCTACTGGTATGAAATCAGACGTGACACGAGA	187				
Db	1	GACAGAAATCTGGATAGTAGCTTTCATGGCACTGGGATGAAATCAGACTCCGACGAGAAA	60				
Qy	188	AGCCGGAAAAATGGAGTAGACGTTAGCACCGAGAGGACACCTTACCTTTCTTAAAAATGCTATT	247				
Db	61	AGTCAGAAAAATGGAGTAACCTTAGCACCGAGGATACCTTGCCCTTTTAAAGTGCTATT	120				
Qy	248	GCTCAGGACACTGCCAGATGACGCTATTATAACACATGCAATAACTAATGCCCATTGCT	307				
Db	121	GCTCAGGGCACTGTCAGATGATGCTATTATAACACATGCAATAACTAATGCACATTGCT	180				
Qy	308	TTGCCATTATAGAGAAGATGATCAGGGAGAGAACCAAGTTAACTTCTGGGTGTATGAAGT	367				
Db	181	TTGCCATCATAGAGAAGATGACCAAGGGAGAGAACCAATTAGCTTTCAGGGTGTATGAAT	240				
Qy	368	ATGAAGGCTCTGATTTTCAATGCAAGGATTCAACAAAAGCCAGCTACGACGAGCAATAG	427				
Db	241	ATGAAGGATCTGATTTTCAGTGCAGAGATTTCCAAAAGCCAGCTACGCCGCAATATAG	300				
Qy	428	AATGTTGTGGACCAATTTGTCAACCAATATTTGCAGCCTPACACTGCCCTCTCGTTA	487				
Db	301	AATCTTCTCGACCAATTTATGTAAACAGTATTTTGCAACCCACACTGCCCTCTGTGCA	360				
Qy	488	TAGGCCATCTTTGATGGCAGCGTCGATGGCTGGCTGTCTCATCTCTATGGCTGTCT	547				
Db	361	TAGTCCGCTTTTGTGATGGCAGCAATTCGATGGCTGGTTTGTCTCATTTCTATGGCTGTCT	420				
Qy	548	GTAATTGTGCAATCATCGCTCTTCTCCAGCTGCTTCTGTACAAACATTACTGTGAAGTA	607				
Db	421	GCATAATTGCTATGATCATCTTCTCCAGCTGCTTTTGTACAAACATTAATTGCAAGAGCA	480				
Qy	608	TCTCAAGCAGAGGTCGTTTACAACCGTGACTTGGAAACAGGATGAAGCAATTTATTCAGCTAG	667				
Db	481	TCTCAAGCAGACGTCGTTTACAACTCGTATTTGGAACAGGATGAAGCAATTTATTCAGTTG	540				
Qy	668	GAGAACTCACTGAAGACCTGATTGACCAAGTCAAAAGCTCTGGTAGTGAAATCTGGATAC	727				
Db	541	GAGAACTCACTAAAGACCTTATTGACCAAGTCACAAAGTTCTTGGTAGTGGGCTCTGCACTAC	600				
Qy	728	CTTTATTGGTTTCAGCGAACTATTGCCAAAACAGATTACAGATGGTTCGCGACGGTTGGTAAGG	787				
Db	601	CTTTATTGGTTTCAGCGAACTATTGCCAAAACAGATTACAGATGGTTCGCGCAAGTTGGTAAG	660				
Qy	788	GCCGGTATGAGAAAGTATGGATGGTAAATGGCGTGGTGAAAAAGTGGCTGTCAAGTAT	847				
Db	661	GCCGATATGAGAAAGTATGATGGGCAATGGCGTGGCGGAAAAAGTGGCGGTGAAAGTAT	720				
Qy	848	TTTTTTACCACTGAAGAGCTAGCTGGTPTTAGAGAAAACAGAAATCTACCAAGACGGTGTTAA	907				
Db	721	TCTTTACCACTGAAGAGCCAGCTGGTTTCGAGAAAACAGAAATCTACCAAACTGTGCTAA	780				
Qy	908	TGCGTCATGAAATATACTTGGTTTTATAGCTGCAGACATTAAGGCACCGGTTCTTGGA	967				
Db	781	TGCGCCATGAAACATACTTGGTTTTATAGCGCGAGCAATTAAGGTACAGGTTCTCTGGA	840				
Qy	968	CTCAGCTGTAATTGATTACTGATTACCATCAGAAATGGTCTCTCTATGACTTCCCTGAAAT	1027				
Db	841	CTCAGCTCTAATTGATTACTGATTACCATGAAATGGATCTCTATGACTTCCCTGAAAT	900				
Qy	1028	GTGCCACCTTGGACACGAGACCCCTACTCAAGTTAGCTTATTCTGCTGCCCTGTGGTCTGT	1087				
Db	901	GTGCTACACTGGACACGAGACCCCTGCTTAAATTGGCTTATTTCAGCTGCCCTGTGGTCTGT	960				
Qy	1088	GCCACCTCCACAGAAAAATTTATGGACGCAAGCAAGCAAGCTGCAATTTGCTCATCGAGACC	1147				
Db	961	GCCACCTGCACAGAAAAATTTATGGACCCCAAGCAAGCCGCAATTTGCTCATCGAGACC	1020				

Qy	1008	TCTCTATG-AC	TTCTCTGAAATGTGCCACCTCGACACCCAGAGGCCCTACTCAAGTTAGCTTT	1066
Db	841	TCTCTATGAAC	TTCTCTGAAATGTGCTACACTGGACACACAGAGCCCTGCTTTAAATTGGCTT	900
Qy	1067	ATTCTGCT-CCCTGTG	TGTGTGCCACCTCCACACAGAAATTTATGCGACGCAGGCAA-1124	
Db	901	ATCCAGTGCCT	TGGGNCCTGCCCCAGAAATTTATGGGCCCCCAAGAAA	960
Qy	1125	-GCCGTGCAAT	TGCTCAT-CGAGACCTGGAAGAGCAAAACATCCTTTATTAAGAAAAA	1178
Db	961	GCCCGCAAT	TGGCTTCTCCGAACCTTTAAGGAGCAAAACATCTCTTCTCCAAAAAAA	1016

Query Match	42.7%;	Score 774.6;	DB 3;	Length 1121;
Best Local Similarity	87.7%;	Pred. No. 1.8e-220;		
Matches 891;	Conservative	0;	Mismatches 120;	Indels 5; Gaps 4;
QY	168	ATCAGACGTGACACAGAGAAGACGCGAAATATGGAGTGAAGTTACACCCAGAGGACACCTT	227	
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QY	228	ACCTTTCTTAAAAATGCTATTGCTCAGGACACTGGCCAGATGACGCTATTATAACACATG	287	
DB	61	GCCTTTTTAAAGTGCTATTGCTCAGGCACTGTCCAGATGATGCTATTATAACACATG	120	
QY	288	CATTAACTAATUGCCATTGCTTTTGCCATTATAGAAAGATGATCAGGAGAAAAACACGTT	347	
DB	121	CATAACTAATGGACATTGCTTTGGCATCATAGAAAGATGACCCAGGAGAAAAACCATT	180	
QY	348	AACTTCTGGGTATGAAGTATGAAGCTCTGATTTTCAATGCAAGGATTCACCAAAAGC	407	
DB	181	AGCTTCAGGGTGTATGAATAATGAAGGATCTGATTTTCAGTGCAAAAGATTCTCCAAAAGC	240	
QY	408	CCAGCTACGCAAGGCAATAGAAATGTTGTCGCAACCAATTTGTGCAACCAATATTTGCGAGCC	467	
DB	241	CCAGCTAGCCGGAACATAGAAATGTTGTCGAGACCAATTTATGTAACAGATATTTGCAACC	300	
QY	468	TACACTGCCCTCTGCTTATAGCCCAATCTTTTGATGGCAGCGTCCGATGGCTGGCTGT	527	
DB	301	CACACTGCCCTCTGTTGTCATAGTCCGTTTTTTTGTATGGCAGCATTCGATGGCTGGTTTT	360	
QY	528	GCTCATCTATGGCTGCTGTATTGTCGCCATGATGCTCTTCTCAGCTGCTTCTGTTA	587	
DB	361	GCTCATTTCTATGGCTGCTGCATAATTGCTATGATCATCTTCTCAGCTGCTTTTGTTA	420	
QY	588	CAAACTTACTGTAAAGTACTCAAGCAGAGGTCGTTTACAACCGTCGACTTGGAAACAGGA	647	
DB	421	CAAACTATTTCGAAGAGCATCTCAAGCAGACGTCGTTTACAATCGTATTTGGAAACAGGA	480	
QY	648	TGAAGCATTTATTCAGTAGAGAGAAATCACTGAAAAGACCTGATTGACCAAGTCAACAAAGCTC	707	
DB	481	TGAAGCATTTATTCAGTTGAGAAATCACTAAAGACCTTATTGACCAAGTCACAAAGTTC	540	
QY	708	TGGTAGTGGATCTGGATTACCTTTATTGGTTTCAGCGAACTATTGCCAAAACAGATTTCAGAT	767	
DB	541	TGGTAGTGGGTCTGGACTACCTTTATTGGTTTCAGCGAACTATTGCCAAAACAGATTTCAGAT	600	
QY	768	GGTTCCGCAGGTTGGTAGGCGCCGGTATGGAGAGTATGATGGTAAATGGCGTGTGA	827	
DB	601	GGTCCGGCAAGTTGGTAAGGCCCATATGGAGAAAGTATGGAGTGGCAAAATGGCGGTGGCGA	660	
QY	828	AAAAAGTGGCTGCAAAATATTTTTTACCACCTGAAGAAGCTAGCTGGTTTTAGAGAAAACAGA	887	
DB	661	AAAAGTGGCGTGAAGATTTCTTTTACCACTGAAGAAGCCAGCTGGTTTTCGAGAAAACAGA	720	
QY	888	AATCTACAGACGGTGTAAATGCGCTCATGAAAATATATCTTGGTTTTTATAGCTGCAGACAT	947	
DB	721	AATCTACCAAACCTGTGCTAATGCGCCATGAAAACATATCTTGGTTTTTATAGCGGCAGACAT	780	
QY	948	TAAAGGCACCGGTTCTGGACTCAGCTGTATTTCGATTTACTGATTTACCATGAGAAATGGGTC	1007	
DB	781	TAAAGGTACAGGTTCTGGACTCAGCTCTTAATTTGATTTACTGATTTACCATGAAATGGATC	840	

[illegible]

QY 1479 CGTGTGTGTAACCGCTTGGGCCAATCGTCTCTAAACCGCTGGAACAGTGATGAATGTCT 1538
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541 TGTGTGTGTAACCGCTTGGGCCAATCGTGTCTAAACCGCTGGAACAGCGATGAATGTCT 600
QY 1539 TCGAGCGGTTTGAAGCTGATGTCAGAAATGCTGGGCCCAATATCCAGACTCCAGACTCAC 1598
Db |||||||
601 TCGAGCAGTTTGAAGCTAATGTGAGAAATGTTGGGCCCAATATCCAGCTCCAGACTCAC 660
QY 1599 AGCTTTGAGAAATCAAGAAGCGCTCGCAAGATGGTTGAATCCAGGATGTAAGATTTG 1658
Db |||||||
661 AGCTTTGAGAAATCAAGAAGCGCTCGCAAGATGGTTGAATCCAGGATGTAAGATTTG 720
QY 1659 AC----AAACAGTTTTGAGAAAGAAATTTAGACTGCAAGAAATTC----ACCCGAGGAAG 1710
Db |||||||
721 ACAATTAACAAATTTTGGGAGAAATTTAGACTGCAAGAAATTTCTTCCACCAAGGAATG 780
QY 1711 GTGGAGTTAGCATGAGTAGGATGTCGGCTTGGTTTCCAGACTCTCTCTTACCATCTT 1770
Db |||||||
781 GTGGGATTAGCATGGAATAGGATGTTGACTTGGTTTCCAGACTCTCTCTCTA-CATCTT 839
QY 1771 CACAGGCTGCTAACAGTAAACCTTTCAGGACTCTGCAGAAATGC 1813
Db |||||||
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RESULT 7
CX204646 842 bp mRNA linear EST 29-DEC-2004
LOCUS MNS07540 Mouse Neurosphere Normalized cdna library Mus musculus
DEFINITION cdna 5', mRNA sequence.
ACCESSION CX204646
VERSION CX204646.1 GI:56859818
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 842)
AUTHORS Williams, C., Wirtz, V., Lundberg, J. and Frisen, J.
TITLE Expressed sequence tags of cdna clones from murine neurospheres
JOURNAL Unpublished (2005)
COMMENT Contact: Williams, C.
Molecular Biotechnology
Institution of Biotechnology
Albion University Center, KTH-Royal Institute of Technology, 106
91 Stockholm, Sweden
Tel: +46855378332.
Fax: +46855378481
Email: cecilia.williams@biotech.kth.se
Seq primer: M13REV

FEATURES
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/organism="Mus musculus"
/mol_type="mRNA"
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/sex="MALE"
/tissue_type="Lateral wall of lateral ventricle"
/cell_type="Early passage neurosphere"
/dev_stage="Adult"
/clone_lib="Mouse Neurosphere Normalized cdna library"
/note="Organ: Adult brain; Vector: pCMVSPORT6.0; A cdna
library was constructed in pCMVSPORT6.0 from RNA isolated
from neurospheres of adult male and female mice. Custom
normalized cdna library by Invitrogen/ResGen"

ORIGIN
Query Match 40.2%; Score 728.6; DB 8; Length 842;
Best Local Similarity 93.6%; Pred. No. 1.1e-206;
Matches 793; Conservative 0; Mismatches 49; Indels 5; Gaps 3;
QY 329 ATCAGGAGAAACACGCTTAACCTTCTGGGTGATGAAGTATGAAGCTCTGATTTTCAAT 388

Db |||||||
1 ATCAGGAGAAACACCACTTAACCTTCTGGGTGATGAAGTATGAAGCTCTGATTTTCAAT 60
QY |||||||
389 GCAAGGATTCACAAAGCCAGCTACGAGAGACAATAGAAATGTTGTTCGACCAATTTGT 448
Db |||||||
61 GCAAGGATTCACGAAAGCCAGCTACGAGAGACAATAGAAATGTTGTTCGACCAATTTGT 120
QY |||||||
449 GCAACCAATATTTGCAGCCCTACACTGCCCCCTGTGCTTATAGGCCCAATTTTGTATGGCA 508
Db |||||||
121 GCACACAGTATTTGCAGCCCTACACTGCCCCCTGTGCTTATAGGCCCAATTTTGTATGGCA 180
QY |||||||
509 GCGTCCGATGGCTGCTGCTCATCTCTATGCGCTGTCTGTATTTGCGCATGATCGTCT 568
Db |||||||
181 GCATCCGATGGCTGCTGCTCATCTTCCATGCTGCTGTATAGTTGCTATGATCATCT 240
QY |||||||
569 TCTCCAGCTGCTTCTTTACAAACATTTACTGTAAAGTATCTCAAGCAGAGCTCGTTACA 628
Db |||||||
241 TCTCCAGCTGCTTTTGTCTATAAGCATTTATGTAAGAGTATCTCAAGCAGAGCTCGTTACA 300
QY |||||||
629 ACCGTGACTTGGAAACAGGATGAAGCATTTATTTCCAGTAGGAGAAATCACATGAAAGACCTGA 688
Db |||||||
301 ACCGTGATTTGGAAACAGGATGAAGCATTTATTTCCAGTAGGAGAAATCATTTGAAAGACCTGA 360
QY |||||||
689 TTGACCACTCAAAAGCTCTGCTAGTGTGATTTACCTTTATTTGTTTCAGCGCAACTA 748
Db |||||||
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QY |||||||
749 TTGCCAAACAGATTCAGATGTTTCCGAGGTTGGTAAGGCCGCTATGAGAGAAATGATGA 808
Db |||||||
421 TTGCCAAACAGATTCAGATGTTTCCGAGGTTGGTAAGGCCGCTATGAGAGAAATGATGA 480
QY |||||||
809 TGGGTAAATGGCGTGTGAAAAAGTGGCTGTCAAAGTATTTTACCCTGAAAGAGCTA 868
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QY |||||||
989 ATTACCATGAGAAATGGATCTCTATGACTTCTGAAATGTGCCACCTCCACACTAGACACAG 1048
Db |||||||
661 ATTACCATGAGAAATGGATCTCTATGACTTCTGAAATGTGCCACCTCCACACTAGACACAG 720
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1049 CCCTACTCAAGTTAGCTTTATTTCTGCTGCTGTGCTGTGCTGCTGCCACCTCCACACAGAAATTT 1108
Db |||||||
721 CCCTACTCAAGTTAGCTTTATTTCTGCTGCTGTGCTGTGCTGCTGCCACCTCC-CACAGAAATTT 779
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QY |||||||
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836 TAAAAA 842

RESULT 8
AK086130 1911 bp mRNA linear HTC 03-APR-2004
LOCUS AK086130
DEFINITION Mus musculus 15 days embryo head cdna, RIKEN full-length enriched
library, clone:930007102 product:bone morphogenetic protein
receptor, type 1B, full insert sequence.
ACCESSION AK086130
VERSION AK086130.1 GI:26351960
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;


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QY 837 TGTCAAAGTATTTTACCACTGAAGAGCTAGCTGTTTATAGAGAAACAGAAATCTACCA 896
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QY 1077 CTGTGCTGTGGCCACCTCCACAGAGAAATTTATGCGCAGGCAAGCCCTGCAATTCG 1136
D 1081 CAGCGGCTATGCCATTTACACACGGAAATCTTTAGCAGCTCAAGGCAAGCCAGCAATCGC 1140
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D 1141 CAGTCAGACTTGAAAGTAAAAACATCTCTGTTGAAGAAAAATGGAACTTTGCTGATAGC 1200
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D 1441 CTTGTTGCCAGTGCAGCTTCTTATGAGGACATGAGAGAAATGTTGTCATGAAGATT 1500
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D 1621 AACCCTTGCCAAATGTCAGAGTCCCAGGACATTAACCTCTGAC 1664

RESULT 9
CK638737
LOCUS
DEFINITION
IMAGE:30644216 5', mRNA sequence.
EST.
CK638737.1 GI:41364603
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 779)
AUTHORS
NIH-MGC http://mgi.nci.nih.gov/.
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TITLE
JOURNAL
COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pYX-5.

FEATURES
source

Location/Qualifiers

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/dev_stage="9.5-10.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP H00"
/note="Organ: Head; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAAGTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."

ORIGIN

Query Match 39.5%; Score 715.6; DB 7; Length 779;
Best Local Similarity 94.9%; Pred. No. 8.5e-203;
Matches 739; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 322 GAAGATGATCAGGAGAACACAGCTTAACCTCTGGGTGATGAAGTATGAAGCTCTGAT 381
D 1 GAAGATGATCAGGAGAACACCACTTAACCTCTGGGTGATGAAGTATGAAGCTCTGAT 60
QY 382 TTTCAATGCAAGGATTTCACAAAGCCAGCTACGAGGACAAATAGAATGTTGCGGACC 441
D 61 TTTCAATGCAAGGATTTCACGAAAGCCAGCTACGAGGACAAATAGAATGTTGCGGACC 120
QY 442 AATTGTTGCAACAATATTGTCAGCTACACTGCCCCCTGTCGTTATAGCCCATTTCTTT 501
D 121 AATTGTTGCAACCAGTATTGTCAGCTACACTGCCCCCTGTTGTTATAGTCCGTTCTTT 180
QY 502 GATGCGAGCTCCGATGGCTGCTGCTCATCTCTATGGCTGCTGTTATGTCGCATG 561
D 181 GATGCGAGCATCCGATGGCTGTTGCTCATTTCCATGGCTGCTGTTATGTTGTTATG 240
QY 562 ATCTGCTTCTCCAGCTGCTTCTGTTACAAACATTAAGTATGTAAGAGTATCTCAAGCAGAGT 621
D 241 ATCATCTTCTCCAGCTGCTTCTGCTATAGCATTTATGTAAGTATCTCAAGCAGAGT 300
QY 622 CATTACACCGTGAATTGGAAACAGGATGAAGCATTTATTTCCAGTAGGAGAAATCACTGAAA 681
D 301 CGTTACAAACCGTGAATTGGAAACAGGATGAAGCATTTATTTCCAGTAGGAGAAATCACTGAAA 360
QY 682 GACCTGATTGACAGCTCAAAAGCTCTGCTAGTGGATCTGCTGTTATGTTGTTCTAG 741
D 361 GACCTGATTGACAGCTCCCAAAGCTCTGGGAGTGGATCTGCTGTTATGTTGTTCTAG 420
QY 742 CGAACTATTGCCAAACAGATTTCAGATGGTTTCGGCAGGTTGGTAAGGCCGCTATCGAGAA 801

QY 1324 TTCAGGCCCTACATCATGGCTGACATCTACAGCTTTGGTTTGATCATTTGGGAGATGGCC 1383
Db 1174 TTCAGTCCCTACATATATGGCTGACATCTACAGCTTTGGACTCATCTCTGGGAGATTGCA 1233
QY 1384 CGTGCCTGATTACAGGAGGAATCGTGGAGGAATATCAATACCATATTAACATGATG 1443
Db 1234 AGGAGATGTGTTCTGGAGGTATAGTGGAGAAATACCAGCTTCCTATATCAGCACCTGGTG 1293
QY 1444 CCTAGTGACCCATCTTATGAAGACATCGCTGAGGTCTGTGTGTGTAACCGCTTGGCGCCA 1503
Db 1294 CCCAGTGACCTCTTATAGGACATGAGAGAAATTTGTGTGCATGAGAAAGTTACGGCT 1353
QY 1504 ATCGTCTCTAACCGCTCGAAGATGATGAATGCTTCGAGCCGTTTGAAGCTGATGTC 1563
Db 1354 TCATTCGCCAATCGATGGAGCAGTGAATGAGTGTCTCAGGCAGATGGGAAAGCTTATGACA 1413
QY 1564 GAATGCTGGGCCCATATCCAGCATCCAGACTCAGACTTGAAGCTTGAATCAAGAGACGCTC 1623
Db 1414 GAGTGTGGGGCAGAAATCTGCTCCAGGCTGACGGCCCTGAGAGTTAAGAAACCCCT 1473
QY 1624 GCAAAGATGTGTAATCCAGGATGTAAAGATTGA 1659
Db 1474 GCCAAATGTGAGAGTCCAGGACATTAACCTCTGA 1509

RESULT 11
CF744610
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CF744610 783 bp mRNA linear EST 10-OCT-2003
UI-M-GV0-clt-d-20-0-UI.r1 NIH_BMAP_GV0 Mus musculus cDNA clone
IMAGE:30617467 5', mRNA sequence.
CF744610
CF744610.1 GI:37640950
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 783)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-i@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pYX-5.
Location/Qualifiers
1. .783
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/clone="IMAGE:30617467"
/tissue_type="whole brain"
/dev_stage="1, 5, and 15 days newborn"
/lab_host="DH10B (TI phage resistant)"
/clone_lib="NIH_BMAP_GV0"
/note="Organ: Brain; Vector: pYX-Asc; Site: 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction. ligated with
EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag

sequence located between the Not I site and the polyA tail
is CGAAGTCAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN

Query Match 39.0%; Score 707.6; DB 6; Length 783;
Best Local Similarity 95.2%; Pred. No. 2.1e-200;
Matches 739; Conservative 0; Mismatches 36; Indels 1; Gaps 1;

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Db 1 AGAAGAAGATGATCAAGGGAGAAACCACTTAACCTTCTGGGTGATGAAGATGAAGGCT 60
QY 377 CTGATTTTCANATGCAAGGATTACCAAAAGCCAGCTACGAGGACAAATAGATGTTGTC 436
Db 61 CTGATTTTCANATGCAAGGATTACCAAAAGCCAGCTACGAGGACAAATAGATGTTGTC 120
QY 437 GGACCAATTTGTGCAACCAATATTTGCAGCTTACACTGCCCCCTGTCGTTATAGGCCCAT 496
Db 121 GGACCAATTTGTGCAACCAATATTTGCAGCTTACACTGCCCCCTGTCGTTATAGGTCCT 180
QY 497 TCTTTGATGCGACGCTCCGATGGCTGCTGCTCATCTCTATGGGTGCTGTTATGTCG 556
Db 181 TCTTTGATGCGACGCTCCGATGGCTGCTGCTCATCTCTATGGGTGCTGTTATAGGTCCT 240
QY 557 CCATGATGCTCTTCTCCAGCTGCTTCTGTACAAACATTAATCTAGAGATATCTCAAGCA 616
Db 241 CTATGATCATCTTCTCCAGCTGCTTCTGTATTAAGCATTTATTTGAAGAGATCTCTCAAGCA 300
QY 617 GAGGTGCTTACAAACCGTGTGGAACAGGATCAAGCATTTATTTCCAGTAGGAGAATCAC 676
Db 301 GGGGTGCTTACAAACCGTGTGGAACAGGATCAAGCATTTATTTCCAGTAGGAGAATCAT 360
QY 677 TGAAGAAGCTGATGACCAAGCTGCAAGAGCTCTGGTAGTGGATCTGGAATTAACCTTTATG 736
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QY 737 TTCAGGGAATATTGGCAACAGATTCAGATGTTTGGCAGGTTGTTAAGGGCGGATG 796
Db 421 TTCAGGGAATATTGGCAACAGATTCAGATGTTTGGCAGGTTGTTAAGGGCGGATG 480
QY 797 GAGAAGTATGGATGGGTAAATGCGGTGGAAGAGTGGCTGTCAAAGTATTTTATACCA 856
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QY 857 CTGAAGAAGCTAGCTGGTTTAGAGAAACAGAAATCTACCAGACGGTGTAAATCGCTCATG 916
Db 541 CTGAAGAAGCTAGCTGGTTTAGAGAAACAGAAATCTACCAGACGGTGTAAATCGCTCATG 600
QY 917 AAAATATCTGGTTTATAGCTGCAGACATTAAAGGACCGGTTCTTGAGCTCAGCTGT 976
Db 601 AAAATATCTGGTTTATAGCTGCAGACATTAAAGGACCGGTTCTTGAGCTCAGCTGT 660
QY 977 ATTTGATTAATGATTAACCATGGAATGGGTCTCTCTATGACTTCTCGAAATGTGCCACCC 1036
Db 661 ATTTGATTAATGATTAACCATGGAATGGGTCTCTCTATGACTTCTCGAAATGTGCCAC 720
QY 1037 TGGACACAGAGCCCTACTCAAGTTAGCTTATTTCTGCTGCTGGTGTGTCGCCAC 1092
Db 721 TAGACACAGAGCCCTACTCAAGTTAGCTTATTTCTGCTGCTGGTGTGTCGCCAC 776

RESULT 12
DRI56725
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

DRI56725 826 bp mRNA linear EST 16-JUN-2005
HES2C.69.D09.g1.A035.NIH.MGC.258 Homo sapiens cDNA clone
IMAGE:7965451 5', mRNA sequence.
DRI56725
DRI56725.1 GI:67868885
EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 826)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: BresaGen, Inc.
 cDNA Library Preparation: Express Genomics, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Laboratory for Genomics and Bioinformatics, University of Georgia
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
 Plate: LLAM 17072 row: g column: 17
 Seq primer: JENREV (CAGGAACAGCTATGACC)
 High quality sequence stop: 826.
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 /sex="male"
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 /cell_type="human embryonic stem cells"
 /cell_line="BG01"
 /lab_host="DH10B-T1 phage-resistant E. coli"
 /clone_lib="NIH_MGC_258"
 /note="Vector: pExpress-1; Site_1: NotI; Site_2: EcoRV; RNA obtained from human embryonic stem cells isolated from the inner cell mass of blastocyst stage embryos and differentiated to an early endodermal cell type. Cell line id and NIH Registry designation is BG01. Positive for GATA4, MixL1, Msx1, HNF4alpha expression; negative for AFP expression. Passage number 40. cDNA primed using oligo-dT primer: 5'-pGACTAGTCTAGATCGAGCGGCCCC(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. This primary library is non-normalized (normalized primary library is NIH_MGC_259). It was constructed by Express Genomics (Frederick, MD). Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA. Note: this is a Mammalian Gene Collection library."
 ORIGIN
 Query Match 38.9%; Score 705; DB 8; Length 826;
 Best Local Similarity 90.8%; Pred. No. 1.3e-199;
 Matches 750; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
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 Db 1 CTACCGCGACATAGATGTTGTCGGACCAATTTATGTATTAACCATGATTTGCAACCCACA 60
 QY 472 CTGCCCCCTGTCGTTATAGGCCCATCTTTTGATGGCAGGTCGCGATGGCTGGCTGCTC 531
 Db 61 CTGCCCCCTGTTGTCATAGTCCGTTTTTTTGATGGCAGCATTCGATGGCTGTTTTGCTC 120
 QY 532 ATCTCTATGGCTGTCTGTATTGTCGCCATGATCGTCTTCTCAGCTGCTCTGTGTACAAA 591
 Db 121 ATTTCTATGGCTGTCTGCATAATTGCTATGATCATCTTCTCCAGCTGCTTTGTGTACAAA 180
 QY 592 CATTACTGTAAAGATATCTCAGCAGAGGTGCTTTACACCGTGACTTGGACAGATGAA 651

181 CATATTCCAGAGCATCTCAAGCAGACGTCGTACATCGTATTGGAAACGAGTAA 240
 QY 652 GCATTTATCCAGTAGGAGATCACTGAAAGACCTGATTGACCACTCAAAAGCTCTGGT 711
 Db 241 GCATTTATCCAGTTGGAGATCACTAAAAGACCTTATTGACCACTCAAAAGTTCTGGT 300
 QY 712 AGTGGATCTGATTTACCTTTATTTGGTTTCAGCGAACTATTGCCAACAGATTCAGATGTT 771
 Db 301 AGTGGTCTGGACTACCTTTATTGGTTTCAGCGAACTATTGCCAACAGATTCAGATGTT 360
 QY 772 CGCAGGTTGGTAAGCGCGGTATGGAGAAAGTATGGATGGGTAAATGGCGTGGTGA AAA 831
 Db 361 CGCAGGTTGGTAAGCGCGGTATGGAGAAAGTATGGATGGGTAAATGGCGTGGTGA AAA 420
 QY 832 GTGGCTGTCAAAGTATTTTACCACCTGAAGAAGTAGCTGGTTTAGAGAAAACAGAAATC 891
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 QY 892 TACCAGACGGTGTAAATCGGTCATGAAATATACCTTGGTTTATAGCTGCAGACATTA AAA 951
 Db 481 TACCAAACTGTGCTAAATCGGTCATGAAACACATCTTGGTTTCATAGCGCAGACATTA AAA 540
 QY 952 GGCACCGGTTCTCGACTCAGCTGATTGTTGATTACTGATTACCATGAGATGGGTCTCTC 1011
 Db 541 GGTACAGGTTCTCGACTCAGCTCTATTGTTGATTACTGATTACCATGAAATGGATCTCTC 600
 QY 1012 TATGACTTCTGAAATGTGCCACCTGGACACCGAGCCCTACTCAAGTTAGCTTTATTTCT 1071
 Db 601 TATGACTTCTGAAATGTGCTACACTGGACACCGAGCCCTGCTTAAATTTGCTTTATTTCA 660
 QY 1072 GCTGCTGTGTTGTCACCTCCACACAGAAATTTATGGCAGCAGGCGAGCTGCA 1131
 Db 661 GCTGCTGTGTTGTCACCTCCACACAGAAATTTATGGCAGCAGGCGAGGCGCA 720
 QY 1132 ATTGCTCATCAGACCTCAAGAGCAAAAACATCTTATTAAAGAAAAATGGTAGTTGCTGT 1191
 Db 721 ATTGCTCATCAGACCTTAAGAGCAAAAACATCTTATCAAGAAAAATGGGAGTTGCTGC 780
 QY 1192 ATTGCTGACCTGGCGCTAGCTGTTAAATTCACAGTGCACAAATG 1237
 Db 781 ATTGCTGACCTGGCGCTGTTGTTAAATTCACAGTGCACAAATG 826
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 DEFINITION IMAGE:30695271 5', mRNA sequence.
 CV557698
 ACCESSION CV557698
 VERSION CV557698.1 GI:54443523
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 763)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tissue Procurement: Dr. James Lin University of Iowa
 Email: cgapbs-remail.nih.gov
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/mousefl.html>
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
 Seq primer: pyx-5.
 Location/Qualifiers

FEATURES

Qy	1538	TTGAGCCGTTTTGAAGCTGATGTCAAGATGCTGGGCCCAATAATCCAGCATTCAGACTCA	1599
Db	661	TTTGAGCAGTTTTTGAAGCTAATGTCAAAATGTTGGGCCCAATAATCCAGCCTCCAGACTCA	720
Qy	1598	CAGCTTTGAGAAATCAAGAAGACGCTCGCAAAGATGTTGAATC	1640
Db	721	CAGCTTTGAGAAATCAAGAAGACACTTTGCAAAATGTTGAATC	763
RESULT 14			
LOCUS	AY418113	1509 bp DNA linear	GSS 17-DEC-2003
DEFINITION	Homo sapiens BMPRIIB gene, VIRTUAL TRANSCRIPT, partial sequence,		
ACCESSION	AY418113	genomic survey sequence.	
VERSION	AY418113.1	GI:39774073	
KEYWORDS	GSS.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
TITLE	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M. Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios		
JOURNAL	Science 302 (5652), 1960-1963 (2003)		
PUBMED	14671302		
REFERENCE	2 (bases 1 to 1509) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M. Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment.		
FEATURES	Location/Qualifiers		
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ORIGIN			
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Best Local Similarity	68.2%; Pred. No. 1.3e-198;		
Matches 1007; Conservative	0; Mismatches 460; Indels 9; Gaps 2;		
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Qy	247	TGCTCAGGACACTGCCACATGACGCTATTATAACACATGATGAATACTAATGCCATTCG	306
Db	100	TGCCACCACATTTGCCAAGAAGCTCAGTCAACAATATTTGAGCACACACGGATATGTT	159
Qy	307	TTTGGCAATTTATAGAAGAAGATGATCAGGGAGAAAACAAGTTCTCGGGTGTATGAAG	366
Db	160	TTCAACGATGATAGAAGAGATGACTCTGGGTTGGCCTGTGGTCACTTCTGGTTCCTAGGA	219
Qy	367	TATGAAGGCTCTGATTTTCAATGCAAGGATTACCACAAAGCCCAGCTACGACGAGCAATA	426
Db	220	CTAGAAGGCTCAGATTTTTCAGTGTGGGGACATCTCCATTCCTCATTCAAGAAGATCAATT	279
Qy	427	GAATGTTG---TCGGACCAAAATTTGTGCAACCAATATTTTGCACCTACACTGCCCCCTGTC	483

Db 1 GGAGCGGTGGAATCAGACAATGACTCAGCTATACACTTACATCAGATTACTGGAGCCT 60
Qy 101 GTCTGTTTCATCTTCTCATGTTCAAGGCGAGAACTCTAGATAGTAGTCTCCATGGTACTG 160
Db 61 GTCTGTTTCATCTTCTCATGTTCAAGGCGAGAACTCTAGATAGTAGTCTCCATGGCACTG 120
Qy 161 GTATGAATCAGACGTGGACAGAGAAGCCGGAATAATGGAGTGACGTTAGCACACAGAGG 220
Db 121 GTATGAATCAGACGTGGACAGAGAAGCCGGAATAATGGAGTGACGTTAGCACACAGAGG 180
Qy 221 ACACCTTACCTTCTTAAATGCTATTGCTCAGGACACTGCCCCAGATGACGCTATTAAATA 280
Db 181 ATACCTTGGCTTCTTAAAGTGCTATTGCTCAGGACACTGCCCCAGATGATGCTATTAAATA 240
Qy 281 ACACATGCATAACTAATGGCCATTGCTTGGCCATTATAGAAAGATGATCAGGGAGAAA 340
Db 241 ACACATGCATAACTAATGGCCATTGCTTGGCCATTATAGAAAGATGATCAGGGAGAAA 300
Qy 341 CCACGTTAATCTCTGGGTGATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTAC 400
Db 301 CCACATTAACTCTGGGTGATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTAC 360
Qy 401 CAAAAGCCGAGCTACCGAGACAATAGAAATGTTGTCGGACCAATTTTGTCAACCAATATT 460
Db 361 CGAAAGCCGAGCTACCGAGACAATAGAAATGTTGTCGGACCAATTTTGTCAACCAATATT 420
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Db 421 TGCAGCCTACACTGCCCCCTGTTGTTATAGGTCGGTCTTTGATGGCAGCATCCGATGGC 480
Qy 521 TGGCTGTGCTCATCTTATGGCTGTCTGATATGTCGCCATGATCGTCTTCTCCAGCTGCT 580
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Db 541 TTTGCTATAAGCAATTATTGAAGATATCTCAAGCAGGGGTGTTTACAACCGTGATTGG 600
Qy 641 AACAGGATGAAGCATTTTATCCAGTAGGAGAATCACTGAAAGACCTGATTGACCACTCAC-700 600
Db 601 AACAGGATGAAGCATTTTATCCAGTAGGAGAATCACTGAAAGACCTGATTGACCACTCAC-700 659
Qy 701 AAAGCTCTGCTAGTGGATCTGGATTACCTTTATTTGTTTCAGCGAACTATTGCCAAACAGA 760
Db 660 CAAGCTNCTGGAGTGGATCTGGATTGCCCTTTATTGGTTTCAGCGAACTATTGCCAAACAGA 719
Qy 761 TTCAGATGGTTCGGCAGGTTGGTAAGGGCCGGTATGGAGAGTATGGATGG 811
Db 720 TTCAGATGGTTCGGCAGGTTGGTAA-GGCCGCTATGGAGAAGTATGGATGG 769

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Job time : 5040 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2005, 05:59:53 ; Search time 188 Seconds
(without alignments)
1243.348 Million cell updates/sec

Title: US-10-600-645-2
Perfect score: 2838
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Scoring table: BLOSUM62
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Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Genesecp1980s.*
2: Genesecp1990s.*
3: Genesecp2000s.*
4: Genesecp2001s.*
5: Genesecp2002s.*
6: Genesecp2003as.*
7: Genesecp2003bs.*
8: Genesecp2004s.*
9: Genesecp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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2	2838	100.0	532	7	ADE61817	Adq9878 Antagonis
3	2838	100.0	532	7	ADE61815	Adw28798 Human bon
4	2838	100.0	532	9	ADW28803	Adw28803 Rat bone
5	2838	100.0	532	9	ADW28802	Adw28802 Rat bone
6	2838	100.0	532	9	ADW28801	Adw28801 Rat bone
7	2838	100.0	532	9	ADW28806	Adw28806 Rat bone
8	2838	100.0	532	9	ADX97416	Adx97416 Rat bone
9	2838	100.0	532	9	ADX97415	Adx97415 Rat bone
10	2838	100.0	532	9	ADX97414	Adx97414 Rat bone
11	2838	100.0	532	9	ADX97419	Adx97419 Rat bone
12	2838	99.5	532	2	AAR74343	BRK-1 pro
13	2823	99.5	532	2	AAR96201	Bone morph
14	2823	99.5	532	2	AAR95225	Mouse BMP
15	2823	99.5	532	2	AAR96248	Mouse BMP
16	2823	99.5	532	2	AAY33305	Aay33305 Human MAL
17	2823	99.5	532	9	ADY51876	Murine AL
18	2769	97.6	532	2	AAR55368	Human ACT
19	2769	97.6	532	2	AAR95207	Human ALK
20	2769	97.6	532	2	AAY33301	Human HAL
21	2769	97.6	532	6	AAE35259	Protein u
22	2769	97.6	532	6	ABO07221	Human p53
23	2769	97.6	532	7	ABR62828	Human bon
24	2769	97.6	532	7	ADE61821	Human Pro

25	2769	97.6	532	7	ADE61817	Ade61817 Human Pro
26	2769	97.6	532	8	ADQ9878	Adq9878 Antagonis
27	2769	97.6	532	9	ADW28798	Adw28798 Human bon
28	2769	97.6	532	9	ADX07491	Cyclin-de
29	2769	97.6	532	9	ADX97411	Adx97411 Human bon
30	2769	97.6	532	9	ADY51868	Ady51868 Human ALK
31	2769	97.6	532	4	ABG22870	Novel hum
32	2763	97.4	532	9	ADY81416	Human act
33	2653	93.5	753	4	ABG22877	Novel hum
34	2635.5	92.9	575	7	ADQ8017	Novel pro
35	2635.5	92.9	575	9	ADU40387	Novel hum
36	2616	92.2	500	2	AAR74342	Truncated
37	2604.5	91.8	637	7	ADQ8018	Novel pro
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39	2129.5	75.0	564	4	ABG22876	Novel hum
40	1950.5	68.7	502	4	AAE06221	Wild-type
41	1941	68.4	502	4	AAE06225	Human BMP
42	1941	68.4	502	5	ABG61890	Prostate
43	1941	68.4	502	5	ABJ05538	Breast ca
44	1941	68.4	502	5	ABG31268	Human bon
45	1941	68.4	502	6	ABJ19801	Androgen-

ALIGNMENTS

RESULT 1
AAR70237
ID AAR70237 standard; protein; 532 AA.
XX AC AAR70237;
XX AC
XX 25-MAR-2003 (revised)
DT 28-SEP-1995 (first entry)
XX
DE Bone morphogenic protein receptor CFK1-23a.
XX Bone morphogenic protein; receptor; serine/threonine kinase; BMP; bone;
KW cartilage; injury; treatment; inhibition.
XX
OS Rattus rattus.
XX
PN WO9507982-A1.
XX
PD 23-MAR-1995.
XX
PF 07-SEP-1994; 94WO-US010080.
XX
PR 17-SEP-1993; 93US-00123934.
XX
PI (GEMY) GENETICS INST INC.
XX Wozney JM, Celeste AJ, Thies RS, Yamaji N;
WPI; 1995-131350/17.
N-PSDB; AAQ83530.
XX
PT Truncated BMP and serine/threonine kinase receptor proteins - used to
inhibit the effects of BMP-2 and/or BMP-4.
XX
PS Claim 16; Page 50-51; 83pp; English.
XX
CC Truncated bone morphogenic protein (BMP) receptors and serine/threonine
kinase receptors may be used in compositions to inhibit the effects of
BMP's such as BMP-2 and BMP-4. The truncated receptors prof. comprise the
ligand binding domain, but not the serine/threonine kinase and
transmembrane domains. The truncated proteins are soluble and will be
excreted into supernatant by recombinant mammalian cells expressing them.
CC Such cells can be delivered in a medium or matrix which partially impedes
their mobility, thereby localising the cells to a site of bone or
cartilage injury. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 532 AA;

```
Query Match 100.0%; Score 2838; DB 2; Length 532;
Best Local Similarity 100.0%; Pred. No. 8.6e-279;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTQLTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKPKENGVTLPAPEDTLPLFK 60
DB 1 MTQLTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKPKENGVTLPAPEDTLPLFK 60
QY 61 CYCSGHCPDDAINNCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120
DB 61 CYCSGHCPDDAINNCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120
QY 121 TTECCRTNLCNQYLQPTLPVVIQPFDDGSVRWLAVLISMAVCIVAMIVFSSCFCKHYC 180
DB 121 TTECCRTNLCNQYLQPTLPVVIQPFDDGSVRWLAVLISMAVCIVAMIVFSSCFCKHYC 180
QY 181 KSISGRGRYNRDLQDEAFIPVGSLSKDLIDQSQSGSGGLPLVQRTIAKQIOMVRQV 240
DB 181 KSISGRGRYNRDLQDEAFIPVGSLSKDLIDQSQSGSGGLPLVQRTIAKQIOMVRQV 240
QY 241 GKGRYGEVMMGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFTAAADIKGTG 300
DB 241 GKGRYGEVMMGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFTAAADIKGTG 300
QY 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
DB 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
QY 361 RDLKSKNILIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYNAPEVLDESLSKN 420
DB 361 RDLKSKNILIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYNAPEVLDESLSKN 420
QY 421 HFQPYIMADYISFGLIIWEMARRCITGGIVEEYQLPYYNMVPSDPSYEDMREVVCVKRLR 480
DB 421 HFQPYIMADYISFGLIIWEMARRCITGGIVEEYQLPYYNMVPSDPSYEDMREVVCVKRLR 480

RESULT 2
ID ADE61819 standard; protein; 532 AA.
XX ADE61819;
XX AC ADE61819;
XX DT 29-JAN-2004 (first entry)
XX DE Rat Protein AAB33865, SEQ ID NO 7747.
XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX OS Rattus norvegicus.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GEMO ) GEN HOSPITAL CORP.
XX PA (FARB ) BAYER AG.
XX FI Woolf C, D'urso D, Befort K, Costigan M;
XX DR WPI; 2003-268312/26.
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GENBANK; AAB33865.

New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 532 AA;

Query Match 100.0%; Score 2838; DB 7; Length 532;
Best Local Similarity 100.0%; Pred. No. 8.6e-279;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTQLTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKPKENGVTLPAPEDTLPLFK 60
DB 1 MTQLTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKPKENGVTLPAPEDTLPLFK 60
QY 61 CYCSGHCPDDAINNCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120
DB 61 CYCSGHCPDDAINNCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120
QY 121 TTECCRTNLCNQYLQPTLPVVIQPFDDGSVRWLAVLISMAVCIVAMIVFSSCFCKHYC 180
DB 121 TTECCRTNLCNQYLQPTLPVVIQPFDDGSVRWLAVLISMAVCIVAMIVFSSCFCKHYC 180
QY 181 KSISGRGRYNRDLQDEAFIPVGSLSKDLIDQSQSGSGGLPLVQRTIAKQIOMVRQV 240
DB 181 KSISGRGRYNRDLQDEAFIPVGSLSKDLIDQSQSGSGGLPLVQRTIAKQIOMVRQV 240
QY 241 GKGRYGEVMMGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFTAAADIKGTG 300
DB 241 GKGRYGEVMMGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFTAAADIKGTG 300
QY 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
DB 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
QY 361 RDLKSKNILIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYNAPEVLDESLSKN 420
DB 361 RDLKSKNILIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYNAPEVLDESLSKN 420
QY 421 HFQPYIMADYISFGLIIWEMARRCITGGIVEEYQLPYYNMVPSDPSYEDMREVVCVKRLR 480
DB 421 HFQPYIMADYISFGLIIWEMARRCITGGIVEEYQLPYYNMVPSDPSYEDMREVVCVKRLR 480

QY 481 PIVSNRWSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
DB 481 PIVSNRWSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532

RESULT 3
ID ADE61815
AC ADE61815 standard; protein; 532 AA.
AC ADE61815;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein AAB33865, SEQ ID NO 7743.
XX

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.

PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; AAB33865.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX

Claim 1; Page: 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

Sequence 532 AA;

Query Match 100.0%; Score 2838; DB 7; Length 532;
Best Local Similarity 100.0%; Pred No. 8.6e-279;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTOLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPLFLK 60
DB 1 MTOLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPLFLK 60
QY 61 CYCSGHCDDDAINTCITNGHCFALIEEDDQGETTLTSCMKYEGSDFOCKSPKQALRR 120
DB 61 CYCSGHCDDDAINTCITNGHCFALIEEDDQGETTLTSCMKYEGSDFOCKSPKQALRR 120
QY 121 TIECCRTNLCNOYLQPTLPVVGPFDDGSVRWLAVLISMAVCIVAMIVFSSFCYKHYC 180
DB 121 TIECCRTNLCNOYLQPTLPVVGPFDDGSVRWLAVLISMAVCIVAMIVFSSFCYKHYC 180
QY 181 KSISRGYRNRDLEQDEAFIPVGESLKDLIDQSQSSGSGGLPLLQVORTIAKIQMVQV 240
DB 181 KSISRGYRNRDLEQDEAFIPVGESLKDLIDQSQSSGSGGLPLLQVORTIAKIQMVQV 240
QY 241 GKGRYGEVWGMKGRCVAVKVFVFTTEASWFERETIYQTVLMRHNILGFTAAIDIKGTG 300
DB 241 GKGRYGEVWGMKGRCVAVKVFVFTTEASWFERETIYQTVLMRHNILGFTAAIDIKGTG 300
QY 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAISAAACGLCHLHTEIYGTQKPAIAH 360
DB 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAISAAACGLCHLHTEIYGTQKPAIAH 360
QY 361 RDLKSKNLIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDESLSKN 420
DB 361 RDLKSKNLIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDESLSKN 420
QY 421 HFQPYIMADIYSFGLIIMEMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVCKRLR 480
DB 421 HFQPYIMADIYSFGLIIMEMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVCKRLR 480
QY 481 PIVSNRWSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
DB 481 PIVSNRWSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532

RESULT 4

ADW28803

ID ADW28803 standard; protein; 532 AA.

XX AC ADW28803;

XX DT 07-APR-2005 (first entry)

XX DE Rat bone morphogenetic protein (BMP) receptor type 1 Seq 107.

XX KW receptor; bone morphogenetic protein; bone injury; antibody production;
KW TGF beta antagonist; BMP-antagonist; osteopathic; osteopenias;
XX osteoporosis.

XX OS Rattus norvegicus.

XX PN WO2005003158-A2.

XX PD 13-JAN-2005.

XX PF 15-JUN-2004; 2004WO-US018910.

XX PR 16-JUN-2003; 2003US-00463190.

XX XX (CLLT) CELLTech R & D INC.

XX PI Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepfer BW;

XX PI Van Ness J, Winkler DG;

XX XX WPI; 2005-081936/09.

XX DR N-PSDB; ADW28817.

XX XX

PT	New antibody or antigen-binding fragment that binds specifically to
PT	sclerostin polypeptide and which inhibits binding of sclerostin
PT	polypeptide to a bone morphogenic protein, useful for increasing bone
PT	mineral content or density.
XX	
XX	Claim 1; SEQ ID NO 107; 205pp; English.
XX	
CC	This invention relates to a novel antibody or antigen-binding fragment
CC	that binds specifically to a sclerostin (SOST) polypeptide and impairs
CC	formation of a sclerostin homodimer. Specifically, it refers to an
CC	antibody that competitively inhibits binding of the sclerostin
CC	polypeptide to a bone morphogenic protein (BMP) Type I receptor binding
CC	site or a BMP Type II receptor binding site. The present invention
CC	describes a hybridoma cell capable of producing the antibody and a host
CC	cell for antibody expression. Furthermore, it provides a nucleic acid
CC	molecule encoding a transforming growth factor-beta (TGF-beta) binding
CC	protein known as SOST (and also BEER) and methods for detection thereof.
CC	Accordingly, such antibodies and osteopathic compositions of the
CC	invention can be used for treating osteopenia, osteoporosis, fractures
CC	and other disorders related to low bone mineral content and density. As
CC	such, these compositions improve bone mineralization and can be described
CC	as TGF-beta antagonists and/ or BMP-antagonists. This polypeptide
CC	sequence is a bone morphogenetic protein receptor type 1 given in an
CC	embodiment of the invention.
XX	
XX	Sequence 532 AA:
XX	

Query Match	100.0%	Score 2838	DB 9	Length 532
Best Local Similarity	100.0%	Prod. No. 8.6e-279		
Matches 532	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	MTQLYTIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDOKKPEBNGVTTLAPEDTLPKL	60	
Db	1	MTQLYTIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDOKKPEBNGVTTLAPEDTLPKL	60	
Qy	61	CYSGHCHPDDAINNTCITNGHCFAIIEEDDOGETTTLTSGCMKYEGSDPCKDSPAQLRR	120	
Db	61	CYSGHCHPDDAINNTCITNGHCFAIIEEDDOGETTTLTSGCMKYEGSDPCKDSPAQLRR	120	
Qy	121	TIECCRTNLNQNLYLOPTLPVVIQPFDFGSVRWLAVLISMAVCIVAMIVFSSCFYKHYC	180	
Db	121	TIECCRTNLNQNLYLOPTLPVVIQPFDFGSVRWLAVLISMAVCIVAMIVFSSCFYKHYC	180	
Qy	181	KSISRRGRYNRDLBQDEAFIPVGSLSKDLIDQSSGSGGLPLLVTAKQIQMVRQV	240	
Db	181	KSISRRGRYNRDLBQDEAFIPVGSLSKDLIDQSSGSGGLPLLVTAKQIQMVRQV	240	
Qy	241	GKGRYGEVMGKWRGEVAVKVFTTBEASWFRETEIYQTVLMRHNILGFIADIKGTG	300	
Db	241	GKGRYGEVMGKWRGEVAVKVFTTBEASWFRETEIYQTVLMRHNILGFIADIKGTG	300	
Qy	301	SWTQLYLITDYHENGSLYDFLKCATLDTLRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH	360	
Db	301	SWTQLYLITDYHENGSLYDFLKCATLDTLRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH	360	
Qy	361	RDLSKSNILIKONGSCCIIADGLAVKNSDNEVDIPLNTRVGTTRRYMAPEVLDESLSKN	420	
Db	361	RDLSKSNILIKONGSCCIIADGLAVKNSDNEVDIPLNTRVGTTRRYMAPEVLDESLSKN	420	
Qy	421	HFQPYIMADIIYSFGLIIWEMARRCITGGIVBEEYQLPYNNMVPSPDSEDMREVCVKRLR	480	
Db	421	HFQPYIMADIIYSFGLIIWEMARRCITGGIVBEEYQLPYNNMVPSPDSEDMREVCVKRLR	480	
Qy	481	PIVSNRNRNSDECLRAVLKLMSECAWHPASRLTALRIKKTIAKVVESQDVKI	532	
Db	481	PIVSNRNRNSDECLRAVLKLMSECAWHPASRLTALRIKKTIAKVVESQDVKI	532	

RESULT 5
ADW28802
ID ADW28802 standard; protein; 532 AA.
XX
AC ADW28802;

XX	07-APR-2005	(first entry)
XX		
XX		Rat bone morphogenetic protein (BMP) receptor type 1 Seq 106.
XX		
XX		receptor; bone morphogenetic protein; bone injury; antibody production;
KW		TGF-beta antagonist; BMP-antagonist; osteopathic; osteopenias;
KW		osteoporosis.
XX		
XX		Rattus norvegicus.
OS		
XX		WQ2005003158-A2.
PN		
XX		13-JAN-2005.
XX		
XX		15-JUN-2004; 2004WO-US018910.
XX		
XX		16-JUN-2003; 2003US-00463190.
PR		
XX		(CLLT) CELLTECH R & D INC.
PA		
XX		Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepser BW;
PI		Van Ness J, Winkler DG;
PI		
XX		WPI; 2005-081936/09.
DR		N-PSDB; ADW28816.
DR		
XX		
XX		New antibody or antigen-binding fragment that binds specifically to
PT		sclerostin polypeptide and which inhibits binding of sclerostin
PT		polypeptide to a bone morphogenic protein, useful for increasing bone
PT		mineral content or density.
XX		
XX		Claim 1; SEQ ID NO 106; 205pp; English.
XX		
CC		This invention relates to a novel antibody or antigen-binding fragment
CC		that binds specifically to a sclerostin (SOST) polypeptide and impairs
CC		formation of a sclerostin homodimer. Specifically, it refers to an
CC		antibody that competitively inhibits binding of the sclerostin
CC		polypeptide to a bone morphogenic protein (BMP) Type I receptor binding
CC		site or a BMP Type II receptor binding site. The present invention
CC		describes a hybridoma cell capable of producing the antibody and a host
CC		cell for antibody expression. Furthermore, it provides a nucleic acid
CC		molecule encoding a transforming growth factor-beta (TGF-beta) binding
CC		protein known as SOST (and also BIER) and methods for detection thereof.
CC		Accordingly, such antibodies and osteopathic compositions of the
CC		invention can be used for treating osteopenia, osteoporosis, fractures
CC		and other disorders related to low bone mineral content and density. As
CC		such, these compositions improve bone mineralization and can be described
CC		as TGF-beta antagonists and/ or BMP-antagonists. This polypeptide
CC		sequence is a bone morphogenetic protein receptor type 1 given in an
CC		embodiment of the invention.
XX		
XX		Sequence 532 AA:
SO		

	Query Match	100.0%;	Score 2838;	DB 9;	Length 532;
	Best Local Similarity	100.0%;	Pred. No. 8.6e-279;		
	Matches 532;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGKMSDVDDQKPENGVTTLAPEDTLPFLK	60		
Db	1	MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGKMSDVDDQKPENGVTTLAPEDTLPFLK	60		
Qy	61	CYCSGHCPDDAINTCITNGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR	120		
Db	61	CYCSGHCPDDAINTCITNGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR	120		
Qy	121	TIECCRTNLNCQYQPTLPVWLGPPFDGSRVRLAVLISMAVCIVAMIVSSCFYKHVC	180		
Db	121	TIECCRTNLNCQYQPTLPVWLGPPFDGSRVRLAVLISMAVCIVAMIVSSCFYKHVC	180		
Qy	181	KSTSSRGRYNRDLEQDEAFIPVGESIKLDIDQSSGSGSLPLLVORTIAKIQMVROV	240		
Db	181	KSTSSRGRYNRDLEQDEAFIPVGESIKLDIDQSSGSGSLPLLVORTIAKIQMVROV	240		

(CLLT) CELLTECH R & D INC.
PA Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepers BW;
PI Van Ness J, Winkler DG;
XX WPI; 2005-081936/09.
XX
XX
XX New antibody or antigen-binding fragment that binds specifically to
PT sclerostin polypeptide and which inhibits binding of sclerostin
PT polypeptide to a bone morphogenic protein, useful for increasing bone
PT mineral content or density.
XX
XX
XX Claim 1; SEQ ID NO 110; 205pp; English.
XX
XX This invention relates to a novel antibody or antigen-binding fragment
CC that binds specifically to a sclerostin (SOST) polypeptide and impairs
CC formation of a sclerostin homodimer. Specifically, it refers to an
CC antibody that competitively inhibits binding of the sclerostin
CC polypeptide to a bone morphogenic protein (BMP) Type I receptor binding
CC site or a BMP Type II receptor binding site. The present invention
CC describes a hybridoma cell capable of producing the antibody and a host
CC cell for antibody expression. Furthermore, it provides a nucleic acid
CC molecule encoding a transforming growth factor-beta (TGF-beta) binding
CC protein known as SOST (and also BBER) and methods for detection thereof.
CC Accordingly, such antibodies and osteopathic compositions of the
CC invention can be used for treating osteopenia, osteoporosis, fractures
CC and other disorders related to low bone mineral content and density. As
CC such, these compositions improve bone mineralization and can be described
CC as TGF-beta antagonists and/or BMP-antagonists. This polypeptide
CC sequence is a bone morphogenetic protein receptor type 1 given in an
CC exemplification of the invention.
XX
XX
XX Sequence 532 AA;
PS
PT Query Match 100.0%; Score 2838; DB 9; Length 532;
PT Best Local Similarity 100.0%; Pred. No. 8.6e-279;
PT Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPLK 60
QY 61 CYCSGHCDDAINNCTINGHCFALIEDDQGETTLTSGCMKYSGDFQCKDSPAQLRR 120
Db 61 CYCSGHCDDAINNCTINGHCFALIEDDQGETTLTSGCMKYSGDFQCKDSPAQLRR 120
QY 121 TIECCTNLCNOYLOPTLPVPIGFFDGSVRWLAVLISMAVICIVAMIVFSSCFYKHC 180
Db 121 TIECCTNLCNOYLOPTLPVPIGFFDGSVRWLAVLISMAVICIVAMIVFSSCFYKHC 180
QY 181 KSISRGYNRDLEQDEAFIPVGSLSKDLIDQSSGSGSLPLLVQRTIAKIQMVQRV 240
Db 181 KSISRGYNRDLEQDEAFIPVGSLSKDLIDQSSGSGSLPLLVQRTIAKIQMVQRV 240
QY 241 KGGRYGEVWGMKRGKAVKVPFTEASFRTEIYQTVLMRHENILGFIADIKGTG 300
Db 241 KGGRYGEVWGMKRGKAVKVPFTEASFRTEIYQTVLMRHENILGFIADIKGTG 300
QY 301 SWTQLYLTIDVHENGSLYDFLKCATLDRALLKLAYSACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLTIDVHENGSLYDFLKCATLDRALLKLAYSACGLCHLHTEIYGTQKPAIAH 360
QY 361 RDLKSKNLIKNGSCCIIADLGLAVKFNSTDNEVDIPLNTRVGTTRRYMAPEVLDESLSKN 420
Db 361 RDLKSKNLIKNGSCCIIADLGLAVKFNSTDNEVDIPLNTRVGTTRRYMAPEVLDESLSKN 420
QY 421 HFQPYIMADIYSFGLIIEWEMARRCITGIVEYQLPYNNMVPSPDSYEDMREVVCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIEWEMARRCITGIVEYQLPYNNMVPSPDSYEDMREVVCVKRLR 480
QY 481 PIVSNRWNDSDECLRAVLKLMSECAHNPNASRLTALRIKTKLAKMVESQDVKI 532
Db 481 PIVSNRWNDSDECLRAVLKLMSECAHNPNASRLTALRIKTKLAKMVESQDVKI 532

RESULT 8
ADX97416
ID ADX97416 standard; protein; 532 AA.
XX
XX AC ADX97416;
XX
XX DT 05-MAY-2005 (first entry)
XX
XX DE Rat bone morphogenic protein type I receptor, SEQ ID 76.
XX
XX KW antibody; sclerostin; SOST; bone morphogenic protein receptor;
KW Transforming Growth Factor; osteopathic; gene therapy; bone repair;
KW osteopenia; osteoporosis; bone injury.
XX
XX OS Rattus norvegicus.
XX
XX FN WO2005014650-A2.
XX
XX PD 17-FEB-2005.
XX
XX PF 15-JUN-2004; 2004WO-US018912.
XX
XX PR 16-JUN-2003; 2003US-0478977P.
XX
XX PA (CLLT) CELLTECH R & D INC.
XX
XX PI Winkler DG, Shi J, Latham J;
XX
XX DR WPI; 2005-163219/17.
XX
XX DR N-FSDB; ADX97430.
XX
XX New isolated antibody specific for a sclerostin polypeptide, useful for
PT increasing bone mineralization or for treating or preventing conditions
PT associated with low bone mineral density, e.g. osteoporosis or
PT osteopenia.
XX
XX Claim 1; SEQ ID NO 76; 157pp; English.
XX
XX The invention relates to a novel isolated antibody, or its antigen-
CC binding fragment, which binds specifically to a sclerostin (SOST)
CC polypeptide. The SOST polypeptide comprises any of 6 sequences having 190
CC or 213 amino acids, fully defined in the specification (ADX97341,
CC ADX97360, ADX97398, ADX97400, ADX97402 or ADX97408). The antibody
CC competitively inhibits binding of the SOST polypeptide to a bone
CC morphogenic protein (BMP) Type I Receptor binding site and a BMP Type II
CC Receptor binding site, where the BMP Type I Receptor binding site is
CC capable of binding to a BMP Type I Receptor polypeptide. The invention
CC further comprises: a hybridoma cell producing the new antibody; a host
CC cell that is capable of expressing the new antibody; a composition
CC comprising the new antibody, or its antigen-binding fragment, and a
CC physiological carrier; an immunogen comprising a peptide comprising 6, 7,
CC 8, 9, 10, 11, 12, or at least 21-50 or 20-75 consecutive amino acids of
CC the SOST polypeptide; methods for producing an antibody that specifically
CC binds to the SOST polypeptide; and methods for identifying an antibody
CC that modulates a Transforming Growth Factor (TGF)-beta signaling pathway,
CC that impairs binding of a BMP to the SOST polypeptide, that impairs SOST
CC homodimer formation, or that increases bone mineral content. The novel
CC antibody and compositions have osteopathic activity. The SOST nucleic
CC acids may be used in gene therapy. The composition and methods are useful
CC for increasing bone mineralization, which may treat or prevent diseases
CC or conditions associated with low bone mineral density, such as
CC osteopenia, osteoporosis or bone fractures. This sequence represents a
CC rat bone morphogenic protein type I receptor of the invention.
XX
XX Sequence 532 AA;
PS
PT Query Match 100.0%; Score 2838; DB 9; Length 532;
PT Best Local Similarity 100.0%; Pred. No. 8.6e-279;
PT Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPLK 60

Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTTLAPEDTLPLFLK 60
Qy 61 CYSGHCHPDDAINNCTITNGHCFALIEEDDQGETTLTSGCMKYEVSDFQCKDSPKQALRR 120
Db 61 CYSGHCHPDDAINNCTITNGHCFALIEEDDQGETTLTSGCMKYEVSDFQCKDSPKQALRR 120
Qy 121 TIECCRTNLCNOYLQPTLPPVWIGPPFDGSRVRLAVLISMAVCIVAMIVFSSFCFKHYC 180
Db 121 TIECCRTNLCNOYLQPTLPPVWIGPPFDGSRVRLAVLISMAVCIVAMIVFSSFCFKHYC 180
Qy 181 KSISRRGRYNRDLQDEAFIPVGESLKDLDQSSGSGGLPLLVORTIAKIQMVRQV 240
Db 181 KSISRRGRYNRDLQDEAFIPVGESLKDLDQSSGSGGLPLLVORTIAKIQMVRQV 240
Qy 241 GKGRYGVMMGKWRGEKVAVKVFTTEASWFRTEIYQTVLMRHNILGFIADIKGTG 300
Db 241 GKGRYGVMMGKWRGEKVAVKVFTTEASWFRTEIYQTVLMRHNILGFIADIKGTG 300
Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Qy 361 RDLKSKNILIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSKN 420
Db 361 RDLKSKNILIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSKN 420
Qy 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYNNVPSDPSYEDMRVVCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYNNVPSDPSYEDMRVVCVKRLR 480
Qy 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKWVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKWVESQDVKI 532

RESULT 9

ADX97415
ID ADX97415 standard; protein; 532 AA.
AC ADX97415;
XX
XX 05-MAY-2005 (first entry)
XX Rat bone morphogenic protein type I receptor, SEQ ID 75.
XX antibody; sclerostin; SOST; bone morphogenic protein receptor;
XX Transforming Growth Factor; osteopathic; gene therapy; bone repair;
XX osteopenia; osteoporosis; bone injury.
XX Rattus norvegicus.
XX WO2005014650-A2.
XX
XX 17-FEB-2005.
XX
XX 15-JUN-2004; 2004WO-US018912.
XX
XX 16-JUN-2003; 2003US-0478977P.
XX
XX (CLLT) CELTECH R & D INC.
XX Winkler DG, Shi J, Latham J;
XX
XX WPI; 2005-163219/17.
XX N-PSDB; ADX97429.
XX
XX New isolated antibody specific for a sclerostin polypeptide, useful for
XX increasing bone mineralization or for treating or preventing conditions
XX associated with low bone mineral density, e.g. osteoporosis or
XX osteopenia.
XX
XX Claim 1; SEQ ID NO 75; 157pp; English.

XX The invention relates to a novel isolated antibody, or its antigen-
CC binding fragment, which binds specifically to a sclerostin (SOST)
CC polypeptide. The SOST polypeptide comprises any of 6 sequences having 190
CC or 213 amino acids, fully defined in the specification (ADX97341,
CC ADX97360, ADX97398, ADX97400, ADX97402 or ADX97408). The antibody
CC competitively inhibits binding of the SOST polypeptide to a BMP
CC morphogenic protein (BMP) Type I Receptor binding site and a BMP Type II
CC Receptor binding site, where the BMP Type I Receptor binding site is
CC capable of binding to a BMP Type I Receptor polypeptide. The invention
CC further comprises: a hybridoma cell producing the new antibody; a host
CC cell that is capable of expressing the new antibody; a composition
CC comprising the new antibody, or its antigen-binding fragment, and a
CC physiological carrier; an immunogen comprising a peptide comprising 6, 7,
CC 8, 9, 10, 11, 12, or at least 21-50 or 20-75 consecutive amino acids of
CC the SOST polypeptide; methods for producing an antibody that specifically
CC binds to the SOST polypeptide; and methods for identifying an antibody
CC that modulates a Transforming Growth Factor (TGF)-beta signaling pathway,
CC that impairs binding of a BMP to the SOST polypeptide, that impairs SOST
CC homodimer formation, or that increases bone mineral content. The novel
CC antibody and compositions have osteopathic activity. The SOST nucleic
CC acids may be used in gene therapy. The composition and methods are useful
CC for increasing bone mineralization, which may treat or prevent diseases
CC or conditions associated with low bone mineral density, such as
CC osteopenia, osteoporosis or bone fractures. This sequence represents a
CC rat bone morphogenic protein type I receptor of the invention.
XX
SQ Sequence 532 AA;

Query Match 100.0%; Score 2838; DB 9; Length 532;
Best Local Similarity 100.0%; Pred. NO. 8.6e-279;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTTLAPEDTLPLFLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTTLAPEDTLPLFLK 60
Qy 61 CYSGHCHPDDAINNCTITNGHCFALIEEDDQGETTLTSGCMKYEVSDFQCKDSPKQALRR 120
Db 61 CYSGHCHPDDAINNCTITNGHCFALIEEDDQGETTLTSGCMKYEVSDFQCKDSPKQALRR 120
Qy 121 TIECCRTNLCNOYLQPTLPPVWIGPPFDGSRVRLAVLISMAVCIVAMIVFSSFCFKHYC 180
Db 121 TIECCRTNLCNOYLQPTLPPVWIGPPFDGSRVRLAVLISMAVCIVAMIVFSSFCFKHYC 180
Qy 181 KSISRRGRYNRDLQDEAFIPVGESLKDLDQSSGSGGLPLLVORTIAKIQMVRQV 240
Db 181 KSISRRGRYNRDLQDEAFIPVGESLKDLDQSSGSGGLPLLVORTIAKIQMVRQV 240
Qy 241 GKGRYGVMMGKWRGEKVAVKVFTTEASWFRTEIYQTVLMRHNILGFIADIKGTG 300
Db 241 GKGRYGVMMGKWRGEKVAVKVFTTEASWFRTEIYQTVLMRHNILGFIADIKGTG 300
Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Qy 361 RDLKSKNILIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSKN 420
Db 361 RDLKSKNILIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSKN 420
Qy 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYNNVPSDPSYEDMRVVCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYNNVPSDPSYEDMRVVCVKRLR 480
Qy 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKWVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKWVESQDVKI 532

RESULT 10

ADX97414
ID ADX97414 standard; protein; 532 AA.

XX AC ADX97414;
XX DT 05-MAY-2005 (first entry)
XX DE Rat bone morphogenic protein type I receptor, SEQ ID 74.
XX KW antibody; sclerostin; SOST; bone morphogenic protein receptor;
XX KW Transforming Growth Factor; osteopathic; gene therapy; bone repair;
XX KW osteopenia; osteoporosis; bone injury.
XX OS Rattus sp.
XX PN WO2005014650-A2.
XX PD 17-FEB-2005.
XX PF 15-JUN-2004; 2004WO-US018912.
XX PR 16-JUN-2003; 2003US-0478977P.
XX PA (CLLT) CELLTECH R & D INC.
XX PI Winkler DG, Shi J, Latham J;
XX PI WPI; 2005-163219/17.
XX DR N-PSDB; ADX97428.
XX
XX PT New isolated antibody specific for a sclerostin polypeptide, useful for
XX PT increasing bone mineralization or for treating or preventing conditions
XX PT associated with low bone mineral density, e.g. osteoporosis or
XX PT osteopenia.
XX PS Claim 1; SEQ ID NO 74; 157pp; English.
XX
XX CC The invention relates to a novel isolated antibody, or its antigen-
XX CC binding fragment, which binds specifically to a sclerostin (SOST)
XX CC polypeptide. The SOST polypeptide comprises any of 6 sequences having 190
XX CC or 213 amino acids, fully defined in the specification (ADX97341,
XX CC ADX97360, ADX97398, ADX97400, ADX97402 or ADX97408). The antibody
XX CC competitively inhibits binding of the SOST polypeptide to a bone
XX CC morphogenic protein (BMP) Type I Receptor binding site and a BMP Type II
XX CC Receptor binding site, where the BMP Type I Receptor binding site is
XX CC capable of binding to a BMP type I Receptor polypeptide. The invention
XX CC further comprises: a hybridoma cell producing the new antibody; a host
XX CC cell that is capable of expressing the new antibody; a composition
XX CC comprising the new antibody, or its antigen-binding fragment, and a
XX CC physiological carrier; an immunogen comprising a peptide comprising 6, 7,
XX CC 8, 9, 10, 11, 12, or at least 21-50 or 20-75 consecutive amino acids of
XX CC the SOST polypeptide; methods for producing an antibody that specifically
XX CC binds to the SOST polypeptide; and methods for identifying an antibody
XX CC that modulates a Transforming Growth Factor (TGF)-beta signaling pathway,
XX CC that impairs binding of a BMP to the SOST polypeptide, that impairs SOST
XX CC homodimer formation, or that increases bone mineral content. The novel
XX CC antibody and compositions have osteopathic activity. The SOST nucleic
XX CC acids may be used in gene therapy. The composition and methods are useful
XX CC for increasing bone mineralization, which may treat or prevent diseases
XX CC or conditions associated with low bone mineral density, such as
XX CC osteopenia, osteoporosis or bone fractures. This sequence represents a
XX CC rat bone morphogenic protein type I receptor of the invention.
XX
XX SQ Sequence 532 AA;
Query Match 100.0%; Score 2838; DB 9; Length 532;
Best Local Similarity 100.0%; Pred. No. 8.6e-279;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTQLYTYRLLGACLFILSHVQGNLDSMLHGTGMKSDVDQKPKNGVTLPEDTLPLFK 60
DB 1 MTQLYTYRLLGACLFILSHVQGNLDSMLHGTGMKSDVDQKPKNGVTLPEDTLPLFK 60
QY 61 CYCSGHCPCDDAINNCTITNGHCFALIEEDDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
|||||

Db 61 CYCSGHCPCDDAINNCTITNGHCFALIEEDDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
QY 121 TIECRTLNCQYLQPTLPVVGFFPDGSRVRLAVLISMVAVCIAMIVFSSCFYKHVC 180
|||||
Db 121 TIECRTLNCQYLQPTLPVVGFFPDGSRVRLAVLISMVAVCIAMIVFSSCFYKHVC 180
QY 181 KSISRGYRNDLEQDEAFIPVGSLSKDLIDQSQSSGSGGLPLLVQRTIAKIQIMVRQV 240
Db 181 KSISRGYRNDLEQDEAFIPVGSLSKDLIDQSQSSGSGGLPLLVQRTIAKIQIMVRQV 240
QY 241 GKGRYGEVWGMKGKRGKAVKVVFFTTBEASVFRTEIYQTVLMRHENILGFTAAADIKGTG 300
Db 241 GKGRYGEVWGMKGKRGKAVKVVFFTTBEASVFRTEIYQTVLMRHENILGFTAAADIKGTG 300
QY 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAISAACGLCHLHTEIYGTQGPAAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAISAACGLCHLHTEIYGTQGPAAIAH 360
QY 361 RDLXKNLIIKNGSCCIIADIGLAVKFNDSNDTNEVDIPLNTRVGTTRYMAPEVLDLSLKN 420
Db 361 RDLXKNLIIKNGSCCIIADIGLAVKFNDSNDTNEVDIPLNTRVGTTRYMAPEVLDLSLKN 420
QY 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVVEYQLPYNNMVPSPDSYEDMRVWCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVVEYQLPYNNMVPSPDSYEDMRVWCVKRLR 480
QY 481 PIVSNRWNDSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRWNDSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
RESULT 11
ADX97419
ID ADX97419 standard; protein; 532 AA.
XX AC ADX97419;
XX DT 05-MAY-2005 (first entry)
XX DE Rat bone morphogenic protein type Ia receptor, SEQ ID 79.
XX KW antibody; sclerostin; SOST; bone morphogenic protein receptor;
XX KW Transforming Growth Factor; osteopathic; gene therapy; bone repair;
XX KW osteopenia; osteoporosis; bone injury.
XX OS Rattus sp.
XX PN WO2005014650-A2.
XX PD 17-FEB-2005.
XX PF 15-JUN-2004; 2004WO-US018912.
XX PR 16-JUN-2003; 2003US-0478977P.
XX PA (CLLT) CELLTECH R & D INC.
XX PI Winkler DG, Shi J, Latham J;
XX PI WPI; 2005-163219/17.
XX
XX PT New isolated antibody specific for a sclerostin polypeptide, useful for
XX PT increasing bone mineralization or for treating or preventing conditions
XX PT associated with low bone mineral density, e.g. osteoporosis or
XX PT osteopenia.
XX PS Claim 1; SEQ ID NO 79; 157pp; English.
XX
XX CC The invention relates to a novel isolated antibody, or its antigen-
XX CC binding fragment, which binds specifically to a sclerostin (SOST)
XX CC polypeptide. The SOST polypeptide comprises any of 6 sequences having 190
XX CC or 213 amino acids, fully defined in the specification (ADX97341,
XX CC ADX97360, ADX97398, ADX97400, ADX97402 or ADX97408). The antibody
XX CC competitively inhibits binding of the SOST polypeptide to a bone
XX CC morphogenic protein (BMP) Type I Receptor binding site and a BMP Type II
XX CC Receptor binding site, where the BMP Type I Receptor binding site is
XX CC capable of binding to a BMP type I Receptor polypeptide. The invention
XX CC further comprises: a hybridoma cell producing the new antibody; a host
XX CC cell that is capable of expressing the new antibody; a composition
XX CC comprising the new antibody, or its antigen-binding fragment, and a
XX CC physiological carrier; an immunogen comprising a peptide comprising 6, 7,
XX CC 8, 9, 10, 11, 12, or at least 21-50 or 20-75 consecutive amino acids of
XX CC the SOST polypeptide; methods for producing an antibody that specifically
XX CC binds to the SOST polypeptide; and methods for identifying an antibody
XX CC that modulates a Transforming Growth Factor (TGF)-beta signaling pathway,
XX CC that impairs binding of a BMP to the SOST polypeptide, that impairs SOST
XX CC homodimer formation, or that increases bone mineral content. The novel
XX CC antibody and compositions have osteopathic activity. The SOST nucleic
XX CC acids may be used in gene therapy. The composition and methods are useful
XX CC for increasing bone mineralization, which may treat or prevent diseases
XX CC or conditions associated with low bone mineral density, such as
XX CC osteopenia, osteoporosis or bone fractures. This sequence represents a
XX CC rat bone morphogenic protein type I receptor of the invention.
XX

competitively inhibits binding of the SOST polypeptide to a bone morphogenic protein (BMP) Type I Receptor binding site and a BMP Type II Receptor binding site, where the BMP Type I Receptor binding site is capable of binding to a BMP Type I Receptor polypeptide. The invention further comprises: a hybridoma cell producing the new antibody; a host cell that is capable of expressing the new antibody; a composition comprising the new antibody, or its antigen-binding fragment, and a physiological carrier; an immunogen comprising a peptide comprising 6, 7, 8, 9, 10, 11, 12, or at least 21-50 or 20-75 consecutive amino acids of the SOST polypeptide; methods for producing an antibody that specifically binds to the SOST polypeptide; and methods for identifying an antibody that modulates a Transforming Growth Factor (TGF)-beta signaling pathway, that impairs binding of a BMP to the SOST polypeptide, that impairs SOST homodimer formation, or that increases bone mineral content. The novel antibody and compositions have osteopathic activity. The SOST nucleic acids may be used in gene therapy. The composition and methods are useful for increasing bone mineralization, which may treat or prevent diseases or conditions associated with low bone mineral density, such as osteopenia, osteoporosis or bone fractures. This sequence represents a rat bone morphogenic protein type Ia receptor of the invention.

Query Match	100.0%	Score 2838;	DB 9;	Length 532;
Best Local Similarity	100.0%;	Pred. No. 8.6e-279;		
Matches 532;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MTQLYTYIRLLGACLFIIISHVQGNQDLSMLHGTGKMSDVDOKKPENGVTLAPEDTLPFLK	60	
Db	1	MTQLYTYIRLLGACLFIIISHVQGNQDLSMLHGTGKMSDVDOKKPENGVTLAPEDTLPFLK	60	
Qy	61	CYSGHGPCDDAINNNTCITNGHCFAIIEBDDOGETTTLTSGCMKYEGSDFOCKDSKPAQLRR	120	
Db	61	CYSGHGPCDDAINNNTCITNGHCFAIIEBDDOGETTTLTSGCMKYEGSDFOCKDSKPAQLRR	120	
Qy	121	TIECCRTNLCNQYLQPTLPVVIQPPFDGSVRWLAVLISMAVCITVAMIVSSCFCKYKHYC	180	
Db	121	TIECCRTNLCNQYLQPTLPVVIQPPFDGSVRWLAVLISMAVCITVAMIVSSCFCKYKHYC	180	
Qy	181	KSTSSRGRYNRDLQDDEAFIPVGBESLKDLDQOSSGSGGLPLLQVTTAKQIQMVRQV	240	
Db	181	KSTSSRGRYNRDLQDDEAFIPVGBESLKDLDQOSSGSGGLPLLQVTTAKQIQMVRQV	240	
Qy	241	GKGRYGEVMWKGWGEKVAVKVFTTTEASWFRETEIQTVLMRHNILGFIADIKGTG	300	
Db	241	GKGRYGEVMWKGWGEKVAVKVFTTTEASWFRETEIQTVLMRHNILGFIADIKGTG	300	
Qy	301	SWTQLYLIITDYHENGSLYDFLKCATLDTALLKLAYSAAACGLCHLHTEIYGTQCKPAIAH	360	
Db	301	SWTQLYLIITDYHENGSLYDFLKCATLDTALLKLAYSAAACGLCHLHTEIYGTQCKPAIAH	360	
Qy	361	RDLSKKNILIKONGSCCIIADGLAVKFNSTNEVDIPLNTRVGTGRRYMAPEVLDESLSKN	420	
Db	361	RDLSKKNILIKONGSCCIIADGLAVKFNSTNEVDIPLNTRVGTGRRYMAPEVLDESLSKN	420	
Qy	421	HFQPYIMADIYSFGLIIWEMARRCITGGIVVEEYQLPYNNVPSPDSEYDMREVVVCVKRLR	480	
Db	421	HFQPYIMADIYSFGLIIWEMARRCITGGIVVEEYQLPYNNVPSPDSEYDMREVVVCVKRLR	480	
Qy	481	PIVSNRWNSECLRAVLKLMSECAWHPASRLTALRIKKTIAKNVESQDVKI	532	
Db	481	PIVSNRWNSECLRAVLKLMSECAWHPASRLTALRIKKTIAKNVESQDVKI	532	

RESULT 12

RESOLUTION 12
AAR74343
ID AAR74343 standard; protein: 532 AA.

XX
AC AAR74343;

XX
DT 25-MAR-2003 (revised)

DT 25-MAR-2003 (revised)

DT 01-NOV-1995 (first entry)

XX

DE	BRK-1 protein.
XX	
XX	BRK-1; BMP receptor kinase protein-1; bone morphogenetic protein.
XX	
XX	Mus sp.
XX	
XX	Key
XX	Location/Qualifiers
FT	Peptide
FT	1. .23
FT	/label= Sig_peptide
FT	24. .152
FT	Domain
FT	/label= Extracellular_ligand_binding_domain
FT	153. .176
FT	Domain
FT	/label= Transmembrane_domain
FT	177. .532
FT	Domain
FT	/label= Intracellular_kinase_domain
XX	
XX	W09514778-A2.
XX	
XX	01-JUN-1995.
PD	
XX	
XX	23-NOV-1994; 94WO-US013534.
PF	
XX	
XX	24-NOV-1993; 93US-00158735.
PR	
XX	
XX	(PROC) PROCTER & GAMBLE CO.
PA	
XX	
XX	Cook JS, Correa PE, Koenig BB, Rosenbaum JS, Ting J;
FI	
XX	
XX	WPI; 1995-206935/27.
DR	
DR	N-PSDB; AAQ90184.
XX	
XX	
XX	New bone morphogenetic protein receptor kinase protein - used for
PT	identifying cpds, capable of binding it and for developing therapeutic
FT	cpds, and detection system(s).
PT	
XX	
XX	Claim 1; Page 29-32; 49pp; English.
PS	
XX	
XX	A cDNA library prepared from NIH3T3 poly-A RNA was screened with J159 PCR
CC	fragment to isolate clone BRK-1 (sequence given in AAQ90184) encoding
CC	full-length BMP receptor kinase protein (AAR74343). Vectors including the
CC	DNA were used to express recombinant BRK-1 in CHO and COS-7 hosts.
CC	(Updated on 25-MAR-2003 to correct PN field.)
CC	
XX	
XX	Sequence 532 AA;
SQ	
XX	
XX	Query Match 99.5%; Score 2823; DB 2; Length 532;
XX	Best Local Similarity 98.9%; Pred.No.2.9e-277;
XX	Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Very Match 99.5%: Score 2823: DB 2: Length 532:

Best Local Similarity 98.9%; Pred. No. 2.9e-277;

Matches	Conservative	Mismatches	Indels	Gaps
526	5	1	0	0

Qy	421	HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYNNMVPSPSYEDMREVVCVKRLR	480
Db	421	HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYNNMVPSPSYEDMREVVCVKRLR	480
Qy	481	PIVSNRWNSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI	532
Db	481	PIVSNRWNSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI	532

Search completed: December 3, 2005, 06:07:43
Job time : 193 secs

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OM protein - protein search, using sw model

Run on: December 3, 2005, 06:04:29 ; Search time 45 Seconds
(without alignments)
977.410 Million cell updates/sec

Title: US-10-600-645-2

Perfect score: 2838

Sequence: 1 MTQLYTYIRLLGACLFIIHSHVQGNLSDMLHGTGMSKSDVDQKPKENGVTLPEDTLPFLK 532

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2838	100.0	532	2	US-08-123-934A-2
2	2838	100.0	532	2	US-09-874-628-2
3	2838	100.0	532	4	PCT-US94-10080-2
4	2823	99.5	532	2	US-09-382-256-14
5	2823	99.5	532	2	US-08-158-735A-4
6	2823	99.5	532	2	US-09-395-115-14
7	2823	99.5	532	2	US-08-334-179A-12
8	2823	99.5	532	2	US-08-436-265-14
9	2823	99.5	532	2	US-09-679-187-14
10	2823	99.5	532	2	US-09-267-963D-14
11	2769	97.6	532	1	US-08-481-337A-6
12	2769	97.6	532	2	US-09-382-256-6
13	2769	97.6	532	2	US-09-395-115-6
14	2769	97.6	532	2	US-08-436-265-6
15	2769	97.6	532	2	US-09-679-187-6
16	2769	97.6	532	2	US-08-448-371A-6
17	2769	97.6	532	2	US-09-267-963D-6
18	2769	97.6	532	2	US-09-949-016-6475
19	2769	97.6	532	4	PCT-US95-05467-6
20	2763	97.4	532	2	US-09-949-016-7785
21	2616	92.2	500	2	US-08-158-735A-2
22	1934.5	68.2	502	2	US-08-123-934A-4
23	1934.5	68.2	502	2	US-09-874-628-4
24	1934.5	68.2	502	4	PCT-US94-10080-4
25	1933.5	68.1	502	1	US-08-481-337A-8
26	1933.5	68.1	502	2	US-09-382-256-18
27	1933.5	68.1	502	2	US-09-395-115-18

28	1933.5	68.1	502	2	US-08-436-265-18	Sequence 18, Appl
29	1933.5	68.1	502	2	US-09-679-187-18	Sequence 18, Appl
30	1933.5	68.1	502	2	US-08-448-371A-8	Sequence 8, Appl
31	1933.5	68.1	502	2	US-09-267-963D-18	Sequence 18, Appl
32	1933.5	68.1	502	4	PCT-US95-05467-8	Sequence 8, Appl
33	1926	67.9	502	2	US-08-334-179A-14	Sequence 14, Appl
34	1848.5	65.1	494	2	US-09-949-016-10396	Sequence 10396, A
35	1274	44.9	503	2	US-08-123-934A-10	Sequence 10, Appl
36	1274	44.9	503	2	US-09-874-628-10	Sequence 10, Appl
37	1274	44.9	503	4	PCT-US94-10080-10	Sequence 10, Appl
38	1268	44.7	501	2	US-09-949-016-9766	Sequence 9766, Ap
39	1268	44.7	503	2	US-09-382-256-10	Sequence 10, Appl
40	1268	44.7	503	2	US-09-395-115-10	Sequence 10, Appl
41	1268	44.7	503	2	US-08-436-265-10	Sequence 10, Appl
42	1268	44.7	503	2	US-09-679-187-10	Sequence 10, Appl
43	1268	44.7	503	2	US-09-267-963D-10	Sequence 10, Appl
44	1268	44.7	503	2	US-09-949-016-6528	Sequence 6528, Ap
45	1263.5	44.5	501	1	US-08-149-105-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-123-934A-2
; Sequence 2, Application US/08123934A
; Patent No. 6291206
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; APPLICANT: CELESTE, Anthony J.
; APPLICANT: THIES, R. Scott
; APPLICANT: YAMAJI, No. 6291206oru
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute Inc. - Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,934A
; FILING DATE: 17-SEP-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, Steven R
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 876 1170
; TELEFAX: 617 876 5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-123-934A-2

Query Match 100.0%; Score 2838; DB 2; Length 532;
Best Local Similarity 100.0%; Pred. No. 8.6e-261;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTQLYTYIRLLGACLFIIHSHVQGNLSDMLHGTGMSKSDVDQKPKENGVTLPEDTLPFLK 60

Db 1 MTQLYTYIRLLGACLFIIHSHVQGNLSDMLHGTGMSKSDVDQKPKENGVTLPEDTLPFLK 60

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QY 61 CYCSGHCPCDDAINNTCITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKSPKAQLRR 120
DB 61 CYCSGHCPCDDAINNTCITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKSPKAQLRR 120
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DB 121 TIECCRTNLCNQYLQPTLPVVPVIGPFDGSRWLAVLISMVAVCIAMIVFSSCFCKYKHC 180
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DB 181 KSISGRGRNDRLEODEAFIPVGESLKDLIDQSQSSGSGGLPLLQRTIAKIQMVROV 240
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DB 241 GKGRYGEVMMGKRGKAVKVPFTTEBASWPRETEIYQTVLMRHNILGFTAAADIKGTG 300
QY 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAISAAACGLCHLHTEIYGTQGPAAIAH 360
DB 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAISAAACGLCHLHTEIYGTQGPAAIAH 360
QY 361 RDLKSKNLIKKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDESLSKN 420
DB 361 RDLKSKNLIKKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDESLSKN 420
QY 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEEYQLPYNNMVPSPDPSYEDMRVVCVKRLR 480
DB 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEEYQLPYNNMVPSPDPSYEDMRVVCVKRLR 480
QY 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMYESQDVKI 532
DB 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMYESQDVKI 532
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RESULT 2

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US-09-874-628-2
; Sequence 2, Application US/09874628
; Patent No. 6610513
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; CELESTE, Anthony J.
; THIES, R. Scott
; YAMAJI, No. 6610513oru
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute Inc.- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/874,628
; FILING DATE: 05-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,934
; FILING DATE: 17-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 876 1170
; TELEFAX: 617 876 5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-874-628-2

Query Match      100.0%; Score 2838; DB 2; Length 532;
Best Local Similarity 100.0%; Pred. No. 8.6e-261;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTQLYTIIRLLGACLIIFISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLAPEDTLPLFLK 60
DB 1 MTQLYTIIRLLGACLIIFISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLAPEDTLPLFLK 60
QY 61 CYCSGHCPCDDAINNTCITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKSPKAQLRR 120
DB 61 CYCSGHCPCDDAINNTCITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKSPKAQLRR 120
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DB 181 KSISGRGRNDRLEODEAFIPVGESLKDLIDQSQSSGSGGLPLLQRTIAKIQMVROV 240
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DB 241 GKGRYGEVMMGKRGKAVKVPFTTEBASWPRETEIYQTVLMRHNILGFTAAADIKGTG 300
QY 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAISAAACGLCHLHTEIYGTQGPAAIAH 360
DB 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAISAAACGLCHLHTEIYGTQGPAAIAH 360
QY 361 RDLKSKNLIKKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDESLSKN 420
DB 361 RDLKSKNLIKKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDESLSKN 420
QY 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEEYQLPYNNMVPSPDPSYEDMRVVCVKRLR 480
DB 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEEYQLPYNNMVPSPDPSYEDMRVVCVKRLR 480
QY 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMYESQDVKI 532
DB 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMYESQDVKI 532
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RESULT 3

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PCT-US94-10080-2
; Sequence 2, Application PC/TUS9410080
; GENERAL INFORMATION:
; APPLICANT: GENETICS INSTITUTE, INC.
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute Inc.- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10080
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,934
; FILING DATE: 17-SEP-1993
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5203-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8260
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-10080-2

Query Match 100.0%; Score 2838; DB 4; Length 532;
Best Local Similarity 100.0%; Pred. No. 8.6e-261;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKPKENGVTLLAPEDTLPFLK 60
DB 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKPKENGVTLLAPEDTLPFLK 60
QY 61 CYCSGHCPDDAINNCTITNGHCFALIEEDDQGETTLLTSGCMKYEGSDFOCKDSPKAQLRR 120
DB 61 CYCSGHCPDDAINNCTITNGHCFALIEEDDQGETTLLTSGCMKYEGSDFOCKDSPKAQLRR 120
QY 121 TIECRTLNCQYLQPTLPVVGIPFDGSRVRLAVLISMAVCIVAMIVFSSFCYKHYC 180
DB 121 TIECRTLNCQYLQPTLPVVGIPFDGSRVRLAVLISMAVCIVAMIVFSSFCYKHYC 180
QY 181 KSISSRGYNRDLQDEAFIPVGSLSKDLIDQSSGSGSLPLLVQRTIAKIOIOMVRQV 240
DB 181 KSISSRGYNRDLQDEAFIPVGSLSKDLIDQSSGSGSLPLLVQRTIAKIOIOMVRQV 240
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DB 241 GKGRYGEVMMGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFIADIKGTG 300
QY 301 SWTQLYLITDYHENGSLYDFLKCNTLDRALLKLAYSACGLCHLHTEIYGTGKPAIAH 360
DB 301 SWTQLYLITDYHENGSLYDFLKCNTLDRALLKLAYSACGLCHLHTEIYGTGKPAIAH 360
QY 361 RDLKSKNLIKKGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDESLSKN 420
DB 361 RDLKSKNLIKKGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDESLSKN 420
QY 421 HFQPYIMADIYSFGLIIWEMARRCITGGIIEEYQLPYNNVPDPSYEDMRVVCVKRLR 480
DB 421 HFQPYIMADIYSFGLIIWEMARRCITGGIIEEYQLPYNNVPDPSYEDMRVVCVKRLR 480
QY 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKWVSSQDVKI 532
DB 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKWVSSQDVKI 532

RESULT 4
US-09-382-256-14
Sequence 14, Application US/09382256A
Patent No. 6207814
GENERAL INFORMATION:
APPLICANT: MIYAZONO, Kohei
TEN DIJKE, Peter
FRANZEN, Petra
YAMASHITA, Hidetoshi
HELDIN, Carl-Henrik
TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS,
HAVING SERINE THREONINE KINASE DOMAINS,
AND THEIR USE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.

STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/382,256A
FILING DATE: 24-Aug-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: No. 6207814ember 17, 1993
APPLICATION NUMBER: GB 9224057.1
FILING DATE: No. 6207814ember 17, 1992
APPLICATION NUMBER: GB 9304677.9
FILING DATE: March 8, 1993
APPLICATION NUMBER: GB 9304680.3
FILING DATE: March 8, 1993
APPLICATION NUMBER: 9311047.6
FILING DATE: May 28, 1993
APPLICATION NUMBER: 9313763.6
FILING DATE: July 2, 1993
APPLICATION NUMBER: 9316099.2
FILING DATE: August 3, 1993
APPLICATION NUMBER: 321344.5
FILING DATE: October 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6207814man D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5298.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-382-256-14

Query Match 99.5%; Score 2823; DB 2; Length 532;
Best Local Similarity 98.9%; Pred. No. 2.3e-259;
Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKPKENGVTLLAPEDTLPFLK 60
DB 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKPKENGVTLLAPEDTLPFLK 60
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DB 61 CYCSGHCPDDAINNCTITNGHCFALIEEDDQGETTLLTSGCMKYEGSDFOCKDSPKAQLRR 120
QY 121 TIECRTLNCQYLQPTLPVVGIPFDGSRVRLAVLISMAVCIVAMIVFSSFCYKHYC 180
DB 121 TIECRTLNCQYLQPTLPVVGIPFDGSRVRLAVLISMAVCIVAMIVFSSFCYKHYC 180
QY 181 KSISSRGYNRDLQDEAFIPVGSLSKDLIDQSSGSGSLPLLVQRTIAKIOIOMVRQV 240
DB 181 KSISSRGYNRDLQDEAFIPVGSLSKDLIDQSSGSGSLPLLVQRTIAKIOIOMVRQV 240
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DB 241 GKGRYGEVMMGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFIADIKGTG 300
QY 301 SWTQLYLITDYHENGSLYDFLKCNTLDRALLKLAYSACGLCHLHTEIYGTGKPAIAH 360

Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAISAACGLCHLHTEIYGTQGPAAIAH 360
QY 361 RDLKSKNLIILKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSLKN 420
Db 361 RDLKSKNLIILKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSLKN 420
QY 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEEQVLPYNNVPSDPSYEDMRVVCVKLR 480
Db 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEEQVLPYNNVPSDPSYEDMRVVCVKLR 480
QY 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532

RESULT 5

US-08-158-735A-4
; Sequence 4, Application US/08158735A
; Patent No. 6248554
; GENERAL INFORMATION:
; APPLICANT: COOK, JONATHAN S.
; APPLICANT: CORREA, PAUL E.
; APPLICANT: KOENIG, BETH B.
; APPLICANT: ROSENBAUM, JAN S.
; APPLICANT: TING, JERRY
; TITLE OF INVENTION: DNA SEQUENCE CODING FOR A BMP RECEPTOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE PROCTER & GAMBLE COMPANY
; STREET: 11810 EAST MIAMI RIVER ROAD
; CITY: ROSS
; STATE: OH
; COUNTRY: USA
; ZIP: 45061

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/158,735A
; FILING DATE: 24-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CORSTANJE, BRAHM J.
; REGISTRATION NUMBER: 34,804
; REFERENCE/DOCKET NUMBER: 5088
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 627-2858
; TELEFAX: (513) 627-0260
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-158-735A-4

Query Match 99.5%; Score 2823; DB 2; Length 532;
Best Local Similarity 98.9%; Pred. No. 2.3e-259;
Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTQLYTYIRLLGACLPFIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPLFK 60
Db 1 MTQLYTYIRLLGACLPFIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPLFK 60
QY 61 CYCSGHCPCPDANNTCTINGHCFAIIEEDDQGETTLTSCMKYEGSDFOCKDSPKAQLRR 120
Db 61 CYCSGHCPCPDANNTCTINGHCFAIIEEDDQGETTLTSCMKYEGSDFOCKDSPKAQLRR 120
QY 121 TIECCTNLNCNQLQPTLPVPVIGPFDGSRWLAVLISMVAVCIAMIVFSSCFYKHYC 180
Db 121 TIECCTNLNCNQLQPTLPVPVIGPFDGSRWLAVLISMVAVCIAMIVFSSCFYKHYC 180

QY 181 KSISRGRYNRDLQDEAFIPVGBESLKLIIDQSQSSGSGGLPLLVQRTIAKQIQMVRQV 240
Db 181 KSISRGRYNRDLQDEAFIPVGBESLKLIIDQSQSSGSGGLPLLVQRTIAKQIQMVRQV 240
QY 241 KGGRYGEVVMGKWRGEKVAVKVFFTEEBASWPRETEIYQTVLMRHENILGFTAADIKGKG 300
Db 241 KGGRYGEVVMGKWRGEKVAVKVFFTEEBASWPRETEIYQTVLMRHENILGFTAADIKGKG 300
QY 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAISAACGLCHLHTEIYGTQGPAAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAISAACGLCHLHTEIYGTQGPAAIAH 360
QY 361 RDLKSKNLIILKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSLKN 420
Db 361 RDLKSKNLIILKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSLKN 420
QY 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEEQVLPYNNVPSDPSYEDMRVVCVKLR 480
Db 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEEQVLPYNNVPSDPSYEDMRVVCVKLR 480
QY 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532

RESULT 6

US-09-395-115-14
; Sequence 14, Application US/09395115
; Patent No. 6271365
; GENERAL INFORMATION:

; APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
; APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
; TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/395,115
; FILING DATE:

CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,265
; FILING DATE: 30-October-1995
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: 17-No. 6271365ember-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9224057.1
; FILING DATE: 17-No. 6271365ember-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304677.9
; FILING DATE: 8-March-1993

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 9304680.3
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9311047.6
; FILING DATE: 28-May-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9313763.6
; FILING DATE: 2-July-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9136099.2

;
; FILING DATE: 3-August-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9321344.5
; FILING DATE: 15-October-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohlel, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-395-115-14

Query Match 99.5%; Score 2823; DB 2; Length 532;
Best Local Similarity 98.9%; Pred. No. 2.3e-259;
Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMSKSDVDQKPKENGVTLPEDTLPFLK 60
DB 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMSKSDVDQKPKENGVTLPEDTLPFLK 60

QY 61 CYCSGHCPCDPAINNTCITNGHCFALIEEDDQGETTLTSGCMKYEAGSDFOCKDSPKQLRR 120
DB 61 CYCSGHCPCDPAINNTCITNGHCFALIEEDDQGETTLTSGCMKYEAGSDFOCKDSPKQLRR 120

QY 121 TIECCRTNLCNQYLQPTLPVWIGPFDGSRVRLAVLISMAVCIVAMIVFSSCFCKYHC 180
DB 121 TIECCRTNLCNQYLQPTLPVWIGPFDGSRVRLAVLISMAVCIVAMIVFSSCFCKYHC 180

QY 181 KSISGRGRNRLDEQDEAFIPVGESLKDLIDQSQSSGSGGLPLLQRTIAKIQMVROV 240
DB 181 KSISGRGRNRLDEQDEAFIPVGESLKDLIDQSQSSGSGGLPLLQRTIAKIQMVROV 240

QY 241 GKGRYGEVWVGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300
DB 241 GKGRYGEVWVGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300

QY 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTGKPAIAH 360
DB 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTGKPAIAH 360

QY 361 RDLKSKNILLIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
DB 361 RDLKSKNILLIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420

QY 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEQYQLPYNNVPSDPSYEDMREVVCKRLR 480
DB 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEQYQLPYNNVPSDPSYEDMREVVCKRLR 480

QY 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
DB 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532

RESULT 7
US-08-334-179A-12
; Sequence 12, Application US/08334179A
; Patent No. 6306622
; GENERAL INFORMATION:
; APPLICANT: ROSENBAUM, JAN S.
; APPLICANT: NOHNO, TSUTOMU
; TITLE OF INVENTION: CDNA ENCODING A BMP TYPE II RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE PROCTER AND GAMBLE COMPANY
; STREET: 11810 EAST MIAMI RIVER ROAD
; CITY: ROSS

;
; STATE: OH
; COUNTRY: US
; ZIP: 45061
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.30, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/334,179A
; FILING DATE: 04-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CORSTANJE, BRAHM J.
; REGISTRATION NUMBER: 34,804
; REFERENCE/DOCKET NUMBER: 5473
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 513-627-2858
; TELEFAX: 513-627-0260
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-334-179A-12

Query Match 99.5%; Score 2823; DB 2; Length 532;
Best Local Similarity 98.9%; Pred. No. 2.3e-259;
Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMSKSDVDQKPKENGVTLPEDTLPFLK 60
DB 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMSKSDVDQKPKENGVTLPEDTLPFLK 60

QY 61 CYCSGHCPCDPAINNTCITNGHCFALIEEDDQGETTLTSGCMKYEAGSDFOCKDSPKQLRR 120
DB 61 CYCSGHCPCDPAINNTCITNGHCFALIEEDDQGETTLTSGCMKYEAGSDFOCKDSPKQLRR 120

QY 121 TIECCRTNLCNQYLQPTLPVWIGPFDGSRVRLAVLISMAVCIVAMIVFSSCFCKYHC 180
DB 121 TIECCRTNLCNQYLQPTLPVWIGPFDGSRVRLAVLISMAVCIVAMIVFSSCFCKYHC 180

QY 181 KSISGRGRNRLDEQDEAFIPVGESLKDLIDQSQSSGSGGLPLLQRTIAKIQMVROV 240
DB 181 KSISGRGRNRLDEQDEAFIPVGESLKDLIDQSQSSGSGGLPLLQRTIAKIQMVROV 240

QY 241 GKGRYGEVWVGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300
DB 241 GKGRYGEVWVGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300

QY 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTGKPAIAH 360
DB 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTGKPAIAH 360

QY 361 RDLKSKNILLIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
DB 361 RDLKSKNILLIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420

QY 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEQYQLPYNNVPSDPSYEDMREVVCKRLR 480
DB 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEQYQLPYNNVPSDPSYEDMREVVCKRLR 480

QY 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
DB 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532

RESULT 8
US-08-436-265-14
; Sequence 14, Application US/08436265
; Patent No. 6316217
; GENERAL INFORMATION:

APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6316217ember-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6316217ember-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304680.3
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9311047.6
FILING DATE: 28-May-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9136099.2
FILING DATE: 3-August-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-265-14

Query Match 99.5%; Score 2823; DB 2; Length 532;
Best Local Similarity 98.9%; Pred. No. 2.3e-259;
Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTQVLYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPAPEDTLPLK 60
Db 1 MTQVLYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDLDQKKPENGVTLPAPEDTLPLK 60
QY 61 CYCSGHCDDAINNTCTINGHCFALIEDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120
Db 61 CYCSGHCDDAINNTCTINGHCFALIEDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120
QY 121 TTECRRTNLCNQLOPTLPVVGPPFGDSIRLWLVLLISMAVCIVAMIVFSSCFCKHYC 180

Db 121 TTECRRTNLCNQLOPTLPVVGPPFGDSIRLWLVLLISMAVCIVAMIVFSSCFCKHYC 180
QY 181 KSISRGYNRDLQDEAFIPVGSLSKDLIDQSSSGSGGLPLLQVQRTIAKQIQMVRQV 240
Db 181 KSISRGYNRDLQDEAFIPVGSLSKDLIDQSSSGSGGLPLLQVQRTIAKQIQMVRQV 240
QY 241 GKGRYGEVMGKWRGEKVAVKVFPTTEBASFRTEIYQTVLMRHNILGFTAAADIKGTG 300
Db 241 GKGRYGEVMGKWRGEKVAVKVFPTTEBASFRTEIYQTVLMRHNILGFTAAADIKGTG 300
QY 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTQGRPAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTQGRPAIAH 360
QY 361 RDLKSKNLIKKNGSCCIIADLGLAVKFNSTDNEVDIPLNTRVGTGTRRYMAPEVLDSSLKN 420
Db 361 RDLKSKNLIKKNGSCCIIADLGLAVKFNSTDNEVDIPLNTRVGTGTRRYMAPEVLDSSLKN 420
QY 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEYQLPYNNMVPSPDSYEDMREVVCKRLR 480
Db 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEYQLPYNNMVPSPDSYEDMREVVCKRLR 480
QY 481 PIVSNRWNDSDECLRAVLKLMSECHWHPASRLTALRIKKTAKMKNVESODVKI 532
Db 481 PIVSNRWNDSDECLRAVLKLMSECHWHPASRLTALRIKKTAKMKNVESODVKI 532

RESULT 9
US-09-679-187-14
Sequence 14, Application US/09679187
Patent No. 6331621
GENERAL INFORMATION:
APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/679,187
FILING DATE: 03-OCT-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6331621ember-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6331621ember-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304680.3
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9311047.6
FILING DATE: 28-May-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 9136099.2
; FILING DATE: 3-August-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9321344.5
; FILING DATE: 15-October-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohlei, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-679-187-14

Query Match          99.5%; Score 2823; DB 2; Length 532;
Best Local Similarity 98.9%; Pred. No. 2.3e-259;
Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMSKSDVDQKPKENGVTLPFLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMSKSDLDQKPKENGVTLPFLK 60
Qy 61 CYCSGHCPCPDANNTCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKQLRR 120
Db 61 CYCSGHCPCPDANNTCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKQLRR 120
Qy 121 TIECCRTNLCNOYLQPTLPVWIGPFFDGSVRWLAVLISMAVCIVAMIVFSSCFCKYHYC 180
Db 121 TIECCRTNLCNOYLQPTLPVWIGPFFDGSIRWLVLISMAVCIVAMIVFSSCFCKYHYC 180
Qy 181 KSISGRYNRDLQDEAFIPVGESLKDLIDQSQSGSGSGLPLLQVORTIAKIQMVRQV 240
Db 181 KSISGRYNRDLQDEAFIPVGESLKDLIDQSQSGSGSGLPLLQVORTIAKIQMVRQV 240
Qy 241 GKGRYGEVWVGKRGKEKAVKVPFTTEASWPRETEIYQTVLMRHNILGFIAADIKGTG 300
Db 241 GKGRYGEVWVGKRGKEKAVKVPFTTEASWPRETEIYQTVLMRHNILGFIAADIKGTG 300
Qy 301 SWTQLYLIIDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTGCKPAIAH 360
Db 301 SWTQLYLIIDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTGCKPAIAH 360
Qy 361 RDLKSKNLIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSKN 420
Db 361 RDLKSKNLIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSKN 420
Qy 421 HFQPYIMADIYSFGLIIEWEMARCCITGGIVEEYQLPYNNVPSPDPSYEDMRVVCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIEWEMARCCITGGIVEEYQLPYNNVPSPDPSYEDMRVVCVKRLR 480
Qy 481 PIVSNRWNSECLRAVLKLMSECAWNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAWNPASRLTALRIKKTAKMVESQDVKI 532

RESULT 10
US-09-267-963D-14
; Sequence 14, Application US/09267963D
; Patent No. 6692925
; GENERAL INFORMATION:
; APPLICANT: MIYAZONO, Kohei
; APPLICANT: IMAMURA, Takeshe
; APPLICANT: DEN DIJKE, Peter
; TITLE OF INVENTION: PROTEINS HAVING SERINE/THREONINE KINASE DOMAINS, CORRESPONDING
; FILE REFERENCE: LUD 5539.1 CIP
; CURRENT APPLICATION NUMBER: US/09/267,963D
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; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/GB93/02367
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: US 09/039,177
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-267-963D-14

Query Match          99.5%; Score 2823; DB 2; Length 532;
Best Local Similarity 98.9%; Pred. No. 2.3e-259;
Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMSKSDVDQKPKENGVTLPFLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMSKSDLDQKPKENGVTLPFLK 60
Qy 61 CYCSGHCPCPDANNTCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKQLRR 120
Db 61 CYCSGHCPCPDANNTCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKQLRR 120
Qy 121 TIECCRTNLCNOYLQPTLPVWIGPFFDGSVRWLAVLISMAVCIVAMIVFSSCFCKYHYC 180
Db 121 TIECCRTNLCNOYLQPTLPVWIGPFFDGSIRWLVLISMAVCIVAMIVFSSCFCKYHYC 180
Qy 181 KSISGRYNRDLQDEAFIPVGESLKDLIDQSQSGSGSGLPLLQVORTIAKIQMVRQV 240
Db 181 KSISGRYNRDLQDEAFIPVGESLKDLIDQSQSGSGSGLPLLQVORTIAKIQMVRQV 240
Qy 241 GKGRYGEVWVGKRGKEKAVKVPFTTEASWPRETEIYQTVLMRHNILGFIAADIKGTG 300
Db 241 GKGRYGEVWVGKRGKEKAVKVPFTTEASWPRETEIYQTVLMRHNILGFIAADIKGTG 300
Qy 301 SWTQLYLIIDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTGCKPAIAH 360
Db 301 SWTQLYLIIDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTGCKPAIAH 360
Qy 361 RDLKSKNLIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSKN 420
Db 361 RDLKSKNLIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSKN 420
Qy 421 HFQPYIMADIYSFGLIIEWEMARCCITGGIVEEYQLPYNNVPSPDPSYEDMRVVCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIEWEMARCCITGGIVEEYQLPYNNVPSPDPSYEDMRVVCVKRLR 480
Qy 481 PIVSNRWNSECLRAVLKLMSECAWNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAWNPASRLTALRIKKTAKMVESQDVKI 532

RESULT 11
US-08-481-337A-6
; Sequence 6, Application US/08481337A
; Patent No. 5863738
; GENERAL INFORMATION:
; APPLICANT: TEN DIJKE, Peter
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: MIYAZONO, Kohei
; APPLICANT: SAMPATH, Kuber T.
; TITLE OF INVENTION: Morphogenic Protein-Specific Cell
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
```


Db 181 KSISRRYRNDLEQDEAFIPVGBSLKDLIDQSQSGSGGLPLLQVORTIAKIQIOMVRQV 240
QY 241 GKGRYGEVWVGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300
Db 241 GKGRYGEVWVGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300
QY 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
QY 361 RDLKSKNILLKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
Db 361 RDLKSKNILLKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
QY 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEEYQLPYNNVPSDPSYEDMREYVVCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEEYQLPYNNVPSDPSYEDMREYVVCVKRLR 480
QY 481 PIVSNRWNSECLRAVLKLMSECAWHPASRLTALRIKKTAKWVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAWHPASRLTALRIKKTAKWVESQDVKI 532

RESULT 13
US-09-395-115-6
; Sequence 6, Application US/09395115
; Patent No. 6271365
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
; APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/395,115
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,265
; FILING DATE: 30-October-1995
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: 17-No. 6271365ember-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9224057.1
; FILING DATE: 17-No. 6271365ember-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304677.9
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304680.3
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9311047.6
; FILING DATE: 28-May-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9313763.6
; FILING DATE: 2-July-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9136099.2
; FILING DATE: 3-August-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9321344.5

; FILING DATE: 15-October-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohlei, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-395-115-6

Query Match 97.6%; Score 2769; DB 2; Length 532;
Best Local Similarity 97.2%; Pred. No. 3.1e-254;
Matches 517; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTQLYTYIRLLGACFLFIISHVQGNLDLSMLHGTGMKSDVDOKKPPENGVTLLAPEDTLPLFK 60
Db 1 MTQLYTYIRLLGAYLFIISRQGNLDLSMLHGTGMKSDSDQKXSENGVTLLAPEDTLPLFK 60

QY 61 CYCSGHCPCDDAINTTCITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
Db 61 CYCSGHCPCDDAINTTCITNGHCFALIEEDDQGETTLASGCMKYEGSDFOCKDSPKAQLRR 120

QY 121 TIECCRTNLCNQYLOPTLPVVPFPGDSVRLAVLISMVCIAMIVPSSFCFCYKHYC 180
Db 121 TIECCRTNLCNQYLOPTLPVVPFPGDSIRMLVLLISMVCIAMIIIFSSFCFCYKHYC 180

QY 181 KSISRRGRYRNDLEQDEAFIPVGBSLKDLIDQSQSGSGGLPLLQVORTIAKIQIOMVRQV 240
Db 181 KSISRRYRNDLEQDEAFIPVGBSLKDLIDQSQSGSGGLPLLQVORTIAKIQIOMVRQV 240

QY 241 GKGRYGEVWVGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300
Db 241 GKGRYGEVWVGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300

QY 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
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Db 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEEYQLPYNNVPSDPSYEDMREYVVCVKRLR 480

QY 481 PIVSNRWNSECLRAVLKLMSECAWHPASRLTALRIKKTAKWVESQDVKI 532
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RESULT 14
US-08-436-265-6
; Sequence 6, Application US/08436265
; Patent No. 6316217
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
; APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022

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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICATEE: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/679,187
FILING DATE: 03-OCT-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 631621ember-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 631621ember-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304680.3
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9311047.6
FILING DATE: 28-May-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9136099.2
FILING DATE: 3-August-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5298
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-265-6

Query Match 97.6%; Score 2769; DB 2; Length 532;
Best Local Similarity 97.2%; Pred. No. 3.1e-254;
Matches 517; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

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QY 61 CYCSGHCPCDDAINTCITNGHCFIIEBDDQGETTLTSCMKYEGSDFOCKDSPKAQLRR 120
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TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-679-187-6

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Qy 121 TIECRTLNCQYLOPTLPVVGIPFDGSRVWLAVLISMAVCIAMIVFSSCFYKHYC 180
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Qy 481 PIVSNRWNSECLRAVLKLMSECAWHPASRLTALRIKKTILAKWVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAWHPASRLTALRIKKTILAKWVESQDVKI 532
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Job time : 47 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 06:11:50 ; Search time 166 Seconds
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1339.067 Million cell updates/sec

Title: US-10-600-645-2
Perfect score: 2838
Sequence: 1 MTQLTYTIRLLGACLFIIISH.....TALRIKKTLAKMVESQDVXI 532

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Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2838	100.0	532	3	US-09-874-628-2
2	2838	100.0	532	4	US-10-463-190-105
3	2838	100.0	532	4	US-10-463-190-106
4	2838	100.0	532	4	US-10-463-190-107
5	2838	100.0	532	4	US-10-463-190-110
6	2838	100.0	532	4	US-10-600-645-2
7	2838	100.0	532	5	US-10-868-497-74
8	2838	100.0	532	5	US-10-868-497-75
9	2838	100.0	532	5	US-10-868-497-76
10	2838	100.0	532	5	US-10-868-497-79
11	2823	99.5	532	3	US-09-903-068-14
12	2823	99.5	532	3	US-10-739-413-14
13	2769	97.6	532	3	US-09-903-068-6
14	2769	97.6	532	3	US-09-982-543A-6
15	2769	97.6	532	4	US-10-153-217-2
16	2769	97.6	532	4	US-10-286-152A-38
17	2769	97.6	532	4	US-10-463-190-102
18	2769	97.6	532	5	US-10-739-413-6
19	2769	97.6	532	5	US-10-868-497-71
20	2769	97.6	532	5	US-10-492-380-38
21	2769	97.6	532	5	US-10-745-237-308
22	2769	97.6	532	6	US-11-098-889-6
23	2769	97.6	532	5	US-10-450-763-53229
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26	2604.5	91.8	637	5	US-10-128-558-173
27	2129.5	75.0	564	5	US-10-450-763-53235

28	1950.5	68.7	502	4	US-10-169-051-2	Sequence 2, Appli
29	1946.5	68.6	502	4	US-10-169-051-4	Sequence 4, Appli
30	1941	68.4	502	4	US-10-044-716-14	Sequence 14, Appl
31	1941	68.4	502	4	US-10-286-152A-40	Sequence 40, Appl
32	1941	68.4	502	4	US-10-139-814-14	Sequence 14, Appl
33	1941	68.4	502	4	US-10-241-220-112	Sequence 112, App
34	1941	68.4	502	4	US-10-295-027-68	Sequence 68, Appl
35	1941	68.4	502	4	US-10-295-027-789	Sequence 789, App
36	1941	68.4	502	4	US-10-295-027-837	Sequence 837, App
37	1941	68.4	502	4	US-10-295-027-881	Sequence 881, App
38	1941	68.4	502	4	US-10-173-999-64	Sequence 64, Appl
39	1941	68.4	502	4	US-10-463-190-103	Sequence 103, App
40	1941	68.4	502	4	US-10-463-190-104	Sequence 104, App
41	1941	68.4	502	4	US-10-463-190-108	Sequence 108, App
42	1941	68.4	502	4	US-10-463-190-109	Sequence 109, App
43	1941	68.4	502	4	US-10-058-270A-6	Sequence 6, Appli
44	1941	68.4	502	4	US-10-692-824-14	Sequence 14, Appl
45	1941	68.4	502	5	US-10-872-972-112	Sequence 112, App

ALIGNMENTS

RESULT 1
US-09-874-628-2
; Sequence 2, Application US/09874628
; Patent No. US20020137133A1
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; CELESTE, Anthony J.
; THIES, R. Scott
; YAMAJI, No. US20020137133A1oru
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute Inc.- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/874,628
; FILING DATE: 05-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,934
; FILING DATE: 17-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, Steven R
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 876 1170
; TELEFAX: 617 876 5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-874-628-2

Query Match 100.0%; Score 2838; DB 3; Length 532;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MTOLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDOKKPNGVTLAPEDTLPFLK 60
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QY 421 HFQPYIMADIYSGFLIIWEMARRCITGGIVEYQLPYYNMVPSDPSYEDMREVVCVKRLR 480
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RESULT 2
US-10-463-190-105
; Sequence 105, Application US/10463190
; Publication No. US2004000935A1
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary E.
; APPLICANT: Galas, David J.
; APPLICANT: Kovacevich, Brian
; APPLICANT: Mulligan, John T.
; APPLICANT: Paeper, Bryan W.
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Winkler, David G.
; TITLE OF INVENTION: COMPOSITIONS AND MEHTODS FOR
; TITLE OF INVENTION: INCREASING BONE MINERALIZATION
; FILE REFERENCE: 240083.508C2
; CURRENT APPLICATION NUMBER: US/10/463,190
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 105
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-463-190-105
Query Match 100.0%; Score 2838; DB 4; Length 532;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTOLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDOKKPNGVTLAPEDTLPFLK 60
Db 1 MTOLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDOKKPNGVTLAPEDTLPFLK 60
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QY 421 HFQPYIMADIYSGFLIIWEMARRCITGGIVEYQLPYYNMVPSDPSYEDMREVVCVKRLR 480
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US-10-463-190-106
; Sequence 106, Application US/10463190
; Publication No. US2004000935A1
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary E.
; APPLICANT: Galas, David J.
; APPLICANT: Kovacevich, Brian
; APPLICANT: Mulligan, John T.
; APPLICANT: Paeper, Bryan W.
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Winkler, David G.
; TITLE OF INVENTION: COMPOSITIONS AND MEHTODS FOR
; TITLE OF INVENTION: INCREASING BONE MINERALIZATION
; FILE REFERENCE: 240083.508C2
; CURRENT APPLICATION NUMBER: US/10/463,190
; CURRENT FILING DATE: 2003-06-16
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 106
; LENGTH: 532
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; ORGANISM: Rattus norvegicus
US-10-463-190-106
Query Match 100.0%; Score 2838; DB 4; Length 532;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Publication No. US2004000935A1
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary E.
; APPLICANT: Galas, David J.
; APPLICANT: Kovacevich, Brian
; APPLICANT: Mulligan, John T.
; APPLICANT: Paeper, Bryan W.
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Winkler, David G.
; TITLE OF INVENTION: COMPOSITIONS AND MEHTODS FOR
; TITLE OF INVENTION: INCREASING BONE MINERALIZATION
; FILE REFERENCE: 240083.508C2
; CURRENT APPLICATION NUMBER: US/10/463,190
; CURRENT FILING DATE: 2003-06-16
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 106
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-463-190-106
Query Match 100.0%; Score 2838; DB 4; Length 532;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTOLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDOKKPNGVTLAPEDTLPFLK 60
Db 1 MTOLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDOKKPNGVTLAPEDTLPFLK 60
QY 61 CYCSGHCPCDDAINNCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
Db 61 CYCSGHCPCDDAINNCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
QY 121 TIECCTNLCNQYLOPTLPVPVIGPFFDGSVRWLAVLISMAVCIAMIVFSSCFCKYKHC 180
Db 121 TIECCTNLCNQYLOPTLPVPVIGPFFDGSVRWLAVLISMAVCIAMIVFSSCFCKYKHC 180
QY 181 KSISSRGYNRDLDEDEAFIPVGESLKDLDIOSQSSGSGGLPLLAVORTIAKQIOMVRQV 240
Db 181 KSISSRGYNRDLDEDEAFIPVGESLKDLDIOSQSSGSGGLPLLAVORTIAKQIOMVRQV 240
```

Db 181 KSISRRGRNDRLEQDEAFIPVGSLSKDLIDQSSGSGSGLPLLVORTIAKQIOMVRQV 240
Qy 241 CKGRYGEVMMGKRWGEKVAVKVPFTTEASWFRTEIYQTVLMRHNILGFIADIKGTG 300
Db 241 CKGRYGEVMMGKRWGEKVAVKVPFTTEASWFRTEIYQTVLMRHNILGFIADIKGTG 300
Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDTLRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTLRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Qy 361 RDLKSKNLIKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDSELSKN 420
Db 361 RDLKSKNLIKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDSELSKN 420
Qy 421 HFQPYIMADIYSGLLIWEWARRCITGGIIEEYQLPYNNMVPSPDPSYEDMREVVCKRLR 480
Db 421 HFQPYIMADIYSGLLIWEWARRCITGGIIEEYQLPYNNMVPSPDPSYEDMREVVCKRLR 480
Qy 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532

RESULT 4

US-10-463-190-107
; Sequence 107, Application US/10463190
; Publication No. US20040009535A1
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary E.
; APPLICANT: Galas, David J.
; APPLICANT: Kovacevich, Brian
; APPLICANT: Mulligan, John T.
; APPLICANT: Paepet, Bryan W.
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Winkler, David G.
; TITLE OF INVENTION: COMPOSITIONS AND MEHTODS FOR
; TITLE OF INVENTION: INCREASING BONE MINERALIZATION
; FILE REFERENCE: 240083.508C2
; CURRENT APPLICATION NUMBER: US/10/463.190
; CURRENT FILING DATE: 2003-06-16
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-463-190-107

Query Match 100.0%; Score 2838; DB 4; Length 532;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPFLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPFLK 60
Qy 61 CYCSGHCPCDDAINNCTITNGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKQALRR 120
Db 61 CYCSGHCPCDDAINNCTITNGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKQALRR 120
Qy 121 TIECCRTNLCNOYLQPTLPVVIIGPFDGSRVRLAVLISMVAVCIAMIVFSSCFCKHYC 180
Db 121 TIECCRTNLCNOYLQPTLPVVIIGPFDGSRVRLAVLISMVAVCIAMIVFSSCFCKHYC 180
Qy 181 KSISRRGRNDRLEQDEAFIPVGSLSKDLIDQSSGSGSGLPLLVORTIAKQIOMVRQV 240
Db 181 KSISRRGRNDRLEQDEAFIPVGSLSKDLIDQSSGSGSGLPLLVORTIAKQIOMVRQV 240
Qy 241 CKGRYGEVMMGKRWGEKVAVKVPFTTEASWFRTEIYQTVLMRHNILGFIADIKGTG 300
Db 241 CKGRYGEVMMGKRWGEKVAVKVPFTTEASWFRTEIYQTVLMRHNILGFIADIKGTG 300
Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDTLRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360

Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTLRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Qy 361 RDLKSKNLIKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDSELSKN 420
Db 361 RDLKSKNLIKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDSELSKN 420
Qy 421 HFQPYIMADIYSGLLIWEWARRCITGGIIEEYQLPYNNMVPSPDPSYEDMREVVCKRLR 480
Db 421 HFQPYIMADIYSGLLIWEWARRCITGGIIEEYQLPYNNMVPSPDPSYEDMREVVCKRLR 480
Qy 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532

RESULT 5

US-10-463-190-110
; Sequence 110, Application US/10463190
; Publication No. US20040009535A1
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary E.
; APPLICANT: Galas, David J.
; APPLICANT: Kovacevich, Brian
; APPLICANT: Mulligan, John T.
; APPLICANT: Paepet, Bryan W.
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Winkler, David G.
; TITLE OF INVENTION: COMPOSITIONS AND MEHTODS FOR
; TITLE OF INVENTION: INCREASING BONE MINERALIZATION
; FILE REFERENCE: 240083.508C2
; CURRENT APPLICATION NUMBER: US/10/463.190
; CURRENT FILING DATE: 2003-06-16
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-463-190-110

Query Match 100.0%; Score 2838; DB 4; Length 532;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPFLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPFLK 60
Qy 61 CYCSGHCPCDDAINNCTITNGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKQALRR 120
Db 61 CYCSGHCPCDDAINNCTITNGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKQALRR 120
Qy 121 TIECCRTNLCNOYLQPTLPVVIIGPFDGSRVRLAVLISMVAVCIAMIVFSSCFCKHYC 180
Db 121 TIECCRTNLCNOYLQPTLPVVIIGPFDGSRVRLAVLISMVAVCIAMIVFSSCFCKHYC 180
Qy 181 KSISRRGRNDRLEQDEAFIPVGSLSKDLIDQSSGSGSGLPLLVORTIAKQIOMVRQV 240
Db 181 KSISRRGRNDRLEQDEAFIPVGSLSKDLIDQSSGSGSGLPLLVORTIAKQIOMVRQV 240
Qy 241 CKGRYGEVMMGKRWGEKVAVKVPFTTEASWFRTEIYQTVLMRHNILGFIADIKGTG 300
Db 241 CKGRYGEVMMGKRWGEKVAVKVPFTTEASWFRTEIYQTVLMRHNILGFIADIKGTG 300
Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDTLRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTLRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Qy 361 RDLKSKNLIKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDSELSKN 420
Db 361 RDLKSKNLIKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDSELSKN 420


```
Db 361 RDLKSKNLIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
Qy 421 HFQPYIMADIYSFGLIIEWMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVCKRLR 480
Db 421 HFQPYIMADIYSFGLIIEWMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVCKRLR 480
Qy 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532

RESULT 8
US-10-868-497-75
; Sequence 75, Application US/10868497
; Publication No. US20050106683A1
; GENERAL INFORMATION:
; APPLICANT: Winkler, David G.
; APPLICANT: Shi, Jiye
; APPLICANT: Latham, John
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR SCLEROSTIN AND
; FILE REFERENCE: 60117-128
; CURRENT APPLICATION NUMBER: US/10/868,497
; CURRENT FILING DATE: 2004-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-868-497-75

Query Match 100.0%; Score 2838; DB 5; Length 532;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPFLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPFLK 60
Qy 61 CYCSGHCPCDDAINNCTITNGHCFALIEEDDQGETTLTSCMKYEGSDFOCKDSPKAQLRR 120
Db 61 CYCSGHCPCDDAINNCTITNGHCFALIEEDDQGETTLTSCMKYEGSDFOCKDSPKAQLRR 120
Qy 121 TIECCRTNLCNOYLQPTLPVWIGPFDGSRVRLAVLISMVAVCIAMIVFSSCFYKHYC 180
Db 121 TIECCRTNLCNOYLQPTLPVWIGPFDGSRVRLAVLISMVAVCIAMIVFSSCFYKHYC 180
Qy 181 KSISSRGYNRDLEQDEAFIPVGESLKDLIDQSSGSGGLPLLQRTIAKQIQMVROV 240
Db 181 KSISSRGYNRDLEQDEAFIPVGESLKDLIDQSSGSGGLPLLQRTIAKQIQMVROV 240
Qy 241 GKGRYGEVMGKRWGEKAVKVFVFTTEASWPRETEIYQTVLMRHNILGFAADIKGTG 300
Db 241 GKGRYGEVMGKRWGEKAVKVFVFTTEASWPRETEIYQTVLMRHNILGFAADIKGTG 300
Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTQGPAAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTQGPAAIAH 360
Qy 361 RDLKSKNLIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
Db 361 RDLKSKNLIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
Qy 421 HFQPYIMADIYSFGLIIEWMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVCKRLR 480
Db 421 HFQPYIMADIYSFGLIIEWMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVCKRLR 480
Qy 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
```

```
Query Match 100.0%; Score 2838; DB 5; Length 532;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPFLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPFLK 60
Qy 61 CYCSGHCPCDDAINNCTITNGHCFALIEEDDQGETTLTSCMKYEGSDFOCKDSPKAQLRR 120
Db 61 CYCSGHCPCDDAINNCTITNGHCFALIEEDDQGETTLTSCMKYEGSDFOCKDSPKAQLRR 120
Qy 121 TIECCRTNLCNOYLQPTLPVWIGPFDGSRVRLAVLISMVAVCIAMIVFSSCFYKHYC 180
Db 121 TIECCRTNLCNOYLQPTLPVWIGPFDGSRVRLAVLISMVAVCIAMIVFSSCFYKHYC 180
Qy 181 KSISSRGYNRDLEQDEAFIPVGESLKDLIDQSSGSGGLPLLQRTIAKQIQMVROV 240
Db 181 KSISSRGYNRDLEQDEAFIPVGESLKDLIDQSSGSGGLPLLQRTIAKQIQMVROV 240
Qy 241 GKGRYGEVMGKRWGEKAVKVFVFTTEASWPRETEIYQTVLMRHNILGFAADIKGTG 300
Db 241 GKGRYGEVMGKRWGEKAVKVFVFTTEASWPRETEIYQTVLMRHNILGFAADIKGTG 300
Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTQGPAAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTQGPAAIAH 360
Qy 361 RDLKSKNLIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
Db 361 RDLKSKNLIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
Qy 421 HFQPYIMADIYSFGLIIEWMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVCKRLR 480
Db 421 HFQPYIMADIYSFGLIIEWMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVCKRLR 480
Qy 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
```

```
RESULT 9
US-10-868-497-76
; Sequence 76, Application US/10868497
; Publication No. US20050106683A1
; GENERAL INFORMATION:
; APPLICANT: Winkler, David G.
; APPLICANT: Shi, Jiye
; APPLICANT: Latham, John
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR SCLEROSTIN AND
; FILE REFERENCE: 60117-128
; CURRENT APPLICATION NUMBER: US/10/868,497
; CURRENT FILING DATE: 2004-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-868-497-76

Query Match 100.0%; Score 2838; DB 5; Length 532;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPFLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPFLK 60
Qy 61 CYCSGHCPCDDAINNCTITNGHCFALIEEDDQGETTLTSCMKYEGSDFOCKDSPKAQLRR 120
Db 61 CYCSGHCPCDDAINNCTITNGHCFALIEEDDQGETTLTSCMKYEGSDFOCKDSPKAQLRR 120
Qy 121 TIECCRTNLCNOYLQPTLPVWIGPFDGSRVRLAVLISMVAVCIAMIVFSSCFYKHYC 180
Db 121 TIECCRTNLCNOYLQPTLPVWIGPFDGSRVRLAVLISMVAVCIAMIVFSSCFYKHYC 180
Qy 181 KSISSRGYNRDLEQDEAFIPVGESLKDLIDQSSGSGGLPLLQRTIAKQIQMVROV 240
Db 181 KSISSRGYNRDLEQDEAFIPVGESLKDLIDQSSGSGGLPLLQRTIAKQIQMVROV 240
Qy 241 GKGRYGEVMGKRWGEKAVKVFVFTTEASWPRETEIYQTVLMRHNILGFAADIKGTG 300
Db 241 GKGRYGEVMGKRWGEKAVKVFVFTTEASWPRETEIYQTVLMRHNILGFAADIKGTG 300
Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTQGPAAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTQGPAAIAH 360
Qy 361 RDLKSKNLIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
Db 361 RDLKSKNLIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
Qy 421 HFQPYIMADIYSFGLIIEWMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVCKRLR 480
Db 421 HFQPYIMADIYSFGLIIEWMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVCKRLR 480
Qy 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
```

```
RESULT 10
US-10-868-497-79
; Sequence 79, Application US/10868497
; Publication No. US20050106683A1
; GENERAL INFORMATION:
; APPLICANT: Winkler, David G.
; APPLICANT: Shi, Jiye
; APPLICANT: Latham, John
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR SCLEROSTIN AND
; FILE REFERENCE: 60117-128
; CURRENT APPLICATION NUMBER: US/10/868,497
; CURRENT FILING DATE: 2004-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-868-497-79

Query Match 100.0%; Score 2838; DB 5; Length 532;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPFLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPFLK 60
Qy 61 CYCSGHCPCDDAINNCTITNGHCFALIEEDDQGETTLTSCMKYEGSDFOCKDSPKAQLRR 120
Db 61 CYCSGHCPCDDAINNCTITNGHCFALIEEDDQGETTLTSCMKYEGSDFOCKDSPKAQLRR 120
Qy 121 TIECCRTNLCNOYLQPTLPVWIGPFDGSRVRLAVLISMVAVCIAMIVFSSCFYKHYC 180
Db 121 TIECCRTNLCNOYLQPTLPVWIGPFDGSRVRLAVLISMVAVCIAMIVFSSCFYKHYC 180
Qy 181 KSISSRGYNRDLEQDEAFIPVGESLKDLIDQSSGSGGLPLLQRTIAKQIQMVROV 240
Db 181 KSISSRGYNRDLEQDEAFIPVGESLKDLIDQSSGSGGLPLLQRTIAKQIQMVROV 240
Qy 241 GKGRYGEVMGKRWGEKAVKVFVFTTEASWPRETEIYQTVLMRHNILGFAADIKGTG 300
Db 241 GKGRYGEVMGKRWGEKAVKVFVFTTEASWPRETEIYQTVLMRHNILGFAADIKGTG 300
Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTQGPAAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTQGPAAIAH 360
Qy 361 RDLKSKNLIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
Db 361 RDLKSKNLIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
Qy 421 HFQPYIMADIYSFGLIIEWMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVCKRLR 480
Db 421 HFQPYIMADIYSFGLIIEWMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVCKRLR 480
Qy 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
```

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; FILE REFERENCE: 60117-128
; CURRENT APPLICATION NUMBER: US/10/868,497
; CURRENT FILING DATE: 2004-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-868-497-79

Query Match      100.0%; Score 2838; DB 5; Length 532;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGKMSDVQDKKPKNGVTLAPEDTLPLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGKMSDVQDKKPKNGVTLAPEDTLPLK 60

Qy 61 CYCSGHCPCDDAINNTCTINGHCFAIIBEDDOGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
Db 61 CYCSGHCPCDDAINNTCTINGHCFAIIBEDDOGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120

Qy 121 TIECCRTNLCNQYLQPTLPVVIQPFDDGSVRLAVLISMAVCIIVAMIVFSSCFYKHYC 180
Db 121 TIECCRTNLCNQYLQPTLPVVIQPFDDGSVRLAVLISMAVCIIVAMIVFSSCFYKHYC 180

Qy 181 KSISRGYRNRLDEQEAFFPVGESLKDLDQSSGSGSLPLLVQRTIAKIQIMVRQV 240
Db 181 KSISRGYRNRLDEQEAFFPVGESLKDLDQSSGSGSLPLLVQRTIAKIQIMVRQV 240

Qy 241 KGGRYGEVWVGKRGKQVAVKVFVFTTEASWFRTEIYQTVLMRHENILGFIADIKGTG 300
Db 241 KGGRYGEVWVGKRGKQVAVKVFVFTTEASWFRTEIYQTVLMRHENILGFIADIKGTG 300

Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSACGLCHLHTEIYGTQKPAIAH 360

Qy 361 RDLKSKNILIKNGSCCADIADGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
Db 361 RDLKSKNILIKNGSCCADIADGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420

Qy 421 HFQPYIMADIVSFGLIIEWEMARRCTIGGIVEYQLPYNNMVPSPDPSYEDMREVVCVKLR 480
Db 421 HFQPYIMADIVSFGLIIEWEMARRCTIGGIVEYQLPYNNMVPSPDPSYEDMREVVCVKLR 480

Qy 481 PIVSNRWNSDECLRAVLKIMSECWAHNPASRLTALRIKTKLAKMVESQDVKI 532
Db 481 PIVSNRWNSDECLRAVLKIMSECWAHNPASRLTALRIKTKLAKMVESQDVKI 532

RESULT 11
US-09-903-068-14
; Sequence 14, Application US/09903068
; Patent No. US20020123139A1
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
; Franzen, Petra; Yamashita, Hidetoshi; Helden, Carl-Henrik
; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
; Having Serine Threonine Kinase Domains And Their Use
;
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
```

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;
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/903,068
; FILING DATE: 11-Jul-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/679,187
; FILING DATE: <unknown>
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: 17-No. US20020123139A1ember-1993
; APPLICATION NUMBER: 9224057.1
; FILING DATE: 17-No. US20020123139A1ember-1992
; APPLICATION NUMBER: 9304677.9
; FILING DATE: 8-March-1993
; APPLICATION NUMBER: 9304680.3
; FILING DATE: 8-March-1993
; APPLICATION NUMBER: 9311047.6
; FILING DATE: 28-May-1993
; APPLICATION NUMBER: 9313763.6
; FILING DATE: 2-July-1993
; APPLICATION NUMBER: 9136099.2
; FILING DATE: 3-August-1993
; APPLICATION NUMBER: 9321344.5
; FILING DATE: 15-October-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohlei, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-903-068-14

Query Match      99.5%; Score 2823; DB 3; Length 532;
Best Local Similarity 98.9%; Pred. No. 2.2e-242;
Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGKMSDVQDKKPKNGVTLAPEDTLPLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGKMSDVQDKKPKNGVTLAPEDTLPLK 60

Qy 61 CYCSGHCPCDDAINNTCTINGHCFAIIBEDDOGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
Db 61 CYCSGHCPCDDAINNTCTINGHCFAIIBEDDOGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120

Qy 121 TIECCRTNLCNQYLQPTLPVVIQPFDDGSVRLAVLISMAVCIIVAMIVFSSCFYKHYC 180
Db 121 TIECCRTNLCNQYLQPTLPVVIQPFDDGSVRLAVLISMAVCIIVAMIVFSSCFYKHYC 180

Qy 181 KSISRGYRNRLDEQEAFFPVGESLKDLDQSSGSGSLPLLVQRTIAKIQIMVRQV 240
Db 181 KSISRGYRNRLDEQEAFFPVGESLKDLDQSSGSGSLPLLVQRTIAKIQIMVRQV 240

Qy 241 KGGRYGEVWVGKRGKQVAVKVFVFTTEASWFRTEIYQTVLMRHENILGFIADIKGTG 300
Db 241 KGGRYGEVWVGKRGKQVAVKVFVFTTEASWFRTEIYQTVLMRHENILGFIADIKGTG 300

Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSACGLCHLHTEIYGTQKPAIAH 360

Qy 361 RDLKSKNILIKNGSCCADIADGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
Db 361 RDLKSKNILIKNGSCCADIADGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420

Qy 421 HFQPYIMADIVSFGLIIEWEMARRCTIGGIVEYQLPYNNMVPSPDPSYEDMREVVCVKLR 480
Db 421 HFQPYIMADIVSFGLIIEWEMARRCTIGGIVEYQLPYNNMVPSPDPSYEDMREVVCVKLR 480
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QY 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKWVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKWVESQDVKI 532

RESULT 12
US-10-739-413-14
; Sequence 14, Application US/10739413
; Publication No. US20050048607A1
; GENERAL INFORMATION:
; APPLICANT: MIYAZONO, Kohei
; APPLICANT: IMAMURA, Takeshe
; APPLICANT: DEN DIJKE, Peter
; TITLE OF INVENTION: PROTEINS HAVING SERINE/THREONINE KINASE DOMAINS, CORRESPONDING
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND THEIR USE
; FILE REFERENCE: LUD 5539.1 CIP
; CURRENT APPLICATION NUMBER: US/10739, 413
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US/09/267,963
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/GB93/02367
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: US 09/039,177
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-739-413-14

Query Match 99.5%; Score 2823; DB 5; Length 532;
Best Local Similarity 98.9%; Pred. No. 2.2e-242;
Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTQLYTYIRLLGACFLIISHVQGNLDSMLHGTGMSKSDVDOKKPENGVTLAPEDTLPFLK 60
Db 1 MTQLYTYIRLLGACFLIISHVQGNLDSMLHGTGMSKSDVDOKKPENGVTLAPEDTLPFLK 60
QY 61 CYCSGHCPCDDAINTTCITNGHCFALIEEDDQGETTLTSCGMKYEGSDFOCKSPKAQLRR 120
Db 61 CYCSGHCPCDDAINTTCITNGHCFALIEEDDQGETTLTSCGMKYEGSDFOCKSPKAQLRR 120
QY 121 TIECCRTNLCNOYLQPTLPVPPVIGFFDGSVRWLAVLISMAVCIVAMIVFSSCFCKHYC 180
Db 121 TIECCRTNLCNOYLQPTLPVPPVIGFFDGSVRWLAVLISMAVCIVAMIVFSSCFCKHYC 180
QY 181 KSISSRGRYNRDLQDEAFIPVGESLKDLIDQSSGSGGLPLLQVORTIAQIQMVROV 240
Db 181 KSISSRGRYNRDLQDEAFIPVGESLKDLIDQSSGSGGLPLLQVORTIAQIQMVROV 240
QY 241 GKGRYGEVWVGKRGKAVKVFPTTEASWPRETEIYQTVLMRHNILGFAADIKGTG 300
Db 241 GKGRYGEVWVGKRGKAVKVFPTTEASWPRETEIYQTVLMRHNILGFAADIKGTG 300
QY 301 SWTQLYLTIDYHENGSLYDFLKCATLDTALLKLAYSACGLCHLHTEIYGTQGRPAIAH 360
Db 301 SWTQLYLTIDYHENGSLYDFLKCATLDTALLKLAYSACGLCHLHTEIYGTQGRPAIAH 360
QY 361 RDLKSNKNIILKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSLN 420
Db 361 RDLKSNKNIILKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSLN 420
QY 421 HFQPYIMADYISFGLIIEWEMARCIITGGIVEEYQLPYNNVPSDPSYEDMREVVCKRLR 480
Db 421 HFQPYIMADYISFGLIIEWEMARCIITGGIVEEYQLPYNNVPSDPSYEDMREVVCKRLR 480
QY 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKWVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKWVESQDVKI 532

RESULT 13
US-09-903-068-6
; Sequence 6, Application US/09903068
; Patent No. US20020123139A1
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
; Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
; Having Serine Threonine Kinase Domains And Their Use
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/903,068
; FILING DATE: 11-Jul-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/679,187
; FILING DATE: <Unknown>
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: 17-No. US20020123139A1ember-1993
; APPLICATION NUMBER: 9224057.1
; FILING DATE: 17-No. US20020123139A1ember-1992
; APPLICATION NUMBER: 9304677.9
; FILING DATE: 8-March-1993
; APPLICATION NUMBER: 9304680.3
; FILING DATE: 8-March-1993
; APPLICATION NUMBER: 9311047.6
; FILING DATE: 28-May-1993
; APPLICATION NUMBER: 9113763.6
; FILING DATE: 2-July-1993
; APPLICATION NUMBER: 9136099.2
; FILING DATE: 3-August-1993
; APPLICATION NUMBER: 9321344.5
; FILING DATE: 15-October-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohlei, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-903-068-6
Query Match 97.6%; Score 2769; DB 3; Length 532;
Best Local Similarity 97.2%; Pred. No. 1.4e-237;
Matches 517; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
QY 1 MTQLYTYIRLLGACFLIISHVQGNLDSMLHGTGMSKSDVDOKKPENGVTLAPEDTLPFLK 60
Db 1 MTQLYTYIRLLGACFLIISHVQGNLDSMLHGTGMSKSDVDOKKPENGVTLAPEDTLPFLK 60
QY 61 CYCSGHCPCDDAINTTCITNGHCFALIEEDDQGETTLTSCGMKYEGSDFOCKSPKAQLRR 120
Db 61 CYCSGHCPCDDAINTTCITNGHCFALIEEDDQGETTLTSCGMKYEGSDFOCKSPKAQLRR 120
QY 121 TIECCRTNLCNOYLQPTLPVPPVIGFFDGSVRWLAVLISMAVCIVAMIVFSSCFCKHYC 180

Db 121 TIECCTNLCNQYLQPTLPVPPVIGFPGSIRWLVLISMVACIIAMIFSSCFCKHYC 180
QY 181 KSISRRGRNRLDEQEAFFIPVGESLKDLIDQSQSSGSGGLPLLVQRTIAKIQIMVRQV 240
Db 181 KSISRRGRNRLDEQEAFFIPVGESLKDLIDQSQSSGSGGLPLLVQRTIAKIQIMVRQV 240
QY 241 GKGRYGEVMMGKWRGEKAVKVVFFTTBEASWFRTEIYQTVLMRHNILGFTAAIDIKGTG 300
Db 241 GKGRYGEVMMGKWRGEKAVKVVFFTTBEASWFRTEIYQTVLMRHNILGFTAAIDIKGTG 300
QY 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAISAACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAISAACGLCHLHTEIYGTQKPAIAH 360
QY 361 RDLKSKNLIKKNGSCCIIADLGLAVKFNSDTNEVDIPLNTRVGTTRRYMAPEVLDLSKN 420
Db 361 RDLKSKNLIKKNGSCCIIADLGLAVKFNSDTNEVDIPLNTRVGTTRRYMAPEVLDLSKN 420
QY 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEYQLPYYNMVPSDPSYEDMREVVCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEYQLPYYNMVPSDPSYEDMREVVCVKRLR 480
QY 481 PIVSNRNSDECLRAVLKMSCEWHPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRNSDECLRAVLKMSCEWHPASRLTALRIKKTAKMVESQDVKI 532

RESULT 14
US-09-982-543A-6
; Sequence 6, Application US/09982543A
; Patent No. US20020155500A1
; GENERAL INFORMATION:
; APPLICANT: Dijke, P.
; APPLICANT: Miyazano, K.
; APPLICANT: Sampath, K.
; APPLICANT: Heldin, C.
; TITLE OF INVENTION: MORPHOGENIC PROTEIN-SPECIFIC CELL SURFACE RECEPTORS AND USES
; FILE REFERENCE: THEREFOR
; CURRENT APPLICATION NUMBER: US/09/982,543A
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 08/448,371
; PRIOR FILING DATE: 1995-06-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-982-543A-6

Query Match 97.6%; Score 2769; DB 3; Length 532;
Best Local Similarity 97.2%; Pred. No. 1.4e-237;
Matches 517; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
QY 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVT LAPEDTLPLFK 60
Db 1 MTQLYTYIRLLGAYLFIISRVOGNLDSMLHGTGMKSDVDQKKSENGVT LAPEDTLPLFK 60
QY 61 CYCSGHCPCDDAINNTCITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
Db 61 CYCSGHCPCDDAINNTCITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
QY 121 TIECCTNLCNQYLQPTLPVPPVIGFPGSIRWLVLISMVACIIAMIFSSCFCKHYC 180
Db 121 TIECCTNLCNQYLQPTLPVPPVIGFPGSIRWLVLISMVACIIAMIFSSCFCKHYC 180
QY 181 KSISRRGRNRLDEQEAFFIPVGESLKDLIDQSQSSGSGGLPLLVQRTIAKIQIMVRQV 240
Db 181 KSISRRGRNRLDEQEAFFIPVGESLKDLIDQSQSSGSGGLPLLVQRTIAKIQIMVRQV 240
QY 241 GKGRYGEVMMGKWRGEKAVKVVFFTTBEASWFRTEIYQTVLMRHNILGFTAAIDIKGTG 300
Db 241 GKGRYGEVMMGKWRGEKAVKVVFFTTBEASWFRTEIYQTVLMRHNILGFTAAIDIKGTG 300

Db 241 GKGRYGEVMMGKWRGEKAVKVVFFTTBEASWFRTEIYQTVLMRHNILGFTAAIDIKGTG 300
QY 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAISAACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAISAACGLCHLHTEIYGTQKPAIAH 360
QY 361 RDLKSKNLIKKNGSCCIIADLGLAVKFNSDTNEVDIPLNTRVGTTRRYMAPEVLDLSKN 420
Db 361 RDLKSKNLIKKNGSCCIIADLGLAVKFNSDTNEVDIPLNTRVGTTRRYMAPEVLDLSKN 420
QY 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEYQLPYYNMVPSDPSYEDMREVVCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEYQLPYYNMVPSDPSYEDMREVVCVKRLR 480
QY 481 PIVSNRNSDECLRAVLKMSCEWHPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRNSDECLRAVLKMSCEWHPASRLTALRIKKTAKMVESQDVKI 532

RESULT 15
US-10-153-217-2
; Sequence 2, Application US/10153217
; Publication No. US20030072758A1
; GENERAL INFORMATION:
; APPLICANT: HOWE, JAMES R.
; TITLE OF INVENTION: EMPRIA INVOLVEMENT IN JUVENILE POLYPOSIS
; FILE REFERENCE: IOWA:037US
; CURRENT APPLICATION NUMBER: US/10/153,217
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: 60/292,691
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-153-217-2

Query Match 97.6%; Score 2769; DB 4; Length 532;
Best Local Similarity 97.2%; Pred. No. 1.4e-237;
Matches 517; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
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Db 1 MTQLYTYIRLLGAYLFIISRVOGNLDSMLHGTGMKSDVDQKKSENGVT LAPEDTLPLFK 60
QY 61 CYCSGHCPCDDAINNTCITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
Db 61 CYCSGHCPCDDAINNTCITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
QY 121 TIECCTNLCNQYLQPTLPVPPVIGFPGSIRWLVLISMVACIIAMIFSSCFCKHYC 180
Db 121 TIECCTNLCNQYLQPTLPVPPVIGFPGSIRWLVLISMVACIIAMIFSSCFCKHYC 180
QY 181 KSISRRGRNRLDEQEAFFIPVGESLKDLIDQSQSSGSGGLPLLVQRTIAKIQIMVRQV 240
Db 181 KSISRRGRNRLDEQEAFFIPVGESLKDLIDQSQSSGSGGLPLLVQRTIAKIQIMVRQV 240
QY 241 GKGRYGEVMMGKWRGEKAVKVVFFTTBEASWFRTEIYQTVLMRHNILGFTAAIDIKGTG 300
Db 241 GKGRYGEVMMGKWRGEKAVKVVFFTTBEASWFRTEIYQTVLMRHNILGFTAAIDIKGTG 300
QY 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAISAACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAISAACGLCHLHTEIYGTQKPAIAH 360
QY 361 RDLKSKNLIKKNGSCCIIADLGLAVKFNSDTNEVDIPLNTRVGTTRRYMAPEVLDLSKN 420
Db 361 RDLKSKNLIKKNGSCCIIADLGLAVKFNSDTNEVDIPLNTRVGTTRRYMAPEVLDLSKN 420

Qy 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYNNMVPSPDPSYEDMREVVCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYNNMVPSPDPSYEDMREVVCVKRLR 480
Qy 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKWVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKWVESQDVKI 532

Search completed: December 3, 2005, 06:25:48
Job time : 168 secs

us-10-600-645-2.rapbm

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 06:12:35 ; Search time 11 Seconds
(without alignments)
231.581 Million cell updates/sec

Title: US-10-600-645-2
Perfect score: 2838
Sequence: 1 MTQLYTYIRLLGACLFISH.....TALRIKTKLAKMVESQDVKI 532

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues
Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_New.*
1: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pap.*
2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pap.*
3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pap.*
4: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pap.*
5: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pap.*
6: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pap.*
7: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pap.*
8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	561.5	19.8	567	US-10-420-192-8	Sequence 8, Appli
2	287	10.1	450	US-11-109-156-21	Sequence 21, Appl
3	248	8.7	835	US-11-186-283-2	Sequence 2, Appli
4	242	8.5	835	US-11-186-283-8	Sequence 8, Appli
5	241.5	8.5	456	US-11-021-441-18	Sequence 18, Appl
6	241.5	8.5	1035	US-11-021-441-4	Sequence 4, Appli
7	238	8.4	648	US-11-109-156-17	Sequence 17, Appl
8	230.5	8.1	460	US-10-990-276-1	Sequence 1, Appli
9	230	8.1	459	US-10-990-276-3	Sequence 3, Appli
10	228.5	8.1	984	US-11-113-424-60	Sequence 60, Appl
11	225	7.9	995	US-11-113-424-62	Sequence 62, Appl
12	224	7.9	479	US-11-021-441-20	Sequence 20, Appl
13	222	7.8	490	US-11-021-441-26	Sequence 26, Appl
14	222	7.8	497	US-11-021-441-22	Sequence 22, Appl
15	222	7.8	497	US-11-021-441-24	Sequence 24, Appl
16	222	7.8	985	US-11-113-424-61	Sequence 61, Appl
17	219	7.7	256	US-11-113-424-183	Sequence 183, App
18	212.5	7.5	987	US-10-949-720-395	Sequence 395, App
19	212.5	7.5	990	US-10-821-234-1201	Sequence 1201, Ap
20	211	7.4	998	US-10-510-524-1	Sequence 1, Appli
21	210	7.4	983	US-11-113-424-59	Sequence 59, Appl
22	207.5	7.3	1142	US-11-109-156-22	Sequence 22, Appl
23	206.5	7.3	1005	US-11-113-424-63	Sequence 63, Appl
24	203.5	7.2	656	US-10-821-234-1121	Sequence 1121, Ap
25	199	7.0	379	US-11-109-156-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-10-420-192-8
; Sequence 8, Application US/10420192
; Publication No. US20050260579A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Herbert Y.
; APPLICANT: Wang, Xiao-Fan
; APPLICANT: Weinberg, Robert A.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded Products and Uses
; FILE REFERENCE: 0399.1086-022
; CURRENT APPLICATION NUMBER: US/10/420,192
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US 09/584,929
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 08/446,936
; PRIOR FILING DATE: 1995-05-23
; PRIOR APPLICATION NUMBER: US 08/311,703
; PRIOR FILING DATE: 1994-09-23
; PRIOR APPLICATION NUMBER: US 07/786,063
; PRIOR FILING DATE: 1991-10-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 567
; TYPE: PRT
; ORGANISM: genomic
US-10-420-192-8

Query Match 19.8%; Score 561.5; DB 6; Length 567;
Best Local Similarity 29.1%; Pred. No. 8.5e+46;
Matches 144; Conservative 104; Mismatches 195; Indels 51; Gaps 13;
QY 63 CSGHCPDAINNCTITNGH-CFAIIEEDDQGGTTLTSGC--MKYEGSDPCKD--SPKQAQ 117
Db 67 CMSCN--SITSICEKPOEVCVAVWRKND-NITLETCHDPKLPVHDFILEDAASPCKI 122
QY 118 LRRTE-----CCTNLCNOYL-----OPLTPPVVIGFFDGSVRLAVLISM 160
Db 123 MKKKKPGETPFMCSCSSDECNDNIFSEYNTSNPDLLLVI-----QVTGISLLPPL 176
QY 161 AKVICAMIVFSCFCYKHYCKYKYSRGRVNRDL--ODEAFIPVGESLKDLDQSSGSS 218
Db 177 GVAISVIIIF-----YCYRVNRQOKLSSTWTGTRKLMFESEHCAIILEDSDSIL 228
QY 219 GSGLLLVQRTIAKIQIMVRQVKGKRYGEVWMGKWRG-----EKVAVKVFVFTTEASNF 272

Db 229 STCANNINHTELLPIELDTLVCKGRFAEYVYKAKLKQNTSEQFETVAVKIFPEYEEYASWK 288
QY 273 RETEIVQTVLMRHNILGFIADIKGTGWTQYLYLTDYHENGSLYDFLKCATLDTALL 332
Db 289 TEKDFIPDINLKHENILQFLTAERKTELKGQWLITAFHAKGNLQEYLTRHVISWEDLR 348
QY 333 KLAYSACGLCHLHTEIYGTQGP--AIAHRDLKSNHILKNGSCCIADLGLAVKFNSD 390
Db 349 KLGSSUARGIAHLHSD-HTPCGRPKMPIVHRDLKSNHILVKNDLTCCCLDFGLSLRLDPT 407
QY 391 TNEVDIPLNTRVGTTRYMAPEVLDESLSKNHFPQYIMADIYSFGLIIMEMARRCITGGIV 450
Db 408 LSVDDLANSQGVGTARYMAPEVLESRMNLENAESFKQTDVYSMALVIMEMTGRCAVAGEV 467
QY 451 EYQIPLYNMPSDPSYEDMREVVVCVKRLRPTVSNRNWNSDECLRAVLKMLSMSCWAHPNAS 510
Db 468 KDVEPPFGSKVREHPCVESMKDNVLRDRGRPEIPSPFLNHOQIQMWYCTLTCEWHDHDEA 527
QY 511 RLTAIRIKKTLAKM 524
Db 528 RUTAQCVAERFSEL 541

RESULT 2
US-11-109-156-21
; Sequence 21, Application US/11109156
; Publication No. US20050250144A1
; GENERAL INFORMATION:
; APPLICANT: Toshio Ota
; APPLICANT: Takao Isogai
; APPLICANT: Tetsuo Nishikawa
; APPLICANT: Koji Hayashi
; APPLICANT: Kaoru Otsuka
; APPLICANT: Jun-ichi Yamamoto
; APPLICANT: Shizuko Ishii
; APPLICANT: Tomoyasu Sugiyama
; APPLICANT: Ai Wakamatsu
; APPLICANT: Keiichi Nagai
; APPLICANT: Tetsuji Otsuki
; APPLICANT: Shin-ichi Funahashi
; APPLICANT: Chiaki Senoo
; APPLICANT: Jun-ichi Nezu
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
; TITLE OF INVENTION: PHOSPHATASE
; FILE REFERENCE: 06501-099002
; CURRENT APPLICATION NUMBER: US/11/109,156
; CURRENT FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: US/10/060,065
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05061
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-109-156-21

Query Match 10.1%; Score 287; DB 7; Length 450;
Best Local Similarity 25.4%; Pred. No. 7.1e-20;

Matches 87; Conservative 67; Mismatches 116; Indels 72; Gaps 14;
QY 204 ESLKDLIDOSSSGSGSL----PLLVRTIA-----KQIQMVRQVKGGRY 245
Db 147 ENLMQLVEHYTSDADGLCTRLIKPKVMEGTAAQDEFYRSGWALNMKELKLQTIKGGEF 206
QY 246 GEVMGKVRGEKAVKVFTEEASWPRETEIYQTVLMRHNILGFIADIKGTGWTQY 305
Db 207 GDVMLGDYRGKNAVAKCIKNDATAQAFLAEASVMTQL-RHSNVLQVLLGVIVBEKGG--L 262
QY 306 YLITDYHENGSLYDFLKC---ATLDTALLKLAYSAAACGLCHLHTEIYGTQCPAIAHRD 362
Db 263 YIVTEYMAKGSGLVDLRSRGRSVLGGDCLLKFSLD----VCEAMEYLEGNN----FVHRD 314
QY 363 LKSKNLIKKNKSCCIADLGLAVKFNPDNEDVIDIPNTRVGTTRYMAPEVLDESLSKNHF 422
Db 315 LAARNVLVSEDNVAKVSDFGLTKEASTQDTGKLPV-----KWTAPREALREKKFPST-- 365
QY 423 QPYIMADIYSFGLIIMEMARRCITGGIIVEEQLPYNNVPSDPSYEDMREVVVCVKRLRPI 482
Db 366 ----KSDVMSFGILLWE-----IYSFGRVPY-----PRIP-----LKDVV-----PR 398
QY 483 VSNRNWNSDE---CLRAVLKMLSMSCWAHPNASRLTALRIKKTLL 521
Db 399 VEKGYKMDAPDCCPPAVYEVKMKNCWHLDAAMRPSFLQRLREQ 440

RESULT 3
US-11-186-283-2
; Sequence 2, Application US/11186283
; Publication No. US20050255520A1
; GENERAL INFORMATION:
; APPLICANT: Raju, Jeyaseelan
; TITLE OF INVENTION: NOVEL CARC PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MNI-068CP2
; CURRENT APPLICATION NUMBER: US/11/186,283
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/626,173
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: US/09/947,199A
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/111,938
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 09/291,839
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/458,457
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 835
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-283-2

Query Match 8.7%; Score 248; DB 7; Length 835;
Best Local Similarity 25.9%; Pred. No. 8.6e-16;
Matches 96; Conservative 68; Mismatches 132; Indels 74; Gaps 21;
QY 177 KHY-----CKSISRRGRYNRDLQDEAFIPVCESLKDLIDQSQSSGS-----GSGPL 224
Db 402 KHYKRPQDELPCNEYSQPG-----GDGSSVSVSPISGKTKSMTEKADILLRAGLPS 454
QY 225 LVQRTIAKIQMVRQVKGGRYGEVMGKVRGEKAVK-----VFFTEEASWF-RETEIY 278
Db 455 HFHLQLS-EIEFHEIIGSGSGKVVYKGRNKAIVAKRYANTYCKSDVDMFCREVS- 512
QY 279 QTVLMRHNILGFIADIKGTGWTQYLYLTDYHENGSLYDFL--KCATLDTALLKLAY 336
Db 513 -LCQLNHPCVIQFVGACLNDR---SQFAIVTQYISGSLFSLHBEQKRILDLQSKLIIV 568
QY 337 SAACGLCHLHTEIYGTQCPAIAHRDLKSNILIKKNGSCCIADLGLAVKFNSDINEVDI 396

Db 569 DVAKGMEYLHNL---TQ---PIIHRDLNSHNILLYEDGHAVVADFGES-REFLOSLEDN- 620
Qy 397 PLNTRVGTTRYMAPEVLDESLSKNHFQPYIMADIYSFGLIIEWMARRCITGGIVEEYQLP 456
Db 621 -MTKQPGNLRWMAPEVFTQCTRYT-----IKADVFSYALCLWEI-----LTG-----EIP 664
Qy 457 YNMV-----SDPSYEDMREVVCVKRLRPV-----NRWNS-----DECLRAVLKLMSECV 504
Db 665 FAHLKPAADAAADWAYHHIRPPIGYSIPKPISSLLIRGNWACBPGRPEFSEVVMKL-EECL 723
Qy 505 AH-----NPAS 510
Db 724 CNIELMSPAS 733

RESULT 4
US-11-186-283-8
; Sequence 8, Application US/11186283
; Publication No. US20050255520A1
; GENERAL INFORMATION:
; APPLICANT: Raju, Jeyaseelan
; TITLE OF INVENTION: NOVEL CARC PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MNI-068CP2
; CURRENT APPLICATION NUMBER: US/11/186,283
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/626,173
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: US/09/947,199A
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/111,938
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 09/291,839
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/458,457
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 835
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-186-283-8

Query Match 8.5%; Score 242; DB 7; Length 835;
Best Local Similarity 26.0%; Pred. No. 3.2e-15;
Matches 98; Conservative 65; Mismatches 112; Indels 102; Gaps 21;
Qy 189 YNRDLEQDEAFIPVGSLSKDLIDQSOSGSGGL-----PLLVTQRTIAK----- 232
Db 404 YKRPQEE-----LPCNE-----YSQPGDGSYVSPVPLGKIKSMYKEKADVLLRLAEL 452
Qy 233 -----QIQMROVQKRGYGEVMMKWRGEKVAVK-----VFTTEASWF-RETEI 277
Db 453 PSRFLQLSEIPEHFIEHIGSGSGFKVYKGRCKNKAIVAKRYRANTYCSKSDVDMFCREVS 512
Qy 278 YQTVLMRHNILGFIAADIKGTSGWTQLYLITDYHENGSLYDFL--KCATLDTALLKLA 335
Db 513 --LCQLNHPCVQVQVFGACLDPP---SQFAIVTQYISGGSFLSLHBEQKRLDLQSKLIITA 567
Qy 336 YSAAACGLCHLHTEIYQCKPAIAHRDLKSKNLIKNGSCCIAADLGLAVKFNSTNTEVD 395
Db 568 VDVAKGMEYLHLSU---TQ---PIIHRDLNSHNILLYEDGHAVVADFGES-REFLOSLEDN 620
Qy 396 IPLNTRVGTTRYMAPEVLDESLSKNHFQPYIMADIYSFGLIIEWMARRCITGGIVEEYQL 455
Db 621 ---MTKQPGNLRWMAPEVFTQCTRYT-----IKADVFSYSLCLWEL-----LTG-----EI 663
Qy 456 PYNMV-----SDPSYEDMREVVCVKRLRPV-----NRWNS-----DECL 493
Db 664 PPAHLKPAADAAADWAYHHIRPPIGYSIPKPISSLLIRGNWACBPGRPEFSEVVMKLEBCL 723

Qy 494 RAVLKLMSCEWAPAS 510
Db 724 CNV-ELMS-----PAS 733
RESULT 5
US-11-021-441-18
; Sequence 18, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKI, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 282172003900
; CURRENT APPLICATION NUMBER: US/11/021,441
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/616,750
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/615,287
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/599,377
; PRIOR FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: PCT/US2004/23881
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 10/883,599
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/556,744
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-441-18

Query Match 8.5%; Score 241.5; DB 7; Length 456;
Best Local Similarity 24.4%; Pred. No. 1.5e-15;
Matches 97; Conservative 70; Mismatches 156; Indels 75; Gaps 18;
Qy 154 LAVLSIMAVCIVAMIVFSSCFYKHYCKSISSRGYNRDLEQ--DEAFIPVGSLSKDL-- 209
Db 15 LAVIGGVAVGVLLVLLVLAGVGFH-----RRRNQARQSPEDVYFSKSEQLKPLKT 67
Qy 210 -IDQSQSSGSGSGLPLLVTQRTIAKIQMVRQVQKRGYGEVMMG--KWRGEKVAVKYFVTT 266
Db 68 YVDPTYEDDPNQAVLKFTEIHPSCVTRQKVIGAGEFGEVYKGMUKTSSGKKEVPVAIKT 127
Qy 267 EASWFRTEIYQTVLMRHNILGFIA----ADIKGT-GSWTQLYLITDYHENGSLYDFL 321
Db 128 LKAGY---TEKQVDFLGEAGIMGQFHHNIIRLEGVISKYKPPMIIITEYMENGALDKFL 184
Qy 322 --KCATLDTALLKLAYSAAACGLCHLHTEIYQCKPAIAHRDLKSKNLIKNGSCCIA 379
Db 185 REKGEFVQLVGMRLGRTAGMKYLANNNY-----VHRDLAARNILVNSLVCKVS 236
Qy 380 DLGLAVKFNSD-----TNEVDIPLNTRVGTTRYMAPEVLDESLSKNHFQPYIMA-DIYS 432
Db 237 DFGLSRVLEDDPEATYTTSGGKIPI-----RWTAPEAIS-----YRKFTSADVWS 282
Qy 433 FGLIIEWMARRCITGGIVEEYQLPYNNMVPSDFSDREVVVCVKRL-RPIVSNRWNSDE 491
Db 283 FGIVMVEV---MTYG-----ERYWEL----SNHEVMKAIINDGFRLPPTM-----D 321
Qy 492 CLRAVLKLMSCEWAPASRLTALRIKKTAKWVESQD 529
Db 322 CPSAIYQLMQCQOQERARRPKFADIVSLDKLIRAPD 359

RESULT 6
US-11-021-441-4
; Sequence 4, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 282172003900
; CURRENT APPLICATION NUMBER: US/11/021,441
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/616,750
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/615,287
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/599,377
; PRIOR FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: PCT/US2004/23881
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 10/883,599
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/556,744
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1035
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein
US-11-021-441-4

Query Match 8.5%; Score 241.5; DB 7; Length 1035;
Best Local Similarity 24.4%; Pred. No. 4.8e-15;
Matches 97; Conservative 70; Mismatches 156; Indels 75; Gaps 18;

Qy 154 LAVLISMVAVICVAMIVFSCFCYKHYCKSISSRGYNRDLEQ--DEAFIPVGESLKDL-- 209
Db LAVIGGVAVGVVLLVLVAGVGFFH-----RRRNQARQSPEDVYFSKSEQLKPKLT 646

Qy 210 -IDQSQSSGSGSLPLVQRTIAKQIQMVROVQKGRYGEVWMG--KWRGEKVAVKVFTT 266
Db YVDPHTYEDPNQAVLKFTTEIHPSCVTRQKVGAGFGEVYKGLKTSKGKKEVPVAIKT 706

Qy 267 EASWFRTEIYQTVLMRHENTLGFIA-----ADIKGT-GSWTQLYLITDYHENGSLYDPL 321
Db LKAGY---TEKORVDFLGGAGIMGQFSHHNIIRLEGVISKYKPKMMIITEYMENGALDKPL 763

Qy 322 --KCATLDRALLKLAYSAAAGLCHLHTEIYGTQKPAIAHRDLKSNILIKKNGSCCIA 379
Db REKDEGFSVLQVGLRGIAAGMKYLANNY-----VHRDLAARILVNSNLVCKVS 815

Qy 380 DLGLAVKFNSD-----TNEVDIPLNTRVGTTRYMAPEVLDLSKNHFQPYIMA-DIYS 432
Db DFLGSLRVLEDDPEATYTTSGGKIPI-----RWTAPEAIS-----YRKFTSADVWS 861

Qy 433 FGLLIWEMARRCITGGIIVEEYQLPYNNVMPSPDSYEDMRVVCVQRLL-RPIVSNRWNSDE 491
Db FGIWVMEV-----MTYG-----BRPYWEL-----SNHEVMKAINDGFRLPTPM-----D 900

Qy 492 CURAVLKLMSCEWNAHPASRLTALRIKKTAKWVESQD 529
Db CPSAIYQLMMQCQWERARRPKFADIVSILDKLIRAPD 938

RESULT 7
US-11-109-156-17
; Sequence 17, Application US/11109156

; Publication No. US20050250144A1
; GENERAL INFORMATION:
; APPLICANT: Toshio Ota
; APPLICANT: Takao Isogai
; APPLICANT: Tetsuo Nishikawa
; APPLICANT: Koji Hayashi
; APPLICANT: Kaoru Otsuka
; APPLICANT: Jun-ichi Yamamoto
; APPLICANT: Shizuko Ishii
; APPLICANT: Tomoyasu Sugiyama
; APPLICANT: Ai Wakamatsu
; APPLICANT: Keiichi Nagai
; APPLICANT: Tetsuji Otsuki
; APPLICANT: Shin-ichi Funahashi
; APPLICANT: Chiaki Senoo
; APPLICANT: Jun-ichi Nezu
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
; TITLE OF INVENTION: PHOSPHATASE
; FILE REFERENCE: 06501-099002
; CURRENT APPLICATION NUMBER: US/11/109,156
; CURRENT FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: US/10/060,065
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05061
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 17
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-109-156-17

Query Match 8.4%; Score 238; DB 7; Length 648;
Best Local Similarity 29.2%; Pred. No. 5.3e-15;
Matches 84; Conservative 56; Mismatches 88; Indels 60; Gaps 18;

Qy 231 AKQIQMVROVQKGRYGEVWMGKWRGEKVAVKVFF-----TTBEASWFRTEIYQTVLMRHE 286
Db ASEVMLSTRIGSGSGFTYKYGKWHGD-VAVKILKVVDPTPEQQAFR-NEVAVLRKTRHV 403

Qy 287 NIL---GFIAADIKGTGSGWTQLYLITDYHENGSLYDLKCATLDR---ALLKLAYSAA 339
Db NILFLFMGTWKD-----NLAIVTQMCBSSLYKHLH--VQETKFMQFQIDIRQTA 453

Qy 340 CGLCHLHTEIYGTQKPAIAHRDLKSNILIKKNGSCCIA DLGLA-VKFN-SDTNVEDIP 397
Db QGMDYLHAK-----NIIHRDMKSNNI FLHEGLTVKIGDFGLATVKSRSQSQVEQP 505

Qy 398 LNRVGTTRYMAPEVLDLSKNHFQPYIMADIYFGLIIEWEMARRCITGGIIVEEYQLPY 457
Db TGSVLWMAPEV--RMQDNPPFS--FQSDVYSYGVLYEL-----MTG-----ELPY 548

Qy 458 YNMVSPDSPSYEDMRVVCVKR--LRPIVSNRWNSDECLRAVLKLMSEC 503
Db SHINRD-----QIIFWVGRGYASPDLSKLYKN--CPKMKRLVADC 588

RESULT 8
US-10-990-276-1
; Sequence 1, Application US/10990276

Publication No. US20050255549A1

GENERAL INFORMATION:
APPLICANT: Wesche, Holger
APPLICANT: Li, Shyun
APPLICANT: Tularik Inc.

TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use

FILE REFERENCE: 018781-003910US

CURRENT APPLICATION NUMBER: US/10/990,276

CURRENT FILING DATE: 2004-11-15

PRIOR APPLICATION NUMBER: US/09/759,595

PRIOR FILING DATE: 2001-01-13

PRIOR APPLICATION NUMBER: US 60/176,395

PRIOR FILING DATE: 2000-01-13

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 460

TYPE: PRT

ORGANISM: Homo sapiens

US-10-990-276-1

Query Match 8.1%; Score 230.5; DB 6; Length 460;

Best Local Similarity 28.4%; Pred. No. 1.7e-14;

Matches 87; Conservative 48; Mismatches 118; Indels 53; Gaps 12;

QY 239 QVKGGRYGVWGMKRGKAVK-----VFPTTEASWFRTEIYQTVLMRHN---ILG 290

Db 191 KMGEGGFGVYKGVNNVTAVKLAAMVDITTEELKQKQDFQBIKVMKCOHENVELLG 250

QY 291 FTAADIKGTGSWTQLYLTDYHENGSLYDFLKC-----ATLDTRALKLAYSACGLCHLH 346

Db 251 F-----SSDGDCLVYVYMPNGSLDLRLSCLDGTPPLSWHMRCKIAQGAANGINFLH 303

QY 347 TEIYGTQGRPAIAHRDLKSNILIKNGSCCIADLGLAVKFNSDTNEVDIPLNTRVGTTR 406

Db 304 ENHH-----IHRDIKSANILLDEAFTAKISDFGLARA--SEKFAQTVMTSRIVGTGA 353

QY 407 YMAPEVLDESLSKNHFQPYIMADYISFGLIIEWMARRCITG-GIVEEYOLPYNNMVPSPD 465

Db 354 YMAPEALRGEITPK-----SDIYSGVVLLEI---ITGLPAVDHEHPQLLL----- 397

QY 466 SYEDMEVY--CVKRLRPVSNRNWSD--CLRAVLKLMSECAWHPASRLTALRIKTL 521

Db 398 ---DIKEEIEDEKTIEDVIDKMNDAADSTSVAMYSVASQCLHLEKKNRPDIKKVQQLL 454

QY 522 AKWVES 527

Db 455 QEMTAS 460

RESULT 9

US-10-990-276-3

Sequence 3, Application US/10990276

Publication No. US20050255549A1

GENERAL INFORMATION:

APPLICANT: Wesche, Holger

APPLICANT: Li, Shyun

APPLICANT: Tularik Inc.

TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use

FILE REFERENCE: 018781-003910US

CURRENT APPLICATION NUMBER: US/10/990,276

CURRENT FILING DATE: 2004-11-15

PRIOR APPLICATION NUMBER: US/09/759,595

PRIOR FILING DATE: 2001-01-13

PRIOR APPLICATION NUMBER: US 60/176,395

PRIOR FILING DATE: 2000-01-13

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3

LENGTH: 459

TYPE: PRT

ORGANISM: Mus sp.

US-10-990-276-3

Query Match 8.1%; Score 230; DB 6; Length 459;

Best Local Similarity 29.1%; Pred. No. 1.9e-14;

Matches 87; Conservative 40; Mismatches 106; Indels 66; Gaps 13;

QY 177 KHYCKSISSRGYRNRLD-QDEAFIPVG-----ESLKDLDIOSQSSGSGGLPLLVRTIA 231

Db 142 EHSCEPPDSSSDPNRSESSDTRFHSFSPHELKSIITNDFEQPASAGN----- 190

QY 232 KQIQMVRQVKGGRYGVWGMKRGKAVK-----VFPTTEASWFRTEIYQTVLMRHE 286

Db 191 -----RMGEGGFGVYKGVNNVTAVKLAAMVDITTEELKQKQDFQBIKVMKCOHE 243

QY 287 N---ILGFTAADIKGTGSWTQLYLTDYHENGSLYDFLKC-----ATLDTRALKLAYSAA 339

Db 244 NLVELLGF-----SSSDNCLVYVYMPNGSLDLRLSCLDGTPPLSWHTRCKVAGTGA 296

QY 340 CGLCHLHTEIYGTQGRPAIAHRDLKSNILIKNGSCCIADLGLAVKFNSDTNEVDIPLN 399

Db 297 NGIRFLHENHH-----IHRDIKSANILLDKDFTAKISDFGLA---RASARLAQTVM 345

QY 400 TR-VGTRRYMAPEVLDESLSKNHFQPYIMADYISFGLIIEWMARRCITG-GIVEEYOLP 456

Db 346 SRIVGTTAYMAPEALRGEITPK-----SDIYSGVVLLEI---ITGLAAVDENREP 393

RESULT 10

US-11-113-424-60

Sequence 60, Application US/11113424

Publication No. US20050260713A1

GENERAL INFORMATION:

APPLICANT: Gangolli et al.

TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-225

CURRENT APPLICATION NUMBER: US/11/113,424

PRIOR FILING DATE: 2005-04-21

PRIOR APPLICATION NUMBER: 60/256,704

PRIOR FILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: 60/311,590

PRIOR FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: 60/257,314

PRIOR FILING DATE: 2000-12-20

PRIOR APPLICATION NUMBER: 60/311,613

PRIOR FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: 60/315,617

PRIOR FILING DATE: 2001-08-29

PRIOR APPLICATION NUMBER: 60/307,506

PRIOR FILING DATE: 2001-07-24

PRIOR APPLICATION NUMBER: 60/322,358

PRIOR FILING DATE: 2001-09-14

PRIOR APPLICATION NUMBER: 60/294,075

PRIOR FILING DATE: 2001-05-29

PRIOR APPLICATION NUMBER: 60/288,153

PRIOR FILING DATE: 2001-05-02

NUMBER OF SEQ ID NOS: 190

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 60

LENGTH: 984

TYPE: PRT

ORGANISM: Rattus norvegicus

US-11-113-424-60

Query Match 8.1%; Score 228.5; DB 7; Length 984;

Best Local Similarity 20.9%; Pred. No. 7.7e-14;

Matches 102; Conservative 74; Mismatches 144; Indels 169; Gaps 22;

QY 82 CFAIIEEDDQGETTLTSGCMKYEGSDFCCKDSPKAQLRRTIECCRTNLCNQVLPV 141

Db 522 CQGTUTDDY-----KSELREQ----- 539

QY 142 VIGPFPGDSVRWLAVLISMVAVIVFSSCFCKYKHYCKSISSRGYRNRLDEQDEAFIP 201

Db 540 ---PLIAGSA-----AAGVVFVSVLSVAISIVC-----SRKRAYSKEAVYSKDL-- 579

Db 56 KH--ADLEHRRRNQARQSPEDVYFSKSQLKPLKTYVDPHTYEDPNQAVLKFTTEIHP 113
QY 232 KOIQMVROVQGRYGEVWMG--KWRGKQAVKVFVFTTEASWPRETEIYQTVLMRHNIL 289
Db 114 SCVTRQKVIAGGEGEVYKGMKLTSSGKKEVPVAIKTKAGY---TEKQVDFLGEAGIM 170
QY 290 GFIA----ADIKGT-GSWTQLYLITDYHENGSLYDFL--KCATLDTALLKLAYSAAACGL 342
Db 171 GQFSHHNIIRLEGVISKPMIITEYMGALDKFLREKDGESVQLVGLMRLGIAAGM 230
QY 343 CHLHTEYGTQGRPAIAHRLKSNLILKNGSCCTADLGLAVKFNDS-----TNEVDI 396
Db 231 KYLANMNY-----VHRDLARNILVNSNLCKVDFGLSRVLEDDPEATYTTSGGKI 282
QY 397 PLNTRVGTTRYMAPEVLDESLSKNHFQPIYMA-DIYSEGLIIEWMARRCITGGIVEEYQL 455
Db 283 PI-----RWTAPeAIS-----YRKFTSASDVMSFGIWMNEV-----MTYG-----ER 319
QY 456 PYNMVPSPSYEDMREVVCVKRL-RPIVSNRNWNSDECLRAVLKLMSECAHNPASRLTA 514
Db 320 PYWEL----SNHEVMKAINDFRLPTPM-----DCPSAIYQLMMQWQOQERARRPKF 367
QY 515 LRIKTKLAKMVESQD 529
Db 368 ADIVSILDKLIRAPD 382

RESULT 13
US-11-021-441-22
; Sequence 26, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; FILE REFERENCE: 282172003900
; CURRENT FILING DATE: 2004-12-23
; PRIOR FILING DATE: 2004-12-23
; PRIOR FILING DATE: 2004-10-06
; PRIOR FILING DATE: 2004-10-01
; PRIOR FILING DATE: 2004-08-05
; PRIOR FILING DATE: 2004-07-23
; PRIOR FILING DATE: 2004-06-30
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein
US-11-021-441-22

Query Match 7.8%; Score 222; DB 7; Length 490;
Best Local Similarity 24.3%; Pred. No. 1.2e-13;
Matches 89; Conservative 63; Mismatches 146; Indels 68; Gaps 17;
QY 186 RGRYNRDLEQ--DEAFIPVGESLKDL---IDQSQSSGSGSLPLLQVRIQIAQIMVROV 240
Db 64 RRRKNQARQSPEDVYFSKSQLKPLKTYVDPHTYEDPNQAVLKFTTEIHPSCVTRQKVI 123
QY 241 GKGRYGEVWMG--KWRGKQAVKVFVFTTEASWPRETEIYQTVLMRHNILGFIA----A 294

Db 124 GAGEFGEVYKGMKLTSSGKKEVPVAIKTKAGY---TEKQVDFLGEAGIMQFSHHNI 180
QY 295 DIKGT-GSWTQLYLITDYHENGSLYDFL--KCATLDTALLKLAYSAAACGLCHLHTEIYG 351
Db 181 RLEGVISKYKPMIITEYMGALDKFLREKDGESVQLVGLMRLGIAAGMKYLANMNY- 239
QY 352 TQCKPAIAHRLKSNLILKNGSCCTADLGLAVKFNDS-----TNEVDIPLNTRVGTG 405
Db 240 -----VHRDLARNILVNSNLCKVDFGLSRVLEDDPEATYTTSGGKIPI----- 285
QY 406 RYMAPEVLDESLSKNHFQPIYMA-DIYSEGLIIEWMARRCITGGIVEEYQLPYNMVPSP 464
Db 286 RWTAPeAIS-----YRKFTSASDVMSFGIWMNEV-----MTYG-----ERPWE 325
QY 465 PSYEDMREVVCVKRL-RPIVSNRNWNSDECLRAVLKLMSECAHNPASRLTALRIKTKL 523
Db 326 SNHEVMKAINDFRLPTPM-----DCPSAIYQLMMQWQOQERARRPKFADIVSILDK 377
QY 524 MVESQD 529
Db 378 LIRAPD 383

RESULT 14
US-11-021-441-22
; Sequence 22, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; FILE REFERENCE: 282172003900
; CURRENT FILING DATE: 2004-12-23
; PRIOR FILING DATE: 2004-12-23
; PRIOR FILING DATE: 2004-10-06
; PRIOR FILING DATE: 2004-10-01
; PRIOR FILING DATE: 2004-08-05
; PRIOR FILING DATE: 2004-07-23
; PRIOR FILING DATE: 2004-06-30
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein
US-11-021-441-22

Query Match 7.8%; Score 222; DB 7; Length 497;
Best Local Similarity 24.3%; Pred. No. 1.2e-13;
Matches 89; Conservative 63; Mismatches 146; Indels 68; Gaps 17;
QY 186 RGRYNRDLEQ--DEAFIPVGESLKDL---IDQSQSSGSGSLPLLQVRIQIAQIMVROV 240
Db 71 RRRKNQARQSPEDVYFSKSQLKPLKTYVDPHTYEDPNQAVLKFTTEIHPSCVTRQKVI 130
QY 241 GKGRYGEVWMG--KWRGKQAVKVFVFTTEASWPRETEIYQTVLMRHNILGFIA----A 294
Db 131 GAGEFGEVYKGMKLTSSGKKEVPVAIKTKAGY---TEKQVDFLGEAGIMQFSHHNI 187

```
QY 295 DIKGT-GSWTQLYLITDYHENGSLYDFL--KCATLDRALLKLAYSAAAGLCHLHTEIYG 351
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 188 RUEGVISKYKPMIITEYWENGALDKFLREKDGESVLQVGMRLGIAAGMKYLANMNY- 246
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 352 TQGPAAIAHRDLKSNKILIKKNGSCCIADLGLAVKFNSD-----TNEVDIPLNTRVGTR 405
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 247 -----VHRDLAARNILVNSLVCKVDFGLSRVLEDDPEATYTTSGKIPi----- 292
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 406 RYMAPEVLDESLSKNHFQPIYMA-DIYSGGLIINEMARRCITGGIVEEQQLPYNNMVPD 464
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 293 RWTAPEAIS-----YRKFTSASDVMSFGIVMWEV---MTYG-----ERYWEL---- 332
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 465 PSYEDMREVVCVKRL-RPIVSNRWNSDECLRAVLKLMSECAHNPASRLTALRIKKTAK 523
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 333 SNHEVMKAINDFRLPTPM-----DCPSAIYQLMMQWQOERARRPKFADIVSILDK 384
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 524 MVESQD 529
      : : : :
Db 385 LIRAPD 390
```

RESULT 15

```
US-11-021-441-24
; Sequence 24, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 282172003900
; CURRENT APPLICATION NUMBER: US/11/021,441
; PRIOR FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/616,750
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/615,287
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/599,377
; PRIOR FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: PCT/US2004/23881
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 10/983,599
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/556,744
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein
US-11-021-441-24
```

```
Query Match 7.8%; Score 222; DB 7; Length 497;
Best Local Similarity 24.3%; Pred No. 1,2e-13;
Matches 89; Conservative 63; Mismatches 146; Indels 58; Gaps 17;

QY 186 RGRYNRDLEQ--DEAFIPVGESLKDl---IDQSQSGSGGLPVLVQRTIAKIQMVQVQ 240
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 71 RRRKNQARQSPEDVYFSKSEQLKPLKYVDPTHEDPNQAVLKFTTEIHPSCVTRQKVI 130
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 241 CGKRGYGVWVG--KWRGEKVAVKVFTTEASWFRTEIYQTVLMRHNILGFIA----A 294
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 131 GAGEFGEVYKGLMKTSSGKKEVFAIKTKAGY---TEKQRVDFLGEAGINGQFSHHNII 187
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 295 DIKGT-GSWTQLYLITDYHENGSLYDFL--KCATLDRALLKLAYSAAAGLCHLHTEIYG 351
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 188 RUEGVISKYKPMIITEYWENGALDKFLREKDGESVLQVGMRLGIAAGMKYLANMNY- 246
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
QY 352 TQGPAAIAHRDLKSNKILIKKNGSCCIADLGLAVKFNSD-----TNEVDIPLNTRVGTR 405
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 247 -----VHRDLAARNILVNSLVCKVDFGLSRVLEDDPEATYTTSGKIPi----- 292
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 406 RYMAPEVLDESLSKNHFQPIYMA-DIYSGGLIINEMARRCITGGIVEEQQLPYNNMVPD 464
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 293 RWTAPEAIS-----YRKFTSASDVMSFGIVMWEV---MTYG-----ERYWEL---- 332
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 465 PSYEDMREVVCVKRL-RPIVSNRWNSDECLRAVLKLMSECAHNPASRLTALRIKKTAK 523
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 333 SNHEVMKAINDFRLPTPM-----DCPSAIYQLMMQWQOERARRPKFADIVSILDK 384
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 524 MVESQD 529
      : : : :
Db 385 LIRAPD 390
```

Search completed: December 3, 2005, 06:26:05
Job time : 13 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 06:01:23 ; Search time 40 Seconds
(without alignments)
1279.683 Million cell updates/sec

Title: US-10-600-645-2
Perfect score: 2838
Sequence: 1 MTQLYTYIRLLGACLFIIH.....TALRIKTKLAKMWESQDVKI 532

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2838	100.0	532	2 JC2387	bone morphogenetic
2	2823	99.5	532	2 A56238	bone morphogenetic
3	2769	97.6	532	2 I37163	ALK-3 - human
4	2223	78.3	527	2 A54985	BMP receptor precu
5	1934.5	68.2	502	2 JC2491	serine/threonine k
6	1933.5	68.1	502	2 A53444	activin receptor-1
7	1926	67.9	502	2 A56683	receptor protein k
8	1274	44.9	503	2 JC2061	transforming growt
9	1274	44.9	509	2 I45713	Dpp receptor TKV,
10	1268	44.7	499	2 JC2062	transforming growt
11	1268	44.7	503	2 A49432	activin receptor-1
12	1208.5	42.6	440	2 A56693	receptor protein k
13	1204.5	42.4	509	2 A45992	activin A receptor
14	1198	42.2	601	2 A55921	serine/threonine k
15	1194	42.1	509	2 A49664	activin type I rec
16	1190.5	41.9	509	2 I59576	transforming growt
17	1184	41.7	505	2 I38959	activin A receptor
18	1180	41.6	505	2 I53417	type I serine-thre
19	1114	39.3	503	2 A49431	activin/TGF-beta-1
20	1093	38.5	502	2 JC4337	activin receptor l
21	1080	38.1	502	2 I48241	ALK-1 - mouse
22	1050	37.0	570	2 I45712	Dpp receptor SAX p
23	1047	36.9	476	2 I80182	activin type I rec
24	896	31.6	487	2 I80183	activin type I rec
25	754	26.6	247	2 PC4260	activin type I rec
26	751.5	26.5	636	2 T15734	hypothetical prote
27	686	24.2	514	2 JQ1317	activin receptor p
28	674.5	23.8	512	2 S21171	activin receptor S
29	665	23.4	513	2 A39896	activin receptor p

30	665	23.4	513	2 I45850	activin receptor t
31	664	23.4	513	1 JQ1486	activin receptor I
32	664	23.4	513	2 A49193	type II activin re
33	664	23.4	513	2 S27258	activin receptor t
34	661	23.3	513	2 S23089	activin receptor t
35	657.5	23.2	669	2 A35103	cell surface recep
36	587	20.7	592	2 S51371	transforming growt
37	584	20.6	516	2 A48678	activin receptor I
38	583.5	20.6	510	1 A42635	activin receptor S
39	578.5	20.4	510	1 A56926	activin receptor I
40	577	20.3	512	2 D40829	activin receptor I
41	577	20.3	536	2 A40829	activin receptor I
42	576.5	20.3	567	2 A44225	transforming growt
43	575	20.3	504	2 B40829	activin receptor i
44	575	20.3	512	2 I37134	activin type II re
45	575	20.3	528	2 C40829	activin receptor i

ALIGNMENTS

RESULT 1
JC2387

bone morphogenetic protein type IA receptor precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Oct-2004

C;Accession: JC2387

R;Takeda, K.; Oida, S.; Ichijo, H.; Iimura, T.; Maruoka, Y.; Amagasa, T.; Sasaki, S.

Biochem. Biophys. Res. Commun. 204, 203-209, 1994

A;Title: Molecular cloning of rat bone morphogenetic protein (BMP) type IA receptor and

A;Reference number: JC2387; MUID:95032096; PMID:7945360

A;Accession: JC2387

A;Molecule type: mRNA

A;Residues: 1-532 <TAK>

A;Cross-references: UNIPROT:Q64308; UNIPARC:UPT000008BA68; DBJ:D38082; NID:gl398909; P

C;Keywords: ATP; glycoprotein; receptor; transmembrane protein

F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-527/Product: bone morphogenetic protein type IA receptor #status predicted <BMP>

F;153-175/Domain: transmembrane #status predicted <TM>

F;232-528/Domain: protein kinase homology <KIN>

F;236-527/Region: kinase domain

F;240-248/Region: protein kinase ATP-binding motif

F;73/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	100.0%;	Score 2838;	DB 2;	Length 532;
Best Local Similarity	100.0%;	Pred. No. 8.7e-145;		
Matches 532;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MTQLYTYIRLLGACLFII	SHVQGNLDSMLHGTGMSD	VDQKPKENGVTLPEDTLPFLK 60
Db	1	MTQLYTYIRLLGACLFII	SHVQGNLDSMLHGTGMSD	VDQKPKENGVTLPEDTLPFLK 60
QY	61	CYCSCGCPDPAINNTCIT	NGHCFATIEEDDQGETTLT	SGCMKYEGSDFOCKSPKQLRR 120
Db	61	CYCSCGCPDPAINNTCIT	NGHCFATIEEDDQGETTLT	SGCMKYEGSDFOCKSPKQLRR 120
QY	121	TEECRTNLQNYLQPTLP	VPVIGPFDGSRVRLAVLI	SMAVCIIVAMIVSSFCYKHYC 180
Db	121	TEECRTNLQNYLQPTLP	VPVIGPFDGSRVRLAVLI	SMAVCIIVAMIVSSFCYKHYC 180
QY	181	KSISGRNVRNDRLEQDE	AFIPVGESLKDILDSQSSG	SGSGLPLLVORTIAKIQMVRQV 240
Db	181	KSISGRNVRNDRLEQDE	AFIPVGESLKDILDSQSSG	SGSGLPLLVORTIAKIQMVRQV 240
QY	241	GRGRYGEVVMGKRGKE	KAIVKVFVFTTEASWFRE	TEIYQTVLMRHNILGFIAADIKGTG 300
Db	241	GRGRYGEVVMGKRGKE	KAIVKVFVFTTEASWFRE	TEIYQTVLMRHNILGFIAADIKGTG 300
QY	301	SWTQLYLIIDYHENGSL	YDFLKCATLDTALLKLAY	SAACGLCHLHTEIYGTGCKPAIAH 360
Db	301	SWTQLYLIIDYHENGSL	YDFLKCATLDTALLKLAY	SAACGLCHLHTEIYGTGCKPAIAH 360
QY	361	RLDKSKNILLKNGSCC	ADIADGLAVKFNDSNTNE	VDIPLNTRVCTRRYMAPEVLDLSKN 420

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Db 361 RDLKSKNLIKKNGSCCIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
QY 421 HFQPYIMADIYFGLIIEWMARRCITGGIVEEYQLPYNNMVPSPDSYEDMREVVCVKLR 480
Db 421 HFQPYIMADIYFGLIIEWMARRCITGGIVEEYQLPYNNMVPSPDSYEDMREVVCVKLR 480
QY 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKTKLAKMVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKTKLAKMVESQDVKI 532

RESULT 2
A56238
bone morphogenetic protein receptor BRK-1 precursor - mouse
N:Alternate names: ALK-3 protein; BMP receptor
C:Species: Mus musculus (house mouse)
C:Date: 03-Oct-1995 #sequence revision 03-Oct-1995 #text_change 31-Dec-2004
C:Accession: A56238; B56238; S40158; I48242; I49543
R:Koenig, B.B.; Cook, J.S.; Wolsing, D.H.; Ting, J.; Tiesman, J.P.; Correa, P.E.; Olson,
Mol. Cell. Biol. 14, 5961-5974, 1994
A:Title: Characterization and cloning of a receptor for BMP-2 and BMP-4 from NIH 3T3 cel
A:Reference number: A56238; MUID:94344106; PMID:8065329
A:Accession: A56238
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-532 <KOE>
A:Cross-references: UNIPROT:P36895; UNIPARC:UPI000000B293; GB:U04672; NID:9538362; PIDN:
A:Accession: B56238
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-491, VSNSQVPVK, <K02>
A:Cross-references: UNIPARC:UPI0000026097; GB:U04673; NID:9538364; PIDN:AAA21515.1; PID:
R:Myazono, K.; Moren, A.; Grimsby, S.; Ichijo, H.; Heldin, C.; ten Dijke, P.
submitted to the EMBL Data Library, June 1993
A:Description: ALK-3 and ALK-6: the closely related members in the serine/threonine kin
A:Reference number: S40158
A:Accession: S40158
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-532 <MY>
A:Cross-references: UNIPARC:UPI000000B293; EMBL:Z23154; NID:9437868; PIDN:CAA80678.1; PI
R:Dewulf, N.; Verschueren, K.; Lonnoy, O.; Moren, A.; Grimsby, S.; Vande Spieghele, K.; M
Endocrinology 136, 2652-2663, 1995
A:Title: Distinct spatial and temporal expression patterns of two type I receptors for b
A:Reference number: I48241; MUID:95269711; PMID:7750489
A:Accession: I48242
A>Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-532 <RES>
A:Cross-references: UNIPARC:UPI000000B293; EMBL:Z23154; NID:9437868; PIDN:CAA80678.1; PI
R:Suzuki, A.; Thies, R.S.; Yamaji, N.; Song, J.J.; Wozney, J.; Murakami, K.; Kung, H.
Proc. Natl. Acad. Sci. U.S.A. 91, 10255-10259, 1994
A:Title: A truncated bone morphogenetic protein receptor affects dorsal-ventral patterni
A:Reference number: I49543; MUID:95024092; PMID:7937936
A:Accession: I49543
A>Status: translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-532 <RE2>
A:Cross-references: UNIPARC:UPI000000B293; GB:D16250; NID:9577633; PIDN:BAA03769.1; PID:
C:Keywords: ATP; phosphotransferase; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:232-528/Domain: protein kinase homology <KIN>
F:240-248/Region: protein kinase ATP-binding motif

Query Match 99.5%; Score 2823; DB 2; Length 532;
Best Local Similarity 98.9%; Pred. No. 5.5e-144;
Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPFLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPFLK 60
```

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QY 61 CYCSGHCPPDDAINNTCIINGHCFAIIEBDDOGETTTLTSGCMKYEGSDFQCKDSPKAQLRR 120
Db 61 CYCSGHCPPDDAINNTCIINGHCFAIIEBDDOGETTTLTSGCMKYEGSDFQCKDSPKAQLRR 120
QY 121 TIECCRTNLCNQYLOPTLPVVGPFPGSVRWLAVLISMVAVCIIVAMIVFSSCFCKHYC 180
Db 121 TIECCRTNLCNQYLOPTLPVVGPFPGSVRWLAVLISMVAVCIIVAMIVFSSCFCKHYC 180
QY 181 KSISRRGRNDRLEQDEAFIPVGESLKDIDQSQSSGSGGLPLLAVQRTIAKQIOMVRQV 240
Db 181 KSISRRGRNDRLEQDEAFIPVGESLKDIDQSQSSGSGSGGLPLLAVQRTIAKQIOMVRQV 240
QY 241 GKGRYGEVMMGKWRGEKVAVKVFTTEBASWPRETEIYQTVLMRHENILGFTAADIKGTG 300
Db 241 GKGRYGEVMMGKWRGEKVAVKVFTTEBASWPRETEIYQTVLMRHENILGFTAADIKGTG 300
QY 301 SWTQLYLITDTHENGSLYDFLKCATLDRALLKLAYSAAAGLCHLHTEIYGTQGPAAIAH 360
Db 301 SWTQLYLITDTHENGSLYDFLKCATLDRALLKLAYSAAAGLCHLHTEIYGTQGPAAIAH 360
QY 361 RDLKSKNLIKKNGSCCIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
Db 361 RDLKSKNLIKKNGSCCIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
QY 421 HFQPYIMADIYFGLIIEWMARRCITGGIVEEYQLPYNNMVPSPDSYEDMREVVCVKLR 480
Db 421 HFQPYIMADIYFGLIIEWMARRCITGGIVEEYQLPYNNMVPSPDSYEDMREVVCVKLR 480
QY 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKTKLAKMVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKTKLAKMVESQDVKI 532

RESULT 3
ALK-3 - human
C:Species: Homo sapiens (man)
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Oct-2004
C:Accession: I37163; S37183
R:ten Dijke, P.; Ichijo, H.; Franzen, P.; Schulz, P.; Saras, J.; Toyoshima, H.; Heldin,
Oncogene 8, 2879-2887, 1993
A:Title: Activin receptor-like kinases: a novel subclass of cell-surface receptors with
A:Reference number: I37161; MUID:93390967; PMID:8397373
A:Accession: I37163
A>Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-532 <RES>
A:Cross-references: UNIPROT:P36894; UNIPARC:UPI000011D628; EMBL:Z22535; NID:9402186; PI
C:Keywords: ATP
F:232-528/Domain: protein kinase homology <KIN>
F:240-248/Region: protein kinase ATP-binding motif

Query Match 97.6%; Score 2769; DB 2; Length 532;
Best Local Similarity 97.2%; Pred. No. 4.2e-141;
Matches 517; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPFLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPFLK 60
QY 61 CYCSGHCPPDDAINNTCIINGHCFAIIEBDDOGETTTLTSGCMKYEGSDFQCKDSPKAQLRR 120
Db 61 CYCSGHCPPDDAINNTCIINGHCFAIIEBDDOGETTTLTSGCMKYEGSDFQCKDSPKAQLRR 120
QY 121 TIECCRTNLCNQYLOPTLPVVGPFPGSVRWLAVLISMVAVCIIVAMIVFSSCFCKHYC 180
Db 121 TIECCRTNLCNQYLOPTLPVVGPFPGSVRWLAVLISMVAVCIIVAMIVFSSCFCKHYC 180
QY 181 KSISRRGRNDRLEQDEAFIPVGESLKDIDQSQSSGSGGLPLLAVQRTIAKQIOMVRQV 240
Db 181 KSISRRGRNDRLEQDEAFIPVGESLKDIDQSQSSGSGSGGLPLLAVQRTIAKQIOMVRQV 240
```


QY 241 CGRGYGEVMGKRGKGVAVKVFTEEBASWFRTEIYQTVLMRHNILGFIADIKGTG 300
DB 241 CGRGYGEVMGKRGKGVAVKVFTEEBASWFRTEIYQTVLMRHNILGFIADIKGTG 300
QY 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAISAAAGLCHLHTEIYGTQKPAIAH 360
DB 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAISAAAGLCHLHTEIYGTQKPAIAH 360
QY 361 RDLKSKNLIKKNKSGCCCIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSKN 420
DB 361 RDLKSKNLIKKNKSGCCCIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSKN 420
QY 421 HFQYIMADIYVSGLLIWMARRCITGIVEYQLPYNNVPSPSYEDMRVVCVKRLR 480
DB 421 HFQYIMADIYVSGLLIWMARRCITGIVEYQLPYNNVPSPSYEDMRVVCVKRLR 480
QY 481 PIVSNRNSDECLRAVLKIMSECAHNPASRLTALRIKKTAKWVESQDVKI 532
DB 481 PIVSNRNSDECLRAVLKIMSECAHNPASRLTALRIKKTAKWVESQDVKI 532

RESULT 4
A:Accession: A54985
C:Species: Xenopus laevis (African clawed frog)
C:Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 31-Dec-2004
C:Accession: A54985
R:Graff, J.M.; Thies, R.S.; Song, J.J.; Celeste, A.J.; Melton, D.A.
Cell 79, 169-179, 1994
A:Title: Studies with a Xenopus BMP receptor suggest that ventral mesoderm-inducing signal is a BMP
A:Reference number: A54985; PMID:9500777; PMID:7522972
A:Accession: A54985
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-527 <GRA>
A:Cross-references: UNIPROT:Q91578; UNIPARC:UPI00000FD12B; GB:U16654; NID:G609353; PIDN:
F:227-523/Domain: protein kinase homology <KIN>
F:235-243/Region: protein kinase ATP-binding motif

Query Match 78.3%; Score 2223; DB 2; Length 527;
Best Local Similarity 80.0%; Pred. No. 6.3e-112;
Matches 423; Conservative 44; Mismatches 52; Indels 10; Gaps 5;

QY 7 YIRLLGACFLIISHVQGNLDSMLHGTCMSDVKDPKENGVTLAPEDTLPLFKVCYCSGH 66
DB 6 FIACFGALLVI-HTQGDFFNPLPHRTGMKNSDPKKQENGVTLAPEDTLPLFLNCYCSG 64
QY 67 CPDDAINNTCITNGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRRTIECCR 126
DB 65 CPQNAVNTCITNGQCFAMIEEDDHGDIILTSGCMKMGSDFOCKDSPKALSRTIECCR 124
QY 127 TNLNQNQLPTLPVVIPTGPFDDG--SVRLAVLISMAVCIVMIVF--SSCFYKHYCKSI 183
DB 125 TDFCNRLDLEPTLSPKI----SDGEYALRFIALIISLVCLILIVGFTLIITWIKH--KLH 178
QY 184 SSRGRYNDLEQDEAFIPVGSLSKLIIDQSQSGSGSLPLLVQRTIAKIQMVROVKGK 243
DB 179 SQRLMYNRNLDPPDAFIPAGESLKALIDISQSGSGSGSLPLLVQRTIAKIQMVROVKGK 238
QY 244 RYGEVVMGKRGKGVAVKVFTEEBASWFRTEIYQTVLMRHNILGFIADIKGTGWT 303
DB 239 RYGEVVMGKRGKGVAVKVFTEEBASWFRTEIYQTVLMRHNILGFIADIKGTGWT 298
QY 304 QLYLITDYHENGSLYDFLKCATLDRALLKLAISAAAGLCHLHTEIYGTQKPAIAHRL 363
DB 299 QMYLITEYHENGSLYDFLKCATLDRALLKLAISAAAGLCHLHTEIYGTQKPAIAHRL 358
QY 364 KSKNLIKKNKSGCCCIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSKNHFQ 423
DB 359 KSKNLIKKNKSGCCCIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSKNHFQ 418
QY 424 PYIMADIYVSGLLIWMARRCITGIVEYQLPYNNVPSPSYEDMRVVCVKRLRPV 483

DB 419 AYIMADIYVSGLLIWMARRCITGIVEYQLPYDMVPNDPSFEDMRVVCVKLRPTV 478
QY 484 SNRWNSDECLRAVLKIMSECAHNPASRLTALRIKKTAKWVESQDVKI 532
DB 479 SNRWNSDECLRAVLKIMAECAHNPASRLTALRIKKTAKWVESQDVKI 527

RESULT 5
JC2491
serine/threonine kinase receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Apr-1995 #sequence_revision 36-May-1995 #text_change 05-Oct-2004
C:Accession: JC2491
R:Yamaji, N.; Celeste, A.J.; Thies, R.S.; Song, J.J.; Bernier, S.M.; Goltzman, D.; Lyon
Biochem. Biophys. Res. Commun. 205, 1944-1951, 1994
A:Title: A mammalian serine/threonine kinase receptor specifically binds BMP-2 and BMP-
A:Reference number: JC2491; PMID:95110346; PMID:7811286
A:Accession: JC2491
A:Molecule type: mRNA
A:Residues: 1-502 <YAM>
A:Cross-references: UNIPARC:UPI00000B6BDE
C:Keywords: ATP; glycoprotein; transmembrane protein
F:127-148/Domain: transmembrane #status predicted <TM>
F:202-498/Domain: protein kinase homology <KIN>
F:210-218/Region: protein kinase ATP-binding motif
F:284,343,388/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 68.2%; Score 1934.5; DB 2; Length 502;
Best Local Similarity 72.1%; Pred. No. 1.6e-96;
Matches 364; Conservative 60; Mismatches 76; Indels 5; Gaps 5;

QY 29 MLHGTCMSDVKDPKENGVTLAPEDTLPLFKVCYCSGHCPDDAINNTCITNGHCFATIEE 88
DB 2 LLRSSG-KLVNVTGK-EDGESTAPTARPKVLKCKHHHCPEDSVNNICSDGTCFTMIEE 59
QY 89 DQGETTLTSGCMKYEGSDFOCKDSPKAQLRRTIECC-RTNLNQNQLPTLPVVIPTGPF 147
DB 60 DSGTPTVTSGLGLESGDFQCRDIPHPQRSIECTERNECNKOLHPTLPKDRDFV 119
QY 148 DGSVRWLAVLISMAVCIVMIVFSSCFYKHYCKSISSRGRYNDLEQDEAFIPVGSLSK 207
DB 120 DGPFIHKKALLISVTVCSL-LLVLIILFCYFRY-KRQEARPRYSIGLEQDETIYPPGESLR 177
QY 208 DLIDQSQSGSGSLPLLVQRTIAKIQMVROVKGKRGYGEVMGKRGKGVAVKVFTEE 267
DB 178 DLIEQSQSGSGSLPLLVQRTIAKIQMVROVKGKRGYGEVMGKRGKGVAVKVFTEE 237
QY 268 EASWFRTEIYQTVLMRHNILGFIADIKGTGWTQLYLIITDYHENGSLYDFLKCATLD 327
DB 238 EASWFRTEIYQTVLMRHNILGFIADIKGTGWTQLYLIITDYHENGSLYDFLKCATLD 297
QY 328 TRALLKLAISAAAGLCHLHTEIYGTQKPAIAHRLKSNILITKNGSGCCCIADLGLAVKF 387
DB 298 AKSMLKLAISVSSVGLCHLHTEIYGTQKPAIAHRLKSNILVKKNGTCCIADLGLAVKF 357
QY 388 NSDTNEVDIPLNTRVGTTRRYMAPEVLDLSKNHFQPYIMADIYVSGLLIWMARRCITG 447
DB 358 ISDTNEVDIPLNTRVGTTRRYMAPEVLDLSKNHFQPYIMADIYVSGLLIWMARRCITG 417
QY 448 GIVEEYQLPYNNVPSPSYEDMRVVCVKRLRPVSNRNSDECLRAVLKIMSECAH 507
DB 418 GIVEEYQLPYNNVPSPSYEDMRVVCVKRLRPVSNRNSDECLRAVLKIMSECAH 477
QY 508 PASRLTALRIKKTAKWVESQDVKI 532
DB 478 PASRLTALRIKKTAKWVESQDIKL 502

RESULT 6
A53444
activin receptor-like kinase 6 precursor - mouse
C:Species: Mus musculus (house mouse)

C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 05-Oct-2004
C:Accession: A53444; S40159
R:ten Dijke, P.; Yamashita, H.; Ichijo, H.; Franzen, P.; Laiho, M.; Miyazono, K.; Heldin
Science 264, 101-104, 1994
A:Title: Characterization of type I receptors for transforming growth factor-beta and ac
A:Reference number: A53444; MUID:94188705; PMID:8140412
A:Accession: A53444
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-502 <TEN>
A:Cross-references: UNIPROT:P36898; UNIPARC:UPI000000417C; EMBL:Z23143; NID:G437870; PIDN:
R.Miyazono, K.; Moren, A.; Grimsby, S.; Ichijo, H.; Heldin, C.; ten Dijke, P.
submitted to the EMBL Data Library, June 1993
A:Description: ALK-3 and ALK-6: the closely related members in the serine/threonine kin
A:Reference number: S40158
A:Accession: S40159
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-502 <MIY>
A:Cross-references: UNIPARC:UPI000000417C; EMBL:Z23143; NID:G437870; PIDN:CAA80674.1; PI
C:Superfamily: Serine/threonine-specific protein kinase, activin receptor II type; prote
C:Keywords: ATP; serine/threonine-specific protein kinase; transmembrane protein
F:202-498/Domain: protein kinase homology <KIN>
F:210-218/Region: protein kinase ATP-binding motif

Query Match 68.1%; Score 1933.5; DB 2; Length 502;
Best Local Similarity 72.1%; Pred. No. 1.8e-96;
Matches 364; Conservative 60; Mismatches 76; Indels 5; Gaps 5;

QY 29 MLHGTGMKDVQKPKENGVTIAPEDTLPFLKCYCSGHCPCDDAINNCTITNGHCFALIEEDOGETT 88
DB 2 LRRSSG-KLVNGTKK-EDGESTAPTRPKILCKCHHCPEDSVNMCSTDGYCTFIIEE 59

QY 89 DQGETTLTSGCMKYEGDFQCKDSPKAQLRTIECC-RTNLCNOYLQPTLPVVPVIGPFF 147
DB 60 DDSGMPVVTSGCLGEGSDFQCRDTPIPHQRRESIECCTERNECNKDLHPTLPPLKDRDFV 119

QY 148 DGSVRVLAVLSMAVCIVAMIVFSSCFCKYKCHKSISRRGRNRLDEQDEAFIPVGESLJK 207
DB 120 DGPPIHKALLISVTVCSL-LLVLLIIFCYFRY-KRQEARPRYSIGLEQDETYPFGESLR 177

QY 208 DLIDQSQSGSGGLPLLVQRTIAKQIOMVROVGKRYGEVWVGKRGKAVKVFVFFTE 267
DB 178 DLIEQSQSGSGGLPLLVQRTIAKQIOMVQIKGKRYGEVWVGKRGKAVKVFVFFTE 237

QY 268 EASWFRETEIYQTVLMRHNILGFTAAADIKGTGSMTQLYLITDYHENGSLYDLKCATLD 327
DB 238 EASWFRETEIYQTVLMRHNILGFTAAADIKGTGSMTQLYLITDYHENGSLYDLKSTILD 297

QY 328 TRALLKLAYSAGGLCHLHTEIYGTQKPAIAHRDLKSNKILIKNGSCCIIADLGLAVKF 387
DB 298 AKSMLKLAYSVSGGLCHLHTEIFSTQKPAIAHRDLKSNKILVKNKGTCCIIADLGLAVKF 357

QY 388 NSDTNEVDIPLNTRVTRYMAPEVLDESLSKNHFQPYIMADIYSFGLIIEWEMARRCITG 447
DB 358 ISDTNEVDIPLNTRVGTKRYMPEVLDESLSNRNHFSQYIMADMYISFGLIIEWEIAARCISG 417

QY 448 GIVEEYQLPYNNVPSDPSYEDMREVVCVKRLRPVSNRWNSECLRAVLKLMSECAW 507
DB 418 GIVEEYQLPYHDLVPSDPSYEDMREVVCVKRLRPFPNRSWSSDECLRQWGLMTECAW 477

QY 508 PASRLTALRIKTLAKMWESQDVKI 532
DB 478 PASRLTALRVKTLAKMWESQDIKL 502

RESULT 7
A56683
receptor protein kinase RPK-1 precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 05-Oct-2004
C:Accession: A56683
R.Sumitomo, S.; Saito, T.; Nohno, T.

DNA Seq. 3, 297-302, 1993
A:Title: A new receptor protein kinase from chick embryo related to type II receptor fo
A:Reference number: A56683; MUID:94003400; PMID:8400359
A:Accession: A56683
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-502 <SUM>
A:Cross-references: UNIPROT:Q05438; UNIPARC:UPI0000126A3C; GB:D13432; NID:G222862; PIDN
C:Superfamily: Serine/threonine-specific protein kinase, activin receptor II type; prote
C:Keywords: ATP; phosphotransferase; transmembrane protein
F:202-498/Domain: protein kinase homology <KIN>
F:210-218/Region: protein kinase ATP-binding motif

Query Match 67.9%; Score 1926; DB 2; Length 502;
Best Local Similarity 72.3%; Pred. No. 4.4e-96;
Matches 360; Conservative 59; Mismatches 75; Indels 4; Gaps 4;

QY 36 KSDVDQKPKENGVTIAPEDTLPFLKCYCSGHCPCDDAINNCTITNGHCFALIEEDOGETT 95
DB 8 KLSMESRKEDSEGT-APAPPQKKUSCQCHHCPEDSVNMCSTDGYCFTIIEEDSGGHL 66

QY 96 LTSQCMKYEGSDFQCKDSPKAQLRTIECCR-TNLNCNOYLQPTLPVVPVIGPFGDSVRWL 154
DB 67 VTGCGLEGSGDFQCRDTPIPHQRRESIECCTQDQYCNKHLHPTLPPLKNRDPFAENIHK 126

QY 155 AVLISMVAVCIAMIVFSSCFCKYKCHKSISRRGRNRLDEQDEAFIPVGESLKLIDQSQ 214
DB 127 ALLISVTVCSS-LLVLLIIFCYFRY-KRQEARPRYSIGLEQDETYPFGESLKLIEQSQ 184

QY 215 SSGSGGLPLLVQRTIAKQIOMVROVGKRYGEVWVGKRGKAVKVFVFFTEASWPRE 274
DB 195 SSGSGGLPLLVQRTIAKQIOMVQIKGKRYGEVWVGKRGKAVKVFVFFTEASWPRE 244

QY 275 TEIYQTVLMRHNILGFTAAADIKGTGSMTQLYLITDYHENGSLYDLKCATLDTRALLKL 334
DB 245 TEIYQTVLMRHNILGFTAAADIKGTGSMTQLYLITDYHENGSLYDLKSTLTDTKGMLK 304

QY 335 AYSAAAGLCHLHTEIYGTQKPAIAHRDLKSNKILIKNGSCCIIADLGLAVKFNSTNEV 394
DB 305 AYSSVSGGLCHLHTEIFSTQKPAIAHRDLKSNKILVKNKGTCCIIADLGLAVKFI 364

QY 395 DIPNTRVTRYMAPEVLDESLSKNHFQPYIMADIYSFGLIIEWEMARRCITGGIVEEYQ 454
DB 365 DIPNTRVTRYMPEPEVLDESLSNRNHFSQYIMADMYISFGLIIEWEIAARCISG 424

QY 455 LPYNNVPSDPSYEDMREVVCVKRLRPVSNRWNSECLRAVLKLMSECAWNPASRLTA 514
DB 475 LPYHDLVPSDPSYEDMREVVCVKRLRPFPNRSWSSDECLRQWGLMMECAWNPASRLTA 484

QY 515 LRIKTLAKMWESQDVKI 532
DB 485 LRVKTLAKMWESQDIKL 502

RESULT 8
JC2061
transforming growth factor beta receptor type I, ESK 2 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 05-Oct-2004
C:Accession: JC2061
R.Tomoda, T.; Kudoh, T.; Noma, T.; Nakazawa, A.; Muramatsu, M.; Arai, K.
Biochem. Biophys. Res. Commun. 198, 1054-1062, 1994
A:Title: Molecular cloning of a mouse counterpart for human TGF-beta type I receptor.
A:Reference number: JC2061; MUID:94161714; PMID:8117261
A:Accession: JC2061
A:Molecule type: mRNA
A:Residues: 1-503 <TOM>
A:Cross-references: UNIPROT:Q64729; UNIPARC:UPI0000021038; GB:D28526; NID:G467521; PIDN:
C:Comment: This protein is the mouse counterpart for human transforming growth factor be
C:Keywords: ATP; glycoprotein; receptor; transmembrane protein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-501/Product: transforming growth factor-beta type I receptor ESK 2 #status predict
F:126-147/Domain: transmembrane #status predicted <TM>

F;203-499/Domain: protein kinase homology <KIN>
F;211-219/Region: protein kinase ATP-binding motif
F;41/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 44.9%; Score 1274; DB 2; Length 503;
Best Local Similarity 51.4%; Pred. No. 3.1e-61;
Matches 263; Conservative 70; Mismatches 144; Indels 32; Gaps 10;

QY 42 KKPENGVTLPEDTL----PFLKCYCSGH-CPDDAINNTCITNGHCFALIEEDDQGETTL 96
DB 9 RRPQLLIVLVAATLPGAKALQCF--HLCTKD--NFTCETDGLCFVSVTETD-KVJH 63
QY 97 TSCMKY-----EGSDFQCKDSKPAQLRRTIECCRNLCNQYLQPTLPPVVGPFDD--- 148
DB 64 NSMCIAEIDLPRDRPFVCAPSKGTAVTTTCNQDHCNKIELPT-----TGPFSEKQS 118
QY 149 ---GSYRWLAVLISMA--VCIVAMIVFSSCFCKYKCKSISGRYNRDLEQDEAFIPVG 203
DB 119 AGLGPVELAAVIAGPVCFVCIALLMLMVYIC---HNRTVIHHRVNEEDPSLDRPFISEG 174
QY 204 ESLKDLIDOSQSGSGGLPLLIVORTIAQIQMVROVGRGKRGVWKGKRGKAVKVP 263
DB 175 TILKDLIYDWTSSGSGGLPLLIVORTIAQITIVLOESIGKRGVWKGKRGKAVKVP 234
QY 264 FTTEASWPRETEIYQTVLMRHNILGFTAAIKGTGTSWTQLYLITDYHENGSLYDPLK 323
DB 235 SSREERSWPRETEIYQTVLMRHNILGFTAAIKGTGTSWTQLYLITDYHENGSLYDPLK 294
QY 324 ATLDTRALLKLAISACGLHLHTEIYGTGKPAIAHRLKSKNLIKNGSCCIADLGL 383
DB 295 YTVTEGMIKLALSTAGLAHLHTEIYGTGKPAIAHRLKSKNLIKNGSCCIADLGL 354
QY 384 AVKFNSTDNEVDIPLNTRVTRYMAPEVLDESLSKNHFQPYIMADIYFGLIINEMARR 443
DB 355 AVRHDSATDITDIAPNHRVGTTRYMAPEVLDESLSKNHFQPYIMADIYFGLIINEMARR 414
QY 444 CITGIVEEYQLPYNNMVPDSYEDMREVCVKRLRPVSNRNSDECLRAVLKMSRC 503
DB 415 CSIGGIHEDYQLPYDLVSPDSVEEMRKVCEQKLRPNI PNWQSCREALRVMAKIMREC 474
QY 504 WAHNPASRLTALRIKTLAKMVEQDVKI 532
DB 475 WYANGAARLTALRIKTLQSLQSQEGIKM 503

RESULT 9
145713
Dpp receptor TKV, splice form 1 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 05-Oct-2004
C:Accession: 145713
R:Brummel, T.J.; Twombly, V.; Marques, G.; Wrana, J.L.; Newfeld, S.J.; Attisano, L.; Mas
Cell 78, 251-266, 1994
A:Title: Characterization and relationship of Dpp receptors encoded by the saxophone and
F:198-500/Domain: intracellular #status predicted <TMM>
A:Reference number: A54829; MUID:94320137; PMID:8044839
A:Accession: 145713
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-509 <RES>
A:Cross-references: UNIPROT:Q95S10; UNIPARC:UPI000002A1A5; EMBL:U11442; NID:G523341; PID
C:Genetics:
A:Gene: FlyBase:tkv; thickveins
A:Cross-references: FlyBase:FBgn0003716
C:Keywords: alternative splicing; ATP
F:206-214/Region: protein kinase homology <KIN>
F:206-214/Region: protein kinase ATP-binding motif

Query Match 44.9%; Score 1274; DB 2; Length 509;
Best Local Similarity 53.5%; Pred. No. 3.1e-61;
Matches 262; Conservative 63; Mismatches 133; Indels 32; Gaps 12;

QY 59 LKCYSGHCPDDAINNTCIT--NGHCFALIE---EDDQG--ETTLTSGCMKYE--GSDQF 109

DB 15 LTYCDGSCPDVNSNGTCETPRGSCFSVAQQLYDDETTGMVEERTYGCMPPEDENGGFLM 74
QY 110 CXDSPKAQLR-RTIECC-RTNLCNQYLQPTLPPVVGPFDD-----GSYRWLAVL--ISM 160
DB 75 CKVAAPVPHUGKNI VCCDKEDFCNRLDYPTYPKLTTPAPDLPVSSSELHTLAVFGSIII 134
QY 161 AVCIVAMIVFSSCFCKYKCKSISGRYNRDLEQDEAFIPVGESLKDILIDOSQSGSGS; 220
DB 135 SLSVFWLIVASLCFTYKRR-EKLRQKPRILNSMCNSQL-----SPLSQLVE--QSSGSGS; 186
QY 221 GLPLLIVORTIAQIQMVROVGRGKRGVWKGKRGKAVKVPFTTEASWPRETEIYQ 280
DB 187 GLPLLIVORTIAQIQMVRLVGRGKRGVWLAQRDRAVAKFTFTTEASWPRETEIYQ 246
QY 281 VLMRHNILGFTAAIKGTGTSWTQLYLITDYHENGSLYDPLKCATLDTALLKLAISAAC 340
DB 247 VLMRHNILGFTAAIKGTGTSWTQMLLITDYHENGSLYDLSMSVNPQKQLLAFLSLLA; 306
QY 341 GLCHLHTEIYGTGKPAIAHRLKSKNLIKNGSCCIADLGLAVKFNSTDNEVDIPLN 400
DB 307 GLAHLHDEIFGTGKPAIAHRLKSKNLIKNGSCCAIADFGKLVKYNSELDVIHIAQNP 366
QY 401 RVGTRYMAPEVLDESLSKNHFQPYIMADIYFGLIINEMARRCIT-----GGIVEEYQ 454
DB 367 RVGTRYMAPEVLSQLDPKQFEFVKRADMYSGVLVWEMTRRCYTPVSGTKTTTCEDYA 426
QY 455 LPYNNMVPDSYEDMREVCVKRLRPVSNRNSDECLRAVLKMSCEWHAHNPASRLTA 514
DB 427 LPYHVDVSDPTFEDHMAVVCVKGPRPPISRWQEDDVLATVSKINMQECPHNPVTLLTA 486
QY 515 LRIKTLAKM 524
DB 487 LRVKTLGLRL 496

RESULT 10
JC2062
Transforming growth factor beta receptor type I precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Oct-2004
C:Accession: JC2062
R:Suzuki, A.; Shioda, N.; Maeda, T.; Tada, M.; Ueno, N.
Biochem. Biophys. Res. Commun. 198, 1063-1069, 1994
A:Title: A mouse TGF-beta type I receptor that requires type II receptor for ligand bin
A:Reference number: JC2062; MUID:94161715; PMID:8117262
A:Accession: JC2062
A:Molecule type: mRNA
A:Residues: 1-499 <SUZ>
A:Cross-references: UNIPROT:Q64729; UNIPARC:UPI000016D072
C:Keywords: ATP; glycoprotein; growth factor receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-499/Product: transforming growth factor-beta type I receptor #status predicted <KIN>
F:122-145/Domain: transmembrane #status predicted <TMM>
F:146-499/Domain: intracellular #status predicted <TMM>
F:199-495/Domain: protein kinase homology <KIN>
F:207-215/Region: protein kinase ATP-binding motif
F:41/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 44.7%; Score 1268; DB 2; Length 499;
Best Local Similarity 51.4%; Pred. No. 6.3e-61;
Matches 261; Conservative 70; Mismatches 143; Indels 34; Gaps 9;

QY 42 KKPENGVTLPEDTL----PFLKCYCSGH-CPDDAINNTCITNGHCFALIEEDDQGETTL 96
DB 9 RRPQLLIVLVAATLPGAKALQCF--HLCTKD--NFTCETDGLCFVSVTETD-KVJH 63
QY 97 TSGCMKY-----EGSDFQCKDSKPAQLRRTIECCRNLCNQYLQPT-----LPPVWIG 144
DB 64 NSMCIAEIDLPRDRPFVCAPSKGTAVTTTCNQDHCNKIELPTTEKQSGAGLPVELA 123
QY 145 PFDGSGRWLAVLISMAVCIVAMIVFSSCFCKYKCKSISGRYNRDLEQDEAFIPVG 204
DB 124 AVIAGPVCF-----VCIALMLMVYIC---HNRTVIHHRVNEEDPSLDRPFISEGT 171

activin A receptor type I - human
N;Alternate names: activin A receptor type II-like kinase 2; ALK-2; serine/threonine kinase
C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence revision 03-May-1994 #text_change 31-Dec-2004
C;Accession: A45992; I37162; S37182
R;Matuzaki, K.; Xu, J.; Wang, F.; McKeehan, W.L.; Krummen, L.; Kan, M.
J. Biol. Chem. 268, 12719-12723, 1993
A;Title: A widely expressed transmembrane serine/threonine kinase that does not bind actin
A;Reference number: A45992; MUID:93286114; PMID:8389764
A;Accession: A45992
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-509 <MAT>
A;Cross-references: UNIPROT:Q04771; UNIPARC:UPI000000163F; GB:L02911; NID:g338218; PIDN:R12en Dijke, P.; Ichijo, H.; Franzen, P.; Schulz, P.; Saras, J.; Toyoshima, H.; Heldin, Oncogene 8, 2879-2887, 1993
A;Title: Activin receptor-like kinases: a novel subclass of cell-surface receptors with serine/threonine kinase activity
A;Reference number: I37162; MUID:93390967; PMID:8397373
A;Accession: I37162
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-509 <RES>
A;Cross-references: UNIPARC:UPI000000163F; EMBL:Z22534; NID:g402184; PIDN:CAA80256.1; PIDN:CAA80256.1; PIDN:CAA80256.1
C;Genetics:
A;Gene: GDB:ACVR1; ACVRUK2; SKR1; ALK2
A;Cross-references: GDB:216986; OMIM:601298
C;Keywords: ATP; serine/threonine-specific protein kinase; transmembrane protein
F;206-502/Domain: protein kinase homology <KIN>
F;214-222/Region: protein kinase ATP-binding motif

Query Match 42.4%; Score 1204.5; DB 2; Length 509;
Best Local Similarity 48.6%; Pred. No. 1.6e-57;
Matches 253; Conservative 79; Mismatches 132; Indels 57; Gaps 14;

QY 46 NGVTLAP-----EDTLP-----FLKCYCSG-----HCPDDAINNCTITNGH 81
DB 3 DGVNLPVLIMIALPSPSEDEKPNKLYMVCGLSCGNBDHCEGQ-----Q 52

QY 82 CFIAIEDDOGETTLTSGCMK-YEGSDFOCKDQSPKQAQLRRTIECCRTNLCNOYLQPTLPP 140
DB 53 CFSLSIND-GFHVYQKGFQVVEQGMKTCTPSP--GQAVECCGDWCNRNITQLP- 108

QY 141 VTGPFDDGS-----VRNLAVLISMAVCIVAMIVFSSCFYKHYCKSISSRGYN-RDL 193
DB 109 -TKGKSPFGQNPHEVLGLIILSWFAVCLLACLLGVALRKPKR-----RNQERLNPDRV 162

QY 194 EQD--EAFIP--VGES-LKDLIDQSOSGSGGLPVLVQRTIAKQIQMVRQVKGKRYGEV 248
DB 163 EYGTIEGLITNVDGSLADLHDHSCSTSGSGGLPFLVQRTVARQITLLECVCVKGRYGEV 222

QY 249 WMGKWRGEKAVKVFVFTTEASWFRTEIYQTVLMRHNILGFIADIKGTGSWTQLYLI 308
DB 223 WRGSGOGENVAVKIFSRDEKSWFRTEIYQTVLMRHNILGFIADIKGTGSWTQLYLI 282

QY 309 TDYHENGSLYDFLKCATLDTALLKLAYSAAACGLHTEIYQTVCKGPAIAHRDLKSKNI 368
DB 283 THYHENGSLYDYQLTTLDTVSLRIVLSIASGLAHLHTEIYQTVCKGPAIAHRDLKSKNI 342

QY 369 LTKKNGSCCIIADGLAVKNSDNEVDIPLNTRVGTTRRYMAPEVLDSESKNHFQPIYMA 428
DB 343 LVKNGQCCIIADGLAVMHSQSNTQDVGNNRNVGTRKYMAPEVLDSESKNHFQPIYMA 402

QY 429 DIYFGLIIEWMARRCITGGIVEEYQLPYNNMVPSPSYEDMRVVCVKRLRPVNSRW 488
DB 403 DIWAFGLVWEVARRMWSNGIVEDYKPPFDVVPNDPSFEDMRKVKVQDQRRPNIPNRF 462

QY 489 SDECLRAVLKMECWNAHNPASRLTALRIKKTLLAKMVESQD 529
DB 463 SDPTLTSIAKLMKECWNPASRLTALRIKKTLLKIDNSLD 503

RESULT 14
A55921

serine/threonine kinase Atr-1 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 08-Sep-1995 #sequence revision 08-Sep-1995 #text_change 31-Dec-2004
C;Accession: A55921
R;Wana, J.L.; Iran, H.; Attisano, L.; Arora, K.; Childs, S.R.; Massague, J.; O'Connor, Mol. Cell. Biol. 14, 944-950, 1994
A;Title: Two distinct transmembrane serine/threonine kinases from Drosophila melanogaster
A;Reference number: A55921; MUID:94119112; PMID:8289834
A;Accession: A55921
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-601 <WRA>
A;Cross-references: UNIPROT:Q23975; UNIPARC:UPI0000007A851; GB:U04692; NID:g436960; PIDN:Q23975
C;Genetics:
A;Gene: FlyBase:babo
A;Cross-references: FlyBase:FBgn0011300
C;Keywords: ATP
F;301-597/Domain: protein kinase homology <KIN>
F;309-317/Region: protein kinase ATP-binding motif

Query Match 42.2%; Score 1198; DB 2; Length 601;
Best Local Similarity 46.3%; Pred. No. 4.1e-57;
Matches 237; Conservative 83; Mismatches 138; Indels 54; Gaps 10;

QY 42 KKPENGVTLAPEDTLPLFKCYCSGHCPCDDAINNCTITNGHCFIAIEDDOGETTLTSGCM 101
DB 121 KKPENKI-----KCHCD-TCKES--NNICETDGFCTSVSKNSDGSIIFYSYCM 166

QY 102 --KY---EGSDFOCKDQSPKQAQLRRTIECCRTNLCNO-----YLOPTLPVVGIP 145
DB 167 VVKYNNMQRSPSECLTSNERFDYRIDCKSDCFCKNENMKRIFETDYVPHRLT----- 220

QY 146 FPDGSRVLAVLISMAVCIVAMIVFSSCFYK---HYCKSISSRGYNRDLSEDAFIPV 202
DB 221 ----SWEFVAIIIGATLFI-----CFTGTSTWYICORRRKRMASGRTFAKEDSAYDPI 268

QY 203 ---GESLKDLDQSOSGSGGLPVLVQRTIAKQIQMVRQVKGKRYGEVMMGKWRGEKVA 259
DB 269 LNGNTTIHDIEMTTSVSGSGAGLPVLVQRTIAKQIQMVRQVKGKRYGEVMMGKWRGEKVA 328

QY 260 VKVFTTEASWFRTEIYQTVLMRHNILGFIADIKGTGSWTQLYLIYTDYHENGSLYD 319
DB 329 VKIFSREBSCSWFREAIYQTVLMRHNILGFIADIKGTGSWTQLYLIYTDYHENGSLYD 388

QY 320 FLKCATLDTALLKLAYSAAACGLHTEIYQTVCKGPAIAHRDLKSKNLIKNGSCCIA 379
DB 389 YLTHPVDVTNMLNWSLSLSTATGLAHLHMDIVGTGKPAIAHRDLKSKNLIKNGSCCIA 448

QY 380 DLGLAVKNSDNEVDIPLNTRVGTTRRYMAPEVLDSESKNHFQPIYMAIYISFGLIWE 439
DB 449 DLGLAVRHKNSDVIDIPSTHRTVGTTRRYMAPEVLDSESKNHFQPIYMAIYISFGLIWE 508

QY 440 MARRCITGGIVEEYQLPYNNMVPSPSYEDMRVVCVKRLRPVNSRWNSDECLRAVLKL 499
DB 509 IARRCNMGMIYDEYQLPYDYVQDPSPSYEDMRVVCVKRLRPVNSRWNSDECLRAVLKL 568

QY 500 MSECAHNPASRLTALRIKKTLLAKMVESQDVK 531
DB 569 MKECWYPNPVARLTALRIKKTLLASISVEDKVK 600

RESULT 15
A49664
activin type I receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 31-Dec-2004
C;Accession: A49664
R;Tsuchida, K.K.T.; Vale, W.W.
Proc. Natl. Acad. Sci. U.S.A. 90, 11242-11246, 1993
A;Title: Cloning and characterization of a transmembrane serine kinase that acts as an activin type I receptor
A;Reference number: A49664; MUID:94068580; PMID:8248234
A;Accession: A49664
A;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-509 <RES>
A:Cross-References: UNIPROT:P80201; UNIPARC:UP10000126671; GB:L19341; NID:9435431; PIDN:
C:Keywords: ATP
F:206-502/Domain: protein kinase homology <KIN>
F:214-222/Region: protein kinase ATP-binding motif

Query Match 42.1%; Score 1194; DB 2; Length 509;
Best Local Similarity 50.5%; Pred. No. 5.8e-57;
Matches 247; Conservative 75; Mismatches 127; Indels 40; Gaps 12;

QY 61 CYCSG-----HCPDDAINVTCTNGHCFALIEDDQGETTLTSGCMK-YEGSDFQCKD 112
Db 35 CVCEGLSCGNEHCHGQ-----QCFSSLSVND-GFRVYQKGCQVYEQGKWTCKT 83

QY 113 SPKAQLRRTIECRTNLCNOYLQPTLPVYVIGVFFFDGS-----VRWLAVLISMVAVCI 166
Db 84 PFSP--GQAVECCQGDWCNRRNVTARLP--TKGKSPGQNFHLEVGLIILSVVFAVCLFA 139

QY 167 MIVFSSCFYKHYCKYSISRRGRYN-RDLEQD--EAFIP--VGES-LKDLIDQSQSSGSGS 220
Db 140 CILGVALRKFKR-----RNQERLNPRDVEYGTIEGLITTNVGDSTLAELLDHSHCTSGSGS 194

QY 221 GLPLLVORTIAKQIOMVROVGKGRYGEVWMGKRGCEKVAVKVFFTEEASWPRETEIYOT 280
Db 195 GLPFLVQRTVARQITLLECVGKGRYGEVWMRGQNGENVAVKIPSSRDEKSWPRETELYNT 254

QY 281 VLMRHENILGFTAAIDIKGTGWTQLYLTIDYHENGSLYDFLKCATLDTRALLKLAYSAA 340
Db 255 VMLRHENILGFTASDMTSRHSSTQLWLITHYHEMGSLYDYQLQTLTLDTVSCLRIVLSIAS 314

QY 341 GLCHLHTEIYGTQKPAIAHRDLKSNILIKNGSCCTADIGLAVKFNSDTNEVDIPLNT 400
Db 315 GLAHLHIEFTGTQKSAIAHRDLKSNILVKNQCCITADLGLAVMHSQSTNQLDVGNNP 374

QY 401 RVGTRRYMAPEVLDESLSKNHFQPYIMADIYSFGLI IWEMARCIITGGIVEYQLPYNM 460
Db 375 RVGTRRYMAPEVLDETIQVDCFDSTYKRVDIWAFGLVLEVARVMVSNGLVEDYKPPFYDV 434

QY 461 VPSPSYEDMREWVCVKLRPIVSNRWNSDECLRAVLKLMSECAHNPA SRLTALRIKKT 520
Db 435 VNPDPSPEDMRKVCVVDQQRPNIPNRWFSDDPTLTSLAKLMKECWYQNP SARLTALRIKKT 494

QY 521 LAKMVESQD 529
Db 495 LTKIDNSLD 503

Search completed: December 3, 2005, 06:12:27
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 06:00:33 ; Search time 235 Seconds
(without alignments)
1597.196 Million cell updates/sec

Title: US-10-600-645-2

Perfect score: 2838

Sequence: 1 MTQLTYTIRLLGACLFIIISH.....TALRIKKTLAKMVESQDVKI 532

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2838	100.0	532	2 Q64308_RAT	Q64308 rattus norv
2	2838	100.0	532	2 Q78EA7_MOUSE	Q78EA7 rattus sp.
3	2823	99.5	532	1 BMRIA_MOUSE	P36895 mus musculus
4	2823	99.5	532	2 Q53243_MOUSE	P36895 mus musculus
5	2763	97.4	532	1 BMRIA_MOUSE	P36894 homo sapien
6	2616	92.2	500	2 Q60607_MOUSE	Q60607 mus musculus
7	2582.5	91.0	533	2 Q90754_CHICK	Q90754 gallus gall
8	2570.5	90.6	533	2 Q9PUF5_COTCO	Q9PUF5 coturnix co
9	2223	78.3	527	2 Q91578_XENLA	Q91578 xenopus lae
10	2222	78.3	527	2 Q42338_XENLA	Q42338 xenopus lae
11	2211	77.9	527	2 Q42339_XENLA	Q42339 xenopus lae
12	2109	74.3	527	2 Q93243_BRARE	Q93243 brachydanio
13	2107.5	74.3	499	2 Q4RG20_TETNG	Q4RG20 tetraodon n
14	2104.5	74.2	534	2 Q66HY1_BRARE	Q66HY1 brachydanio
15	1950.5	68.7	502	2 Q9BD14_SHEEP	Q9BD14 ovis aries
16	1944.5	68.5	502	2 Q95123_PIG	Q95123 sus scrofa
17	1941	68.4	502	1 BMRIA_MOUSE	Q00238 homo sapien
18	1934.5	68.2	502	2 Q9QVT7_MOUSE	Q9QVT7 rattus sp.
19	1933.5	68.1	502	1 BMRIA_MOUSE	P36898 mus musculus
20	1926.5	67.9	502	2 Q9PUF4_COTCO	Q9PUF4 coturnix co
21	1926	67.9	502	1 BMRIA_MOUSE	Q05438 gallus gall
22	1918.5	67.6	502	2 Q4PRC1_CAPHI	Q4PRC1 capra hircu
23	1894	66.7	530	2 Q9W629_BRARE	Q9W629 brachydanio
24	1878	66.2	508	2 Q4SJF6_TETNG	Q4SJF6 tetraodon n
25	1631	57.5	479	2 Q4RT67_TETNG	Q4RT67 tetraodon n
26	1612	56.8	371	2 Q8SPU3_PIG	Q8SPU3 sus scrofa
27	1591.5	56.1	361	2 Q421Q1_CAPHI	Q421Q1 capra hircu
28	1383	48.7	237	2 Q569A5_RAT	Q569A5 rattus norv
29	1336	47.1	286	2 Q8SPU4_PIG	Q8SPU4 sus scrofa
30	1307.5	46.1	534	2 Q7YXAI_CRAGI	Q7YXAI crassostrea
31	1290	45.5	499	2 Q5CD19_PIG	Q5CD19 sus scrofa

RESULT 1

Q64308_RAT	500	2	Q91595_XENLA	Q91595 xenopus lae
AC Q64308;	45.4	2	Q5CD18_PIG	Q5CD18 sus scrofa
DT 01-NOV-1996 (Tremblrel. 01, Created)	45.3	2	Q5CD21_PIG	Q5CD21 sus scrofa
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)	45.3	2	Q5CD20_PIG	Q5CD20 sus scrofa
DE Bone morphogenetic protein type IA receptor precursor (Bone morphogenetic protein 4 receptor).	548	2	Q7QGF7_ANOGA	Q7QGF7 anopheles g
DE merphogenetic protein 4 receptor).	548	2	Q6PUB5_ANOGA	Q6PUB5 anopheles g
GN Name=ALUK-3;	565	2	Q46680_BOVIN	Q46680 bos taurus
OS Rattus norvegicus (Rat).	531	2	Q81PK9_DROME	Q81PK9 drosophila
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	563	2	Q7JQ37_DROME	Q7JQ37 drosophila
OC NCBI_TaxID=10116;	563	2	Q7KTP1_DROME	Q7KTP1 drosophila
RN [1]	575	2	Q9VMT1_DROME	Q9VMT1 drosophila
RP NUCLEOTIDE SEQUENCE.	503	1	TGFR1_MOUSE	Q64729 mus musculus
RC STRAIN=Wistar; TISSUE=Dental pulp;	503	2	Q4FJL1_MOUSE	Q4FJL1 mus musculus
RX MEDLINE=95032096; PubMed=7945360;	509	2	Q95S10_DROME	Q95S10 drosophila
RA Takeda K., Oida S., Ichijo H., Iimura T., Maruoka Y., Amagasa T., Sasaki S.;				
RT "Molecular cloning of rat bone morphogenetic protein (BMP) type IA receptor and its expression during ectopic bone formation induced by BMP*."				
RT Biochem. Biophys. Res. Commun. 204:203-209(1994).				
RL NUCLEOTIDE SEQUENCE.				
RN [2]				
RP STRAIN=Wistar; TISSUE=Brain;				
RC Ikeda T., Takahashi H.;				
RA "Expression pattern of bone morphogenetic protein 4 receptor in embryo and adult rat."				
RT Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.				
RL AIP1, ACVR2, ACVR1B and MADH3 (By similarity).				
CC -!- SUBUNIT: Interacts with AIP1. Part of a complex consisting of AIP1, ACVR2, ACVR1B and MADH3 (By similarity).				
CC -!- SIMILARITY: Type I membrane protein (By similarity).				
DR EMBL; D38082; BAA07275.1; -; mRNA.				
DR EMBL; D17667; BAA04549.1; -; mRNA.				
DR PIR; J2387; J2387.				
DR HSP; P36894; IES7.				
DR SMR; Q64308; 55-143.				
DR Ensembl; ENSRNOG0000010814; Rattus norvegicus.				
DR RGD; 70989; Bmpria.				
DR GO; GO:0016020; C:membrane; IEA.				
DR GO; GO:0005524; F:ATP binding; IEA.				
DR GO; GO:0004872; F:transforming growth factor beta receptor ac. . .; IEA.				
DR GO; GO:0005024; F:transforming growth factor beta receptor ac. . .; IEA.				
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.				
DR GO; GO:0007178; P:transmembrane receptor protein serine/threo. . .; IEA.				
DR InterPro; IPR000472; Activin_receptor.				
DR InterPro; IPR000333; Actn_receptorII.				
DR InterPro; IPR000719; Prot_kinase.				
DR InterPro; IPR008271; Ser_thr_pkin_AS.				
DR InterPro; IPR003605; TGFbetarecept_GS.				

ALIGNMENTS

DR Pfam; PF01064; Activin_recpt; 1.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00653; ACTIVIN2R.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00467; GS; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding; Receptor;
KW Serine/threonine-protein kinase; Signal; Transferase; Transmembrane.
FT SIGNAL 1 23 Potential.
SQ SEQUENCE 532 AA; 59994 MW; 14ED4C03E2540A0C CRC64;

Query Match 100.0%; Score 2838; DB 2; Length 532;
Best Local Similarity 100.0%; Pred. No. 9.3e-188;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPAPEDTLPLFLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPAPEDTLPLFLK 60

QY 61 CYCSGHCPCDDAINNTCTINGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
Db 61 CYCSGHCPCDDAINNTCTINGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120

QY 121 TIECCRTNLCNQYLOPTLPVVGPFDDGSVRWLAVLISMAVICIVAMIVFSSCFCKHYC 180
Db 121 TIECCRTNLCNQYLOPTLPVVGPFDDGSVRWLAVLISMAVICIVAMIVFSSCFCKHYC 180

QY 181 KSISSRGYNRDLQDEAFIPVGESLKDLDIOSQSGSGGLPLLVQRTIAKIQMVQV 240
Db 181 KSISSRGYNRDLQDEAFIPVGESLKDLDIOSQSGSGGLPLLVQRTIAKIQMVQV 240

QY 241 GKGRYGEVVMGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFTAAIDKGTG 300
Db 241 GKGRYGEVVMGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFTAAIDKGTG 300

QY 301 SWTQLYLTIDYHENGSLYDFLKCATLDTALLKLAYSACGLCHLHTEIYGTQGPAPAH 360
Db 301 SWTQLYLTIDYHENGSLYDFLKCATLDTALLKLAYSACGLCHLHTEIYGTQGPAPAH 360

QY 421 HFQPYIMADYISFGLIIWEMARRCITGGIVEYQLPYNNMVPSPSPSYEDMREVVCVKRLR 480
Db 421 HFQPYIMADYISFGLIIWEMARRCITGGIVEYQLPYNNMVPSPSPSYEDMREVVCVKRLR 480

RESULT 2

Q78EA7_9MURI PRELIMINARY; PRT; 532 AA.
AC Q78EA7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Bone morphogenetic protein type IA receptor.
GN Name=Bmprla;
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95204990; PubMed=7897267;
RA Takeda K.;
RT "Expression of serine/threonine kinase receptors during ectopic bone

formation induced by bone morphogenetic protein (BMP).";
Kokubyo Gakkai Zasshi 61:512-526(1994).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; S75359; AAB33865.1; -; mRNA.
DR HSSP; P36897; 1B6C.
DR SMR; Q78EA7; 55-143.
DR RGD; 70989; Bmprla.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005024; F:transforming growth factor beta receptor ac. .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007178; P:transmembrane receptor protein serine/threo. .; IEA.
DR InterPro; IPR000472; Activin_receptor.
DR InterPro; IPR000333; Actn_receptorII.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR003605; TGFbetarecept_GS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF01064; Activin_recpt; 1.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00653; ACTIVIN2R.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00467; GS; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding; Receptor;
KW Serine/threonine-protein kinase; Transferase; Transmembrane.
SQ SEQUENCE 532 AA; 59994 MW; 14ED4C03E2540A0C CRC64;

Query Match 100.0%; Score 2838; DB 2; Length 532;
Best Local Similarity 100.0%; Pred. No. 9.3e-188;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPAPEDTLPLFLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPAPEDTLPLFLK 60

QY 61 CYCSGHCPCDDAINNTCTINGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
Db 61 CYCSGHCPCDDAINNTCTINGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120

QY 121 TIECCRTNLCNQYLOPTLPVVGPFDDGSVRWLAVLISMAVICIVAMIVFSSCFCKHYC 180
Db 121 TIECCRTNLCNQYLOPTLPVVGPFDDGSVRWLAVLISMAVICIVAMIVFSSCFCKHYC 180

QY 181 KSISSRGYNRDLQDEAFIPVGESLKDLDIOSQSGSGGLPLLVQRTIAKIQMVQV 240
Db 181 KSISSRGYNRDLQDEAFIPVGESLKDLDIOSQSGSGGLPLLVQRTIAKIQMVQV 240

QY 241 GKGRYGEVVMGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFTAAIDKGTG 300
Db 241 GKGRYGEVVMGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFTAAIDKGTG 300

QY 301 SWTQLYLTIDYHENGSLYDFLKCATLDTALLKLAYSACGLCHLHTEIYGTQGPAPAH 360
Db 301 SWTQLYLTIDYHENGSLYDFLKCATLDTALLKLAYSACGLCHLHTEIYGTQGPAPAH 360

QY 361 RDLKSNKILIKNGSCCADIADGLAVKFNSTNEVDIPLNTRVGTTRYNAPEVLDLSKN 420
Db 361 RDLKSNKILIKNGSCCADIADGLAVKFNSTNEVDIPLNTRVGTTRYNAPEVLDLSKN 420

QY 421 HFQPYIMADYISFGLIIWEMARRCITGGIVEYQLPYNNMVPSPSPSYEDMREVVCVKRLR 480
Db 421 HFQPYIMADYISFGLIIWEMARRCITGGIVEYQLPYNNMVPSPSPSYEDMREVVCVKRLR 480


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Db 61 CYCSGHCPCDDAINTNTCTNGHCFALIEEDDQGETTLTSGCMKYEGSDFCQKDSPKAQLRR 120
Qy 121 TIECCTNLCNQYLQPTLPVVGPPFDGSRVRLAVLISMAVCIAMIVFSSCFYKHYC 180
Db 121 TIECCTNLCNQYLQPTLPVVGPPFDGSRVRLAVLISMAVCIAMIVFSSCFYKHYC 180
Qy 181 KSISSRGYNRDLQDEAFIPVGSGLKDLIDQSSGSGGLPLLAVQRTIAKQIOMVRQV 240
Db 181 KSISSRGYNRDLQDEAFIPVGSGLKDLIDQSSGSGGLPLLAVQRTIAKQIOMVRQV 240
Qy 241 GKGRYGEVVMGKWRGEKAVKVFTEEASWFRTEIYQTVLMRHNILGFTAAADIKGTG 300
Db 241 GKGRYGEVVMGKWRGEKAVKVFTEEASWFRTEIYQTVLMRHNILGFTAAADIKGTG 300
Qy 301 SWTQLYLTDYHENGSLYDFLKCATLDTALLKLAISAACGLCHLHTEIYGTQGPATAH 360
Db 301 SWTQLYLTDYHENGSLYDFLKCATLDTALLKLAISAACGLCHLHTEIYGTQGPATAH 360
Qy 361 RDLKSKNLIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYNAPEVLDLSLKN 420
Db 361 RDLKSKNLIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYNAPEVLDLSLKN 420
Qy 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEYQLPYYNMVPSDPSYEDMRVVCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEYQLPYYNMVPSDPSYEDMRVVCVKRLR 480
Qy 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532

RESULT 4
Q53243_MOUSE PRELIMINARY; PRT; 532 AA.
ID Q53243_MOUSE
AC Q53243;
DT 13-SEP-2005 (trEMBLrel. 31, Created)
DT 13-SEP-2005 (trEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (trEMBLrel. 31, Last annotation update)
DE Bone morphogenetic protein receptor type Ia.
GN Name=Bmprla;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Lung;
RA Shalmanov P.D., Morty R.E., Eickelberg O.;
RT "Expression of bone morphogenic protein receptor Ia in the mouse.";
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AY365062; AAQ64630.1; -; mRNA.
DR SMR; Q53243; SS-143.
DR MGI; MGI:1338938; Bmprla.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0016021; P:anterior/posterior pattern formation; IMP.
DR GO; GO:0009952; P:cartilage development; IMP.
DR GO; GO:0051216; P:cell differentiation; IGI.
DR GO; GO:0030154; P:cell differentiation; IGI.
DR GO; GO:0009950; P:dorsal/ventral axis specification; IMP.
DR GO; GO:0007398; P:ectoderm development; IMP.
DR GO; GO:0048382; P:mesoderm development; IMP.
DR GO; GO:0001880; P:Mullerian duct regression; IMP.
DR InterPro; IPR000472; Activin_receptor.
DR InterPro; IPR000333; Actn_receptorII.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR003605; TGPbetarecept_GS.
DR InterPro; IPR001245; Tyr_pkinase.
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DR Pfam; PF01064; Activin_recp; 1.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00653; ACTIVIN2R.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00467; GS; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding; Receptor;
KW Serine/threonine-protein kinase; Transferase; Transmembrane.
SQ SEQUENCE 532 AA; 60063 MW; 70CC83CFB07CE9D5 CRC64;

Query Match 99.5%; Score 2823; DB 2; Length 532;
Best Local Similarity 98.9%; Pred. No. 1e-186;
Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACLPFIISHVQGNLDSMLHGTGMKSDVDOKKPGVYTLAPEDTLPELK 60
Db 1 MTQLYTYIRLLGACLPFIISHVQGNLDSMLHGTGMKSDVDOKKPGVYTLAPEDTLPELK 60

Qy 61 CYCSGHCPCDDAINTNTCTNGHCFALIEEDDQGETTLTSGCMKYEGSDFCQKDSPKAQLRR 120
Db 61 CYCSGHCPCDDAINTNTCTNGHCFALIEEDDQGETTLTSGCMKYEGSDFCQKDSPKAQLRR 120

Qy 121 TIECCTNLCNQYLQPTLPVVGPPFDGSRVRLAVLISMAVCIAMIVFSSCFYKHYC 180
Db 121 TIECCTNLCNQYLQPTLPVVGPPFDGSRVRLAVLISMAVCIAMIVFSSCFYKHYC 180

Qy 181 KSISSRGYNRDLQDEAFIPVGSGLKDLIDQSSGSGGLPLLAVQRTIAKQIOMVRQV 240
Db 181 KSISSRGYNRDLQDEAFIPVGSGLKDLIDQSSGSGGLPLLAVQRTIAKQIOMVRQV 240

Qy 241 GKGRYGEVVMGKWRGEKAVKVFTEEASWFRTEIYQTVLMRHNILGFTAAADIKGTG 300
Db 241 GKGRYGEVVMGKWRGEKAVKVFTEEASWFRTEIYQTVLMRHNILGFTAAADIKGTG 300

Qy 301 SWTQLYLTDYHENGSLYDFLKCATLDTALLKLAISAACGLCHLHTEIYGTQGPATAH 360
Db 301 SWTQLYLTDYHENGSLYDFLKCATLDTALLKLAISAACGLCHLHTEIYGTQGPATAH 360

Qy 361 RDLKSKNLIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYNAPEVLDLSLKN 420
Db 361 RDLKSKNLIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYNAPEVLDLSLKN 420

Qy 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEYQLPYYNMVPSDPSYEDMRVVCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEYQLPYYNMVPSDPSYEDMRVVCVKRLR 480

Qy 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532

RESULT 5
BMRIA HUMAN
ID BMRIA HUMAN STANDARD; PRT; 532 AA.
AC P36894; OGNEN8;
DT 01-JUN-1994 (Rel. 29, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Bone morphogenetic protein receptor type IA precursor (EC 2.7.1.37)
DE (Serine/threonine-protein kinase receptor R5) (SKR5) (Activin
DE receptor-like kinase 3) (ALK-3).
DE Name=BMRIA; Synonyms=ACVRLK3, ALK3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
```

RC TISSUE=Placenta;
 RX MEDLINE=9330967; PubMed=8397373;
 RA ten Dijke P., Ichijo H., Franzen P., Schulz P., Sarraf J.,
 RA Toyoshima H., Heidlin C.-H., Miyazono K.;
 RT "Activin receptor-like kinases: a novel subclass of cell-surface
 RT receptors with predicted serine/threonine kinase activity.";
 RL Oncogene 8:2879-2887(1993).
 RN [2]
 RC NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP TISSUE=Testis;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Ahtschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Heist N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heist F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RX X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 55-143 IN COMPLEX WITH BMP-2.
 RP PubMed=10881198; DOI=10.1038/75903;
 RA Kirsch T., Sebald W., Dreyer M.K.;
 RT "Crystal structure of the BMP-2-BRIA ectodomain complex.";
 RL Nat. Struct. Biol. 7:492-496(2000).
 RN [4]
 RC DISEASE.
 RX MEDLINE=21275975; PubMed=11381269; DOI=10.1038/98919;
 RA Howe J.R., Bair J.L., Sayed M.G., Anderson M.E., Mitros F.A.,
 RA Petersen G.M., Velculescu V.E., Traverso G., Vogelstein B.;
 RT "Germline mutations of the gene encoding bone morphogenetic protein
 RT receptor 1A in juvenile polyposis.";
 RL Nat. Genet. 28:184-187(2001).
 RN [5]
 RP VARIANTS JPS ARG-124 AND TYR-376, AND VARIANT CD ASP-338.
 RX MEDLINE=21426344; PubMed=11536076;
 RA Zhou X.-P., Woodford-Richens K., Lehtonen R., Kurose K., Aldred M.,
 RA Hampel H., Launonen V., Virta S., Pillarski R., Salovaara R.,
 RA Bodmer W.F., Conrad B.A., Dunlop M., Hodgson S.V., Iwama T.,
 RA Jaervinen H., Kellokumpu I., Kim J.C., Leggett B., Markie D.,
 RA Mecklin J.-P., Neale K., Phillips R., Piris J., Rozen P.,
 RA Houllston R.S., Aaltonen L.A., Tomlinson I.P.M., Eng C.;
 RT "Germline mutations in BMPRIA/ALK3 cause a subset of cases of juvenile
 RT polyposis syndrome and of Cowden and Bannayan-Riley-Ruvalcaba
 RT syndromes.";
 RL Am. J. Hum. Genet. 69:704-711(2001).
 RN [6]
 RP VARIANTS JPS ASP-62; TYR-82 AND CYS-443.
 RX PubMed=12417513;
 RA Sayed M.G., Ahmed A.F., Ringold J.R., Anderson M.E., Bair J.L.,
 RA Mitros F.A., Lynch H.T., Tinley S.T., Petersen G.M., Giardiello F.M.,
 RA Vogelstein B., Howe J.R.;
 RT "Germline SMAD4 or BMPRIA mutations and phenotype of juvenile
 RT polyposis.";
 RL Ann. Surg. Oncol. 9:901-906(2002).
 RN [7]
 RP VARIANT JPS ARG-130.
 RX PubMed=12136244; DOI=10.1007/s00439-002-0748-9;
 RA Friedl W., Uhlhaas S., Schulmann K., Stolte M., Loff S., Back W.,
 RA Mangold E., Stern M., Knaebel H.P., Sutter C., Weber R.G.,
 RA Pistorius S., Burger B., Propping P.;
 RT "Juvenile polyposis: massive gastric polyposis is more common in MADH4
 RT mutation carriers than in BMPRIA mutation carriers.";
 RL Hum. Genet. 111:108-111(2002).
 RN [8]
 RP VARIANT JPS THR-470.
 RX PubMed=12630959; DOI=10.1034/j.1399-0004.2003.00008.x;
 RA Kim I.J., Park J.H., Kang H.C., Kim K.H., Kim J.H., Ku J.L.,
 RA Kang S.B., Park S.Y., Lee J.S., Park J.G.;
 RT "Identification of a novel BMPRIA germline mutation in a Korean
 RT juvenile polyposis patient without SMAD4 mutation.";
 RL Clin. Genet. 63:126-130(2003).
 CC -!- FUNCTION: Receptor for BMP-2 and BMP-4.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBUNIT: Heterodimer with a type-II receptor.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Highly expressed in skeletal muscle.
 CC -!- DISEASE: Defects in BMPRIA are a cause of juvenile polyposis
 CC syndrome (JPS) [MIM:174900]; also known as juvenile intestinal
 CC polyposis (JIP). JPS is an autosomal dominant gastrointestinal
 CC hamartomatous polyposis syndrome in which patients are at risk for
 CC developing gastrointestinal cancers. The lesions are typified by a
 CC smooth histological appearance, predominant stroma, cystic spaces
 CC and lack of a smooth muscle core. Multiple juvenile polyps usually
 CC occur in a number of Mendelian disorders. Sometimes, these polyps
 CC occur without associated features as in JPS; here, polyps tend to
 CC occur in the large bowel and are associated with an increased risk
 CC of colon and other gastrointestinal cancers.
 CC -!- DISEASE: Defects in BMPRIA are a cause of Cowden disease (CD)
 CC [MIM:158350]. CD is an autosomal dominant cancer syndrome
 CC characterized by multiple hamartomas and by a high risk for
 CC breast, thyroid and endometrial cancers.
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. TGFB
 CC receptor subfamily.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; Z22535; CAA80257.1; -; mRNA.
 CC EMBL; BC028383; AAH28383.1; -; mRNA.
 CC PIR; I37163; I37163.
 CC PDB; 1ES7; X-ray; B/D=55-143.
 CC PDB; 1BEM; X-ray; C/D=24-152.
 CC Ensembl; ENSG00000107779; Homo sapiens.
 CC HGNC; HGNC:1076; BMPRIA.
 CC MIM; 601299; -.
 CC MIM; 158350; -.
 CC MIM; 174900; -.
 CC GO; GO:0016021; C:integral to membrane; TAS.
 CC GO; GO:0007179; P:transforming growth factor beta receptor si. . . TAS.
 CC InterPro; IPR000472; Activin_receptor.
 CC InterPro; IPR000333; Actn_receptorII.
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR008271; Ser_thr_pkin_AS.
 CC InterPro; IPR002290; Ser_thr_pkinase.
 CC InterPro; IPR003605; TGFbeta_recept_GS.
 CC InterPro; IPR001245; TGFbeta_recept_1.
 CC Pfam; PF01064; Activin_recpt; 1.
 CC Pfam; PF00069; Pkinase; 1.
 CC PRINTS; PR00653; ACTIVIN2R.
 CC PRODOM; P0000001; Prot_kinase; 1.
 CC SMART; SM00467; GS; 1.
 CC SMART; SM00220; S_TKc; 1.
 CC SMART; SM00219; TyrKc; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
 CC PROSITE; PS50011; PROTEIN_KINASE_ST; 1.
 CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 CC 3D-structure; ATP-binding; Disease mutation; Glycoprotein; Kinase;
 KW Nucleotide-binding; Receptor; Serine/threonine-protein kinase; Signal;
 KW Transferrase; Transmembrane.
 KW SIGNAL 1 23 Potential.

FT CHAIN 24 532 Bone morphogenetic protein receptor type
FT IA.
FT TOPO_DOM 24 152 Extracellular (Potential).
FT TRANSMEM 153 176 Potential.
FT TOPO_DOM 177 532 Cytoplasmic (Potential).
FT DOMAIN 234 525 Protein kinase.
FT NP_BIND 240 248 ATP (By similarity).
FT ACT_SITE 362 362 Proton acceptor (By similarity).
FT BINDING 261 261 ATP (By similarity).
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
FT DISULFID 61 82
FT DISULFID 61 82
FT DISULFID 63 67
FT DISULFID 76 100
FT DISULFID 110 124
FT DISULFID 125 130
FT VARIANT 62 62
FT VARIANT 82 82
FT VARIANT 124 124
FT VARIANT 130 130
FT VARIANT 338 338
FT VARIANT 376 376
FT VARIANT 443 443
FT VARIANT 470 470
FT CONFLICT 2 2
FT STRAND 59 62
FT TURN 64 65
FT STRAND 69 70
FT STRAND 75 78
FT STRAND 81 87
FT STRAND 95 101

Query Match 97.4%; Score 2763; DB 1; Length 532;

Best Local Similarity 97.0%; Pred. No. 1.4e-182;

Matches 516; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTQLYTYIRLLGACFLIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPAPEDTLPLFK 60
DB 1 MPQLYIYIRLLGAYLFIISRVOQNLDLSMLHGTGMKSDSDQKKSENGVTLPAPEDTLPLFK 60
QY 61 CYCSGHCPCDDAINNTCTITNGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
DB 61 CYCSGHCPCDDAINNTCTITNGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
QY 121 TIECCTNLCNQYLQPTLPVVPVPPFDGSGVRLAVLISMAVICVIMVFFSCFCYKHYC 180
DB 121 TIECCTNLCNQYLQPTLPVVPVPPFDGSGIRWLILLISMAVICIIMVFFSCFCYKHYC 180
QY 181 KSISRRGRNRDLDEAEFIPGESIKDLIDQSQSGSGGLPLLVORTIAKIQIOWRVQ 240
DB 181 KSISRRGRNRDLDEAEFIPGESIKDLIDQSQSGSGGLPLLVORTIAKIQIOWRVQ 240
QY 241 GKGRYGEVWVGKWRGKVAKVFFFTTEASWFRTEIYQTVLMRHNILGFTAAADIKGTG 300
DB 241 GKGRYGEVWVGKWRGKVAKVFFFTTEASWFRTEIYQTVLMRHNILGFTAAADIKGTG 300
QY 301 SWTQLYLITYDHENGLYDFLKCATLDTRALLKLAYSACGLCHLHTEIYGTQGPATIAH 360
DB 301 SWTQLYLITYDHENGLYDFLKCATLDTRALLKLAYSACGLCHLHTEIYGTQGPATIAH 360
QY 361 RDLKSNILLIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSLNK 420
DB 361 RDLKSNILLIKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSLNK 420
QY 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEYQLPYYNMVPSDPSYEDMREWVCVKRLR 480

DB 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEYQLPYYNMVPSDPSYEDMREWVCVKRLR 480
QY 481 PIVSNRNWNSDECLRAVLKLMSECAHNPAISRLTALRIKKTAKMVESQDVKI 532
DB 481 PIVSNRNWNSDECLRAVLKLMSECAHNPAISRLTALRIKKTAKMVESQDVKI 532
RESULT 6
Q06007 MOUSE
ID Q06007 MOUSE PRELIMINARY; PRT; 500 AA.
AC Q06007;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE BRK-IT.
GN Name=Bmpria;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94344106; PubMed=8065329;
RA Koenig B.B., Cook J.S., Wolsing D.H., Ting J., Tiesman J.P.,
RA Correa P.E., Olson C.A., Pecquet A.L., Ventura P., Grant R.A.,
RA Chen G., Wrana J.B., Massague J., Rosenbaum J.S.;
RT "Characterization and cloning of a receptor for BMP-2 and BMP-4 from
RT NIH 3T3 cells.";
RL Mol. Cell. Biol. 14:5961-5974(1994).
CC -!- SUBUNIT: Interacts with AIP1. Part of a complex consisting of
CC AIP1, ACVR2, ACVR1B and MADH3 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; U04673; AAA21515.1; -; mRNA.
DR HSSP; P36894; 1ES7.
DR SMR; Q06007; 55-143.
DR MGI; MGI:1338938; Bmpria.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0009952; P:anterior/posterior pattern formation; IMP.
DR GO; GO:0051216; P:cartilage development; IMP.
DR GO; GO:0030154; P:cell differentiation; IGI.
DR GO; GO:0009950; P:dorsal/ventral axis specification; IMP.
DR GO; GO:0007396; P:ectoderm development; IMP.
DR GO; GO:0048382; P:mesoderm development; IMP.
DR GO; GO:0001880; P:Mullerian duct regression; IMP.
DR InterPro; IPR000472; Activin_receptor.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR003605; TGFbeta_recept_GS.
DR Pfam; PF01064; Activin_recp; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00467; GS; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase; Transmembrane.
SQ SEQUENCE 500 AA; 56439 MW; 0E7A59A526888DD CRC64;
Query Match 92.2%; Score 2616; DB 2; Length 500;
Best Local Similarity 98.8%; Pred. No. 1.9e-172;
Matches 485; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTQLYTYIRLLGACFLIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPAPEDTLPLFK 60
DB 1 MTQLYTYIRLLGACFLIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPAPEDTLPLFK 60
QY 61 CYCSGHCPCDDAINNTCTITNGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
DB 61 CYCSGHCPCDDAINNTCTITNGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120

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QY 121 TIECCRTNLCNQYLQPTLPVWIGPFDGSRVRLAVLISMAVCIAMIVPSSCFCKYKVC 180
DB 121 TIECCRTNLCNQYLQPTLPVWIGPFDGSRVRLAVLISMAVCIAMIVPSSCFCKYKVC 180
QY 181 KSISRRGRYNRDLQDEAFIPVGSLSKDLIDQSSGSGSLPQLLVQRTIAKIQMVROV 240
DB 181 KSISRRGRYNRDLQDEAFIPVGSLSKDLIDQSSGSGSLPQLLVQRTIAKIQMVROV 240
QY 241 GKGRYGEVWVGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300
DB 241 GKGRYGEVWVGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300
QY 301 SWTQLYLTIDYHENGSLYDFLKCATLDTALLKLAASAACGLCHLHTEIYGTGKPAIAH 360
DB 301 SWTQLYLTIDYHENGSLYDFLKCATLDTALLKLAASAACGLCHLHTEIYGTGKPAIAH 360
QY 361 RDLKSNLIIKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSLKN 420
DB 361 RDLKSNLIIKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSLKN 420
QY 421 HFQPYIMADIYSFGLIIEWMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVCKRLR 480
DB 421 HFQPYIMADIYSFGLIIEWMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVCKRLR 480
QY 481 PIVSNRWNSDE 491
DB 481 PIVSNRWNSDE 491

RESULT 7
Q90754.CHICK
ID Q90754.CHICK PRELIMINARY; PRT; 533 AA.
AC Q90754;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Protein kinase.
GN Name=BRK-1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Shimabara M., Kawakami Y., Nakata Y., Yamamoto S., Nohno T.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; L49204; AAA97421.1; -; mRNA.
DR HSSP; P36894; 1ES7.
DR SMR; Q90754; 55-141.
DR Ensembl; ENSGALG00000002003; Gallus gallus.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005024; F:transforming growth factor beta receptor ac. .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007178; P:transmembrane receptor protein serine/threo. .; IEA.
DR InterPro; IPR000472; Actin receptor.
DR InterPro; IPR000333; Actn receptorII.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR Pfam; PF01064; Activin recp; 1.
DR PRINTS; PR00653; ACTIVIN2R.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00467; GS; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00101; PROTEIN KINASE DOW; 1.
DR PROSITE; PS0108; PROTEIN KINASE ST; 1.
DR ATP-Binding; Kinase; Nucleotide-Binding;
KW Serine/threonine-protein kinase; Transferase; Transmembrane.
SQ SEQUENCE 533 AA; 60283 MW; C39C8267DB494DBE CRC64;
Query Match 91.0%; Score 2582.5; DB 2; Length 533;
Best Local Similarity 90.2%; Pred. No. 4.3e-170;
Matches 481; Conservative 22; Mismatches 29; Indels 1; Gaps 1;
QY 1 MTQLYTYIRLLGACLFIIISHVOGQNLDSMLHGTGMSKSDVDQKKPENGVTILAPEDTILPFLK 60
DB 1 MTRLRVCERLLGAYLLIILHVQGNLDSMLHGTGMSKTNPDQKKQGNVTILAPEDTILPFLK 60
QY 61 CYCSGHCPCPDAINNTCITNGHCFALIEEDDOGETTLTSGCMKYEGSDFOCKDSPKQLRR 120
DB 61 CYCSGHCPCPDAINNTCITNGHCFALIEEDDEHGEPTLASGCMKYEGSDFOCKDSPKQLRR 120
QY 121 TIECCRTNLCNQYLQPTLPV-VIGPPFDGSRVRLAVLISMAVCIAMIVPSSCFCKYKHY 179
DB 121 TIECCRTDFCNQDLQPTLPPLDSTDGLFDGSRVRLAVLISMAVCIAMIVPSSCFCKYKHY 180
QY 180 KSISSRRGRYNRDLQDEAFIPVGSLSKDLIDQSSGSGSLPQLLVQRTIAKIQMVROV 239
DB 181 CKSMARKHCYNRDLQDEAFIPAGESLSKDLIDQSSGSGSLPQLLVQRTIAKIQMVROV 240
QY 240 VGKGRYGEVWVGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFIAADIKGT 299
DB 241 VGKGRYGEVWVGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFIAADIKGT 300
QY 300 GSWTQLYLTIDYHENGSLYDFLKCATLDTALLKLAASAACGLCHLHTEIYGTGKPAIA 359
DB 301 GSWTQLYLTIDYHENGSLYDFLKCTTLDNRALLKLAASAACGLCHLHTEIYGTGKPAIA 360
QY 360 HRDLKSNLIIKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSLKS 419
DB 361 HRDLKSNLIIKNGSGTCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSLKN 420
QY 420 NHFQPYIMADIYSFGLIIEWMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVCKRL 479
DB 421 NHFQPYIMADIYSFGLIIEWMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVCKRL 480
QY 480 RIVSNRWNSDECLRAVLKMSCEWANNPASRLTALRIKTKLAKMVESQDVKI 532
DB 481 RIVSNRWNSDECLRAVLKMSCEWANNPASRLTALRIKTKLAKMVESQDVKI 533

RESULT 8
Q9PUP5.COTCO
ID Q9PUP5.COTCO PRELIMINARY; PRT; 533 AA.
AC Q9PUP5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Bone morphogenetic protein receptor 1A.
GN Name=BMPR-1A;
OS Coturnix coturnix (Common quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=9091;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20237589; PubMed=10772803; DOI=10.1006/dbio.2000.9684;
RA McPherson C.E., Varley J.E., Maxwell G.D.;
RT "Expression and regulation of type I BMP receptors during early avian
sympathetic ganglion development.";
RL Dev. Biol. 221:220-232(2000).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF189777; AAF04582.1; -; mRNA.
DR HSSP; P36894; 1ES7.
DR SMR; Q9PUP5; 55-139.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
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Oy 484 SNRWSDECLRAVLKLMSECHWAHPASRLTALRIKTKTLAKMVESQDVKI 532
Db 479 SNRWSDECLRAVLKLMSECHWAHPASRLTALRIKTKTLAKMVESQDVKI 527

RESULT 10
O42338_XENLA
ID O42338_XENLA PRELIMINARY; PRT; 527 AA.
AC O42338;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE BMP receptor (LOC397711 protein).
GN Name=LOC397711;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Suzuki A., Shioda N., Ueno N.;
RT "Bone morphogenetic protein acts as a ventral mesoderm modifier in
early Xenopus embryos.";
RL Dev. Growth Differ. 37:581-588(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Haie S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Goughwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -| SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
CC -| SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; D32066; BAA22437.1; -; mRNA.
DR EMBL; BC070551; AAR70551.1; -; mRNA.
DR HSP; P36894; IES7.
DR SMR; O42338; 53-140.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005024; F:transforming growth factor beta receptor ac. .; IEA.

Query Match 78.3%; Score 2222; DB 2; Length 527;
Best Local Similarity 80.0%; Pred. No. 3.5e-145; Indels 10; Gaps 5;
Matches 423; Conservative 43; Mismatches 53;

Oy 7 YIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLAPEDTLPLFLKCYCSGH 66
Db 6 FIACFGALLLVI-HTQGQDFNLLPHRTGMKNSDPPKKQENGVTLAPEDTLPLFLNCYCSGY 64

Oy 67 CPDDAINNTCTNGHCFATIEBDDQGETTLTSCGMKVEGSDFOCKDSPKAQLRTIECCR 126
Db 65 CQNAVNNCTITNGQCFAMIEEDHDIILTSCGMKVEGSDFOCKDSPKALSRTIECCR 124

Oy 127 TNLCHQYLOPTLPVPIVGGFFFG--SVRWLAVLISMAVCIVAMIVF--SSCFCKHYCKSI 183
Db 125 TDFCNRLDLEPTISPKI-----SDGEYGLRFALISLVWCLILIVGFILIIYKH--KLH 178

Oy 184 SSGRYNRLEQDEAFIPVGESLKLIDQSQSGSGGLPLLVQRTIAKQIOMVROVGKG 243
Db 179 SQRLMYNRNLDPDDAFIPAGESLKLIDISQSGSGGLPLLVQRTIAKQIOMVROVGKG 238

Oy 244 RYGEVVMGKRGKAVKAVKVFVTEBASWPRETEIYQTVLMRHNILGLFIAADIKGTGWT 303
Db 239 RYGEVVMGKRGKAVKAVKVFVTEBASWPRETEIYQTVLMRHNILGLFIAADIKGTGWT 298

Oy 304 QLYLTDVHENGSLYDFLKCATLDTRALLKLAISAACGLCHLHTEIYGTGPKPAIAHRDL 363
Db 299 QMYLITEYHENGSLYDFLKCCTLDTRSLKLAISAACGLCHLHTEIYGTGPKPAIAHRDL 358

Oy 364 KSKNLIKNGSCCADIAGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDESLSKNHQ 423
Db 359 KSKNLIKENWTCCADIAGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDESLSKNHQ 418

Oy 424 PYIMADIVSFGIIWEMARRCITGIVEYQIPYNNMPSDPSYEDMRVWCVRIRPTV 483
Db 419 AYIMADIVSFLIIWEMTRRCITGIVEYQIPYNNMPSDPSYEDMRVWCVRIRPTV 478

Oy 484 SNRWSDECLRAVLKLMSECHWAHPASRLTALRIKTKTLAKMVESQDVKI 532
Db 479 SNRWSDECLRAVLKLMSECHWAHPASRLTALRIKTKTLAKMVESQDVKI 527

RESULT 11
O42339_XENLA
ID O42339_XENLA PRELIMINARY; PRT; 527 AA.
AC O42339;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE 'BMP receptor' (LOC397712 protein).
GN Name=LOC397712;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
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OX NCBI_TaxID=8355;
RN [1] NUCLEOTIDE SEQUENCE.
RA Suzuki A., Shoda N., Ueno N.;
RT "Bone morphogenetic protein acts as a ventral mesoderm modifier in
RT early Xenopus embryos."
RL Dev. Growth Differ. 37:581-588 (1995).
RN [2] NUCLEOTIDE SEQUENCE.
RX TISSUE=Ovary;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh L.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3] NUCLEOTIDE SEQUENCE.
RP TISSUE=Ovary;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391 (2002).
RN [4] NUCLEOTIDE SEQUENCE.
RP TISSUE=Ovary;
RA Klein S., Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; D32067; BAA22438.1; -; mRNA.
DR EMBL; BC071081; AAH71081.1; -; mRNA.
DR HSSP; P36894; 1ES7.
DR SMR; O42339; 53-140.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005024; F:transforming growth factor beta receptor ac. . ; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007178; P:transmembrane receptor protein serine/threo. . ; IEA.
DR InterPro; IPR000472; Activin receptor.
DR InterPro; IPR000333; Actin receptorII.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_kinase.
DR InterPro; IPR003605; TGFbetarecept_GS.
DR Pfam; PF01064; Activin_recpt; 1.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00653; ACTIVIN2R.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00467; GS; 1_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding; Receptor;
KW Serine/threonine-protein kinase; Transferase; Transmembrane.
SQ SEQUENCE 527 AA; 59807 MW; D24E46D8A1291074 CRC64;

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Query Match 77.9%; Score 2211; DB 2; Length 527;
Best Local Similarity 79.4%; Pred. No. 2e-144;
Matches 421; Conservative 42; Mismatches 55; Indels 12; Gaps 5;

QY 9 RLLGAC---LFTISHVQGNLDSMLHGTGMSKSDVDOKKPKENGVTTLAPEDTLPLPKYCSCG 65
DB 4 RLFIACFGVLLAIIHAQGGDFNLPRTGMSKNSDPKPKQENGVTTLAPEDTLPLPKYCSCG 63

QY 66 HCPDADINNTCITNGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRRTIECC 125
DB 64 YCPQNAVNTCITNGQCFAIEEDDHGDI IWTSGCMKEGSDFOCKDSPKALSRTTIECC 123

QY 126 RTNLCNQYLQPLTPPVVITGPFPDG--SVRWLAVLISMVAVCIAMIVF--SSCFYKHYCKS 182
DB 124 RTDFCNRLQPLTSPKIA---DGEYGLRFLAIIISMVVCVFIAGFIIIIYKXH--KL 177

QY 193 ISSGRVNRDLEODEAFIPVGESLKLIDQSSSGSGSLPLLVTAKQIOMVROVCK 242
DB 178 HSQRLMYNRNLDPPDAFI PAGESL KALIDISQSSSGSGSLPLLVTAKQIOMVROVCK 237

QY 243 GRYGEVMGKVRGEKVAVKVFTTTEASWFRTEIYQTVLMRHNILGFIAADIKGTGSM 302
DB 238 GRYGEVMGKVRGEKVAVKVFTTTEASWFRTEIYQTVLMRHNILGFVAADIKGTGSM 297

QY 303 TOLYLTIDYHENGSLYDFLKCATLDTRALLKLAYSAAAGLCHLHTEIYGTQCKPAIAHRD 362
DB 298 TQWVLTIEYHENGSLYDFLKCATLDTRALLKLAYSAAAGLCHLHTEIYGTQCKPAIAHRD 357

QY 363 LKSNKILIKKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDES LKNHNF 422
DB 358 LKSNKILIKENWTCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDES LKNHNF 417

QY 423 QPYIMADIYSFGLIIEWEMARRCITGGIVEEYQLPYNNMVPSPDPSYEDMREVVCKRLRPI 482
DB 418 QAYIMADIYSFSLIWEWTRCITGGIVEEYQLPYNDVMPNDPSPEDMREVVCKMLRPT 477

QY 483 VSNRWSDECLRAVLKMLSECWAHNPASRLTALRIKKT LAKWVESQDVKI 532
DB 478 VSNRWSDECLRAVLKMLSECWAHNPASRLTALRIKKT LAKWVESQDVKI 527

RESULT 12
O93243_BRARE PRELIMINARY; PRT; 527 AA.
ID O93243_BRARE PRELIMINARY; PRT; 527 AA.
AC O93243;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Type I serin/threonine kinase receptor.
GN Name=bmpria; Synonyms=BMPR-IA;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1] NUCLEOTIDE SEQUENCE.
RP STRAIN=AB line;
RA Nikaido M., Tada M., Takeda H., Kuroiwa A., Ueno N.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AB011826; BAA32748.1; -; mRNA.
DR HSSP; P36894; 1ES7.
DR SMR; O93243; 58-140.
DR ZFIN; ZDB-GENE-000502-1; bmpria.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005024; F:transforming growth factor beta receptor ac. . ; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007178; P:transmembrane receptor protein serine/threo. . ; IEA.

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DR InterPro; IPR000472; Activin_receptor.
DR InterPro; IPR000333; Actn_receptorII.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR InterPro; IPR003605; TGFbeta_recept_GS.
DR Pfam; PF01064; Activin_rec; 1.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00653; ACTIVIN2R.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00467; GS; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding; Receptor;
KW Serine/threonine-protein kinase; Transferase; Transmembrane.
SQ SEQUENCE 527 AA; 59657 MW; 6607C24551D3B9E9 CRC64;

Query Match 74.3%; Score 2109; DB 2; Length 527;
Best Local Similarity 75.8%; Pred. No. 2.2e-137;
Matches 402; Conservative 46; Mismatches 74; Indels 8; Gaps 5;

Qy 4 LYTIVRLGACLF-ISHVQGNLDSMLHGTGKMSDVKQKPEGVTLAPEDTLPLKCY 62
Db 5 LFITVLTGVCLLTCSGAGQNDHVLQGTGVR--LDSRRPGDDSTIAPEDAARFLSCH 62
Qy 63 CSGHCPDDAINNCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRRTI 122
Db 63 CSGHCPDDAKNCTETNGQCFAINNEEDBNGDVLSSGCMKYEGSHFOCKDSQAQRTRTI 122
Qy 123 ECRTNLCNQYLQPTLPVWIGPFFDGSVRWLAVLISMAVICVAMIVFSSCFYKHYCKS 182
Db 123 ECCQFQFCNDLKPBLPRDSEP---PDPHLAFLLISVTVCFCALICV-TVICVYRY-KW 177
Qy 183 ISSRGRVNRLEODEAIPVGESLKULIDQSOGSGSGGLPLLVQRTIAKIQIOMVROVGK 242
Db 178 QTERQVRHRLDQDEAFIPAGESLKULINQSQTSGSGGLPLLVQRTIRKIQIOTVRMIGK 237
Qy 243 GRYGEVVMGKWRGEKVAVKVFYFFTEASWFRETIYQTVLMRHNILGFFIAADIKGTSW 302
Db 238 GRYGEVWLGRGKVKAVKVFYFFTEASWFRETIYQTVLMRHNILGFFIAADINGTAS 297
Qy 303 TQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSACGLCHLHTEIYGTQGPALAHRD 362
Db 298 TQLYLITDYHENGSLYDFLTLLDQTALLRLAFSAACGLCHLHTEIYGTQGPALAHRD 357
Qy 363 LKSNHILIKNGSCCIADGLAVKFNSDTNEVDIPLNTRVGTTRYMAPEVLDLSKNHF 422
Db 358 LKSNHILIKNGTCTCIADGLAVKFNSDTNEVDLPLSTRMGTRYMAPEVLDLTLNKNHF 417
Qy 423 QPYIMADIYFGLIIEWMARRCITGGTVEYQVLPYNNMVPSPSYEDMRVWCVKRLRPI 482
Db 418 QAYIMADIYFGLIIEWMARRCVTGGIIEYHYVPYEMVSPDSYEDMLEVWCVKGLRPT 477
Qy 483 VSNRNSDECLRAVLKLMSCWAHPNRSALTALRIKTKLAKWVESQDVKI 532
Db 478 VSNRNSDECLRAVLKLMSCWAHPNRSALTILRVKTKLAKWVESQDIKI 527

RESULT 13
Q4RGZ0_TETNG
ID Q4RGZ0_TETNG PRELIMINARY; PRT; 499 AA.
AC Q4RGZ0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF15083, whole genome shotgun sequence.
DE (Fragment).
DE ORFNames=GSTENG0034592001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
```

```
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli B., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Landier E.S., Weissenbach J., Roest Casali H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC cycle. It is required in higher cells for entry into S-phase and
CC mitosis. Component of the kinase complex that phosphorylates the
CC repetitive C-terminus of RNA polymerase II. Catalytic component of
CC MPF (By similarity).
CC -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC mature oocytes (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; CAAE01015083; CAG12342.1; -; Genomic_DNA.
DR InterPro; IPR000472; Activin_receptor.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR InterPro; IPR003605; TGFbeta_recept_GS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF01064; Activin_rec; 1.
DR Pfam; PF00069; Pkinase; 1.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00467; GS; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding; Receptor;
KW Serine/threonine-protein kinase; Transferase; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 499 AA; 56419 MW; CDBAC3433C9B5429 CRC64;

Query Match 74.3%; Score 2107.5; DB 2; Length 499;
Best Local Similarity 78.4%; Pred. No. 2.7e-137;
Matches 403; Conservative 40; Mismatches 52; Indels 19; Gaps 7;

Qy 23 GQNLDLMLHGTGKMSDVKQKPEGVTLAPEDTLPLKCYCSGHCPCDDAINTTITNGHC 82
Db 1 GQNPDVVLQGTGKAE-----DSTIAPDAARFLSCYCSGHCPCDDAINTTITNGQC 52
Qy 83 FAIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRRTIECRTNLCNQYLQPTLPVV 142
Db 53 FAIIEDEHGEPLLTSGCMKYEGSHFOCKDSPKAQLRRTIECNTDFCNRELQPTLPPLA 112
Qy 143 -IGPFFDGSVRWLAVLISMAVICVAMIVFSSCFYKHYCKSSSRGY---NRDLEODEA 198
Db 113 PIG----GSPNNLAFLLISMTVC-CMLICVAVVYTRY-KWQSERQRYHKHRLDEQ-EV 165
Qy 199 FIPVGESLKDLDQSSGSGGLPLLVQRTIAKIQIOMVROVGKRGYGEVVMGKWRGEKV 258
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Db 166 FIPAGESLRLDIHQSSGSGSLPLLVTORTIAKQIQMMRQIQKRGYGEVWLGWRGKV 225
Qy 259 AVKVFPTTEASWFRTEIYQTVLMRHNILGFIADIKGTGSWTQLYLITYDHENGSLY 318
Db 226 AVKVFPTTEASWFRTEIYQTVLMRHNILGFIADIKGTGAFTQLFLITYDHENGSLY 285
Qy 319 DFLKCATLDTALLKLAYSACGLCHLHTEIYGTQKPAIAHRDLKSNILIKKNGSCCI 378
Db 286 DYLKUSTLTHMLLRLAYSAACGLCHLHTEIYGTQKPAIAHRDLKSNILIKKNGSCCI 345
Qy 379 ADGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDSELSKNHFPYIMADIYSFGLIIV 438
Db 346 ADGLAVKFNSTNEVDVPLSTRVGTTRYMAPEVLDSELSKNHFPYIMADIYSFGLIIV 405
Qy 439 EMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVVCVKRLRPISVNRNWSDECLRAVLK 498
Db 406 EMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVVCVKRLRPISVNRNWSDECLRAVLK 465
Qy 499 LMSECAWNPASRLTALRKTTLAKMVESQDVKI 532
Db 466 LMSECAWNPASRLTILRVKTKLAKMVESQDIKV 499

RESULT 14
Q66HY1 BRARE
ID Q66HY1_BRARE PRELIMINARY; PRT; 534 AA.
AC Q66HY1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Zgc:92227.
GN ORFNames=zgc:92227;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]_TaxID=7955;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Matusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RX Director MGC Project;
RA Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC081626; AAH81626.1; -; mRNA.
DR SMR; Q66HY1; 63-147.
DR ZFIN; ZDB-GENE-040912-150; zgc:92227.
DR GO; GO:0016020; C.membrane; IEA.
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DR GO; GO:0005524; P.ATP binding; IEA.
DR GO; GO:0004674; P.protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; P.protein-tyrosine kinase activity; IEA.
DR GO; GO:0005024; P.transforming growth factor beta receptor ac. .; IEA.
DR GO; GO:0006468; P.protein amino acid phosphorylation; IEA.
DR InterPro; IPR000472; Activin receptor.
DR InterPro; IPR000719; Prot.kinase.
DR InterPro; IPR008271; Ser_thr_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR003605; TGFbetarecept_Gs.
DR InterPro; IPR001245; Tvr_kinase.
DR Pfam; PF01064; Activin_recp; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00467; GS; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_SF; 1.
KW ATP-binding; Kinase; Nucleotide-binding; Receptor;
KW Serine/threonine-protein kinase; Transferase; Transmembrane.
SQ SEQUENCE 534 AA; 59781 MW; FFOB38D40DA3C212 CRC64;

Query Match 74.2%; Score 2104.5; DB 2; Length 534;
Best Local Similarity 77.2%; Pred. No. 4.6e-137;
Matches 397; Conservative 49; Mismatches 59; Indels 9; Gaps 6;

Qy 23 QNLDLSMLHGTGMKSDVDQKPE--NGVTLAPEDTLPLFKVCYSGCHCPDDAINNTCITNG 80
Db 26 QGNPDYMLHGTGVKPGSDPRAQAGDGTVAPEADAARFLSCYSGCHCEDATNNTCEING 85
Qy 81 HCFAIIEEDDOGETTLTSGCMKYEGSDFOCKDSPKAQLRRTIECRTLNCQYLOPTLPP 140
Db 86 HCFAIIEDEHGEAMLTSKCMKYEGSHFOCKDSPNAQTRRTIECSTDFCNRDLOPTLPP 145
Qy 141 VVIG--PFEDGSRVRLAVLISMVCIAMIVFSSCFYKHYCKSISSSRGRYNRDLEQDEA 198
Db 146 PIPGKPPFNNAHL--LAFLSIVTCCFTLVAI-TIVCYRFP-KLQTGRHRYORDLGPTEA 201
Qy 199 FIPVGESLKDLDIOSQSSGSGSLPLLVTORTIAKQIQMMRQIQKRGYGEVWLGWRGKV 258
Db 202 FIPAGESLKDLDIOSQ-SFGSSGSLPLLVTORTIAKHQIMVRQIQKRGYGEVWLGWRGENV 260
Qy 259 AVKVFPTTEASWFRTEIYQTVLMRHNILGFIADIKGTGSWTQLYLITYDHENGSLY 318
Db 261 AVKVFPTTEASWFRTEIYQTVLMRHNILGFIADIKGTGTFTQLFLITYDHENGSLC 320
Qy 319 DFLKCATLDTALLKLAYSACGLCHLHTEIYGTQKPAIAHRDLKSNILIKKNGSCCI 378
Db 321 DYLYKTTLDTQALLRLAYSACGLCHLHTEIYGTQKPAIAHRDLKSNILIKKNGTCCT 380
Qy 379 ADGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDSELSKNHFPYIMADIYSFGLIIV 438
Db 381 ADGLAVKFNSTNEVDVPLSTRVGTTRYMAPEVLDSELSKNHFPYIMADIYSFGLIIV 440
Qy 439 EMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVVCVKRLRPISVNRNWSDECLRAVLK 498
Db 441 EMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVVCVKMRPVVSVNRNWSDECLRAVLK 500
Qy 499 LMSECAWNPASRLTALRKTTLAKMVESQDVKI 532
Db 501 LMSECAWNPASRLTALRVKTKLAKMVESQDIKI 534

RESULT 15
Q9BDI4 SHEEP
ID Q9BDI4_SHEEP PRELIMINARY; PRT; 502 AA.
AC Q9BDI4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Bone morphogenetic protein receptor type IB (Bone morphogenetic
```

protein type 1B receptor).
 DE Name=EMPR-IB;
 OS Ovis aries (Sheep).
 GN Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Caprinae; Ovis.
 ON NCBI_TaxID=9940;
 RX [1]
 RC NUCLEOTIDE SEQUENCE.
 RC TISSUE=Ovary;
 RX MEDLINE=21211518; PubMed=11312159; DOI=10.1677/joe.0.169R001;
 RA Souza C.J., MacDougall C., MacDougall C., Campbell B.K.,
 RA McNeilly A.S., Baird D.T.;
 RT "The Booroola (FecB) phenotype is associated with a mutation in the
 RT bone morphogenetic receptor type 1 B (BMPRI1B) gene.";
 RL J. Endocrinol. 169:R1-R6(2001).
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=Ovary;
 RA Souza C.J.H., MacDougall C.N., Pathirana S.V., Wood T., Telfer E.,
 RA Campbell B.K., McNeilly A.S., Bownes M., Baird D.T.;
 RA Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=Ovary;
 RX MEDLINE=21159170; PubMed=11259271;
 RA Wilson T., Wu X.Y., Juengel J.L., Ross I.K., Lumsden J.M., Lord E.A.,
 RA Dodds K.G., Walling G.A., McEwan J.C., O'Connell A.R., McNatty K.P.,
 RA Montgomery G.W.;
 RT "Highly prolific Booroola sheep have a mutation in the intracellular
 RT kinase domain of bone morphogenetic protein 1B receptor (ALK-6) that
 RT is expressed in both oocytes and granulosa cells.";
 RL Biol. Reprod. 64:1225-1235(2001).
 RN [4]
 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=Ovary;
 RA Wilson T.M., Ross I.K.;
 RA Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=2121086; PubMed=11320249; DOI=10.1073/pnas.091575998;
 RA Mulsant P., Lecier F., Fabre S., Schibler L., Monget P., Lanneluc I.,
 RA Pisselet C., Riquet J., Monniaux D., Callebaut I., Cribiau E.,
 RA Thimonier J., Teyssier J., Bodin L., Cognie Y., Chitour N.,
 RA Elsen J.-M.;
 RT "Mutation in bone morphogenetic protein receptor-1B is associated with
 RT increased ovulation rate in Booroola Merino ewes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:5104-5109(2001).
 CC -1- SUBUNIT: Interacts with ALP1. Part of a complex consisting of
 CC ALP1, ACVR2, ACVR1B and MAD3. (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AF357007; AAK30296.1; -; mRNA.
 DR EMBL; AF312016; AAK53213.1; -; mRNA.
 DR EMBL; AF298885; AAK48709.1; -; mRNA.
 DR HSSP; P36897; 1IAS.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0005024; F:transforming growth factor beta receptor ac. ; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR GO; GO:0007178; P:transmembrane receptor protein serine/threo. ; IEA.
 DR InterPro; IPR000472; Activin_receptor.
 DR InterPro; IPR000333; Actn_receptorII.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_kin_AS.
 DR InterPro; IPR003605; TGfbeta_recept_GS.
 DR Pfam; PF01064; Activin_recp; 1.
 DR Pfam; PF00069; Pkinase_1.
 DR PRINTS; PR00653; ACTIIN2R.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00467; GS; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Nucleotide-Binding; Receptor;
 KW Serine/threonine-protein kinase; Transferase; Transmembrane.
 SQ SEQUENCE 502 AA; 56907 MW; 6552124A0A24F35C CRC64;
 Query Match 68.7%; Score 1950.5; DB 2; Length 502;
 Best Local Similarity 72.7%; Pred. No. 1.9e-126;
 Matches 367; Conservative 58; Mismatches 75; Indels 5; Gaps 5;
 QY 29 MLHGTCMKSDVDQKPKENGVTLPAPETLPLKCYCSGCHCPDDAINNTCITNGHCFATIEE 88
 DB 2 LLRSSG-KLSVGTGK-EDGESTAPRPKILRCKCHHCPEDSVNNICSTDGGYCFMTIEE 59
 QY 89 DDOGETTLTSGCMKYEGSDPQCKDSKPAQLRRRIECC-RTNLGNQVLOPTLPVPVIGPFF 147
 DB 60 DSGMPVTVTSGCLGEGSDPQCDTPIPHORRSIECTERNECNKOLHPTLPKKNRDFV 119
 QY 148 DGSVRVLAWLISMAVCIVAMIVFSSCFYKHYCKSISSRGYNRDLQDEAFIPVGSGLK 207
 DB 120 DGFPIHKALLISVTVCSL-LLVLIILFCYFRY-KRQEARPRYSIGLEQDETYIPPGESLR 177
 QY 208 DLIDQSSSGSGSLPLLVQRTIAKQIQMVQVQKGRYGEVWVGKRGKGVAVKVFPTTE 267
 DB 178 DLIEQSSSGSGSLPLLVQRTIAKQIQMVQVQKGRYGEVWVGKRGKGVAVKVFPTTE 237
 QY 268 EASWPRETEIYQTVLMRHNILGFIADIKGTGTSWTQLYLTIDYHENGSLYDFLKCATLD 327
 DB 238 EASWPRETEIYQTVLMRHNILGFIADIKGTGTSWTQLYLTIDYHENGSLYDFLKCATLD 297
 QY 328 TRALLKLAYSACGLCHLHTEIYGTQKPAIAHRLDKSKNLIKXGSCCIIADLGLAVKF 387
 DB 328 TRALLKLAYSACGLCHLHTEIYGTQKPAIAHRLDKSKNLIKXGSCCIIADLGLAVKF 357
 QY 388 NSDTNEVDIPLNTRVGTTRYMAPEVLDLSKXHFQPYMADYISFGLIIWEHARRCITG 447
 DB 358 ISDTNEVDIPLNTRVGTTRYMAPEVLDLSKXHFQPYMADYISFGLIIWEHARRCITG 417
 QY 448 GIVEEYQLPYANMVPSPDPSYEDMREYVVCVKRLRPIVSNRNWNSDECLRAVLKLMSECAWN 507
 DB 418 GIVEEYQLPYANMVPSPDPSYEDMREYVVCVKRLRPIVSNRNWNSDECLRAVLKLMSECAWN 477
 QY 508 PASRLTALRIKKTALKWVESQDVKI 532
 DB 478 PASRLTALRVKKTALKWVESQDIKL 502

Search completed: December 3, 2005, 06:11:42
 Job time : 239 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 9, 2005, 19:16:45 ; Search time 5253 Seconds
(without alignments)
5756.847 Million cell updates/sec

Title: US-10-600-645-2
Perfect score: 2838
Sequence: 1 MTQLYTIRLLGACLFIIISH.....TALRIKTKLAKWVESQDVKI 532

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 2842172553 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+pn.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US10600645/runat_02122005_103604_23280/app_query.fasta_1.711
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosu62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -NORM_SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM_ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10600645 @CNG_1_1_3367@runat_02122005_103604_23280 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_ste.*
11: gb_sv.*
12: gb_un.*
13: gb_vi.*
14: gb_hcg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2838	100.0	1599	9	RATRB4R1
2	2838	100.0	1813	6	AR169902 Sequence
3	2838	100.0	1813	6	AR382508 Sequence

4	2838	100.0	3003	6	CQ986812
5	2838	100.0	3003	6	CS027157
6	2838	100.0	3003	9	RATRBALK3
7	2838	100.0	3167	6	CQ986810
8	2838	100.0	3167	6	CQ986811
9	2838	100.0	3167	6	CS027155
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16	2823	99.5	2070	6	AR164274
17	2823	99.5	2070	6	AR264352
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19	2823	99.5	2292	9	MUSBMPRC
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32	2769	97.6	2932	6	AR264348
33	2769	97.6	2932	6	AR408534
34	2769	97.6	2932	6	AR475169
35	2769	97.6	2932	8	HSALK3A
36	2763	97.4	3625	8	BC028383
37	2741	96.6	2892	6	CQ720881
38	2680	94.4	2861	6	CQ718018
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42	2523.5	88.9	239655	14	AC096969
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45	2222	78.3	2395	5	D32066

ALIGNMENTS

RESULT 1
RATRB4R1
LOCUS
Rat mRNA for bone morphogenetic protein 4 receptor, complete cds.
DEFINITION
D17667.1 GI:684975
VERSION
bone morphogenetic protein 4 receptor.
KEYWORDS
Rattus norvegicus (Norway rat)
SOURCE
Rattus norvegicus
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE
1 (bases 1 to 1599)
Ikeda, T. and Takahashi, H.
Expression pattern of bone morphogenetic protein 4 receptor in embryo and adult rat
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 1599)
Takahashi, H.
Direct Submission
TITLE
Submitted (16-SEP-1993) Hiroshi Takahashi, Tokyo Metropolitan
JOURNAL
Institute of Gerontology, Department of Pathology; 35-2 Sakaecho, Itabashi-ku, Tokyo 173, Japan (Tel:03-3964-3241(ex.3034), Fax:03-3579-4776)
LOCATION/Qualifiers
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/db_xref="GI:1405418"
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ORIGIN

Alignment Scores:
Pred. No.: 3 87e-271 Length: 1599
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-600-645-2 (1-532) x RATRBR4R1 (1-1599)

Qy	1	MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis	20
Db	1	ATGACTCAGCTATACACCTACATCAGATTACTTGGGAGCGTCTCTTTCATCATTTCTCAT	60
Qy	21	ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp	40
Db	61	GTTCAAGGCGAGAATCTAGATAGTATGCTTCCATGTTGTTGTTATGAAATCAGACGTGGAC	120
Qy	41	GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys	60
Db	121	CAGAAGAAGCCGGAATAATGGAGTAGCTAGCTAGCAGAGGACACCTTACCTTTCTTAAAA	180
Qy	61	CystTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly	80
Db	181	TGCTATTGCTCAGGACACTGCCACAGATGACGCTATTATACACATGCATAACTAATGGC	240
Qy	81	HisCysPheAlaIleIleGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys	100
Db	241	CATTGCTTTGCCATTATAGAGAAGATGATCAGGGAGAAACACCGTTAACTTCTGGGTGT	300
Qy	101	MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg	120
Db	301	ATGAAGTATGAAGCTCTGATTTTCAATGCAAGGATTCACCAAAAGCCAGCTACGACGG	360
Qy	121	ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro	140
Db	361	ACAATAGAATGTTGTGCGACCAATTTGTGCAACCAATATTTGCACCTACACTGCCCCCT	420
Qy	141	ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet	160
Db	421	GTCGTTATAGGCCCATTTCTTGAATGGCAGCGTCCGATGGCTGGCTCATCTCTATG	480
Qy	161	AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys	180
Db	481	GCTGCTGTTATGTGCCATGATGCTCTTCTCCAGCTGCTTCTGTGTTCAAAACATTACTGT	540
Qy	181	LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle	200
Db	541	AAGAGTATCTCAAGCAGAGGTCGTTACAAACCGTGACTTGGAAACAGGATGAGGCATTATT	600

Qy	201	ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer	220
Db	601	CCAGTAGAGAAATCACTGAAAGACCTGATTGACCAGTCAACAAGCTCTGGTAGTGATCT	660
Qy	221	GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal	240
Db	661	GGATTACCTTTATTGGTTTCAGGAACTATTGCCAAACAGATTCAAGTTGGTTCGGCAGGTT	720
Qy	241	GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTyrTrpArgGlyGluLysValAlaVal	260
Db	721	GGTAAGGCCCGGTATGAGAAAGTAGTGGTAAATGCGTGGTGGTGAAGAAAGTGGCTGTC	780
Qy	261	LysValPhePheThrThrGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr	280
Db	781	AAAGTATTTTTTACCACCTGAAGAAAGTACGTGGTGTGTAGAGAAACAGAAATCTTACCAGACG	840
Qy	281	ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly	300
Db	841	GTGTTAATGCCGTCAATAAATATATCTTGGTTTTATAGCTGCAGACATTAAAGGCCACCGT	900
Qy	301	SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe	320
Db	901	TCCTGGACTCAGCTGATTTCGATTACTGATTACCATGAGATGGGTCTCTCTATGACTTC	960
Qy	321	LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys	340
Db	961	CTGAAATGTGCCACCTGGACACCCAGACCCCTACTCAAGTTAGCTTATTTCTGCTGCCTGT	1020
Qy	341	GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis	360
Db	1021	GGTCTGTGCCACCTCCACACAGAAATTTATGGCAGCAAGGCAAGCCCTGCAATTCCTCAT	1080
Qy	361	ArgAspLeuLysSerLysAsnIleLeuLysLysAsnGlySerCysCysIleAlaAsp	380
Db	1081	CGAGACCTGAAGACGAAAAACATCTCTATTAAAGAAAAATGGTAGTTGCTGTATTGCTGAC	1140
Qy	381	LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr	400
Db	1141	CTGGCGCTAGCTGTATAATTCAACAGTGACACAAATGAAGTTTGACATACCTTGAACACC	1200
Qy	401	ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLysLysAsn	420
Db	1201	AGGTTGGGCACCGCGGTACATGGCTCCAGAAAGTGTGGACGAGAGCTCAGTAAAAAC	1260
Qy	421	HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet	440
Db	1261	CATTTCCAGCCCTACATCATCGCTGACATCTACAGCTTTGGTTTGTATCATTTGGGAGATG	1320
Qy	441	AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet	460
Db	1321	GCCCGTCGCTGTTATTACAGGAGGAATCGTGAGGAATATCAATTACCATTATTTACAAACATG	1380
Qy	461	ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg	480
Db	1381	GTGCCTTAGTACCCTCTTTATGAAGACATGCGTGAGGTGCTGTGTGTGAAACGCTTGCGG	1440
Qy	481	ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet	500
Db	1441	CCAATCGTCTTAACCGCTGGAACAGTGAATGATGCTCTCCAGCCGTTTTGAAGCTGATG	1500
Qy	501	SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr	520
Db	1501	TCAGAAATGCTGGGCCCATTAATCCAGCATCCAGACTCAGAGCTTTGAGAAATCAAGAAGACG	1560
Qy	521	LeuAlaLysMetValGluSerGlnAspValLysIle	532
Db	1561	CTCCAAAGATGGTTGAATCCAGGACGTAAAGATT	1596

RESULT 2
ARI69902
LOCUS
DEFINITION Sequence 1 from patent US 6291206.
1813 bp DNA linear PAT 17-DEC-2001

ACCESSION AR169902
VERSION AR169902.1 GI:17907859
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1813)
AUTHORS Wozney,J.M., Celeste,A.J., Thies,R.Scott. and Yamaji,N.
TITLE BMP receptor proteins
JOURNAL Patent: US 6291206-A 1 18-SEP-2001;
FEATURES Location/Qualifiers
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source /organism="unknown"
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ORIGIN

Alignment Scores:

Pred. No.: 4,54e-271 Length: 1813
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-600-645-2 (1-532) x AR169902 (1-1813)

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Qy      21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db      121 GTTCAAGGGCAGAACTCTAGATGATGCTCCATGGTACTGGTATGAATCAGACGTGAC 180

Qy      41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
Db      181 CAGAAGAAGCCGGAATATGGAGTGACGTTAGCACAGAGGACACCTTTACCTTTCTTAAAA 240

Qy      61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
Db      241 TGTATTGCTCAGGACACTGCCCGATGACGCTATTATTAACATCATCAATACTAATGGC 300

Qy      81 HisCysPheAlaIleIleGluGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db      301 CATTTGCTTTGCCATTATAGAAGAAGATGATCAGGAGAAACACCGTTAACTTCTGGGTG 360

Qy      101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db      361 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCAAAAGCCACGCTACGCAGG 420

Qy      121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db      421 ACAATAGATGTTGTGCGGCAATTTGTGCAACCAATATTGTGAGCCCTACACTGCCCCCT 480

Qy      141 ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
Db      481 GTCGTTATAGGCCCATCTTTTGATGAGCGGTCGATGGCTGGCTGCTCATCTCTATG 540

Qy      161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
Db      541 GCTGCTCTGATTGTGCGCATGATCGTCTTCTCAGCTGCTCTGTTTACAAACATTACTGT 600

Qy      181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGlnAspGluAlaPheIle 200
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Qy      201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
Db      661 CCAGTAGAGATCACTGAAAGACCTGATTGACCAAGTCACAAAGCTCTGGTAGTATCT 720

Qy      221 GlyLeuProLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
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Qy      261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db      841 AAAGTATTTTTTACCACCTGAAGAAGCTAGCTGGTTTAGAGAAACAGAAATCTACCACAG 900

Qy      281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db      901 GTGTTAATGCGTCATGAAATATATCTGGTTTATAGCTGCAGACATTAAGGACCGCGGT 960

Qy      301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db      961 TCCTGGACTCAGCTGTATTGATTACTGATTACATGAGAAATGGGTCTCTCTATGACTTC 1020

Qy      321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db      1021 CTGAATGTGCCACCTGGACACAGAGCCCTACTCAAGTTAGCTTATTCTGCTGCCCTGT 1080

Qy      341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db      1081 GGTCTGTGCCACCTCCACACAGAAATTTATGGCACGCAAGGCAAGCCTGCAATTTGCTCAT 1140

Qy      361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
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Qy      381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
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Qy      401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
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Qy      421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTyrGluMet 440
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Qy      441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db      1381 GCCCGTCGCTGTTATTACAGGAGGAATCGTGGAGGAATATCAATTACATATTACAACATG 1440

Qy      461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
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Qy      481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
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Qy      501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
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RESULT 3

AR382508 1813 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 1 from patent US 6610513.
DEFINITION AR382508
ACCESSION AR382508
VERSION AR382508.1 GI:40091231
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1813)
AUTHORS Wozney,J.M., Celeste,A.J., Thies,R.S. and Yamaji,N.

TITLE Receptor proteins
JOURNAL Patent: US 6610513-A 1 26-AUG-2003;
Genetics Institute, LLC; Cambridge, MA
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/organism="unknown"
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Pred. No.: 4 54e-271 Length: 1813
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-600-645-2 (1-532) x AR382508 (1-1813)
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DB 61 ATGACTCAGCTATACACTTACATCAGATTACTGGGAGCCTGCTGTTCTCATTTCTCAT 120
QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetIysSerAspValAsp 40
DB 121 GTTCAAGGGCAGAACTAGATAGTATGCTCCATGGTACTGGTATGAATCAGACGTGGAC 180
QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
DB 181 CAGAAGAAGCCCGAAATGGAGTGGAGCTTAGCACCAGAGGACACCTTACCTTTCTTAAA 240
QY 61 CysTyrCysSerGlyHisCysProAspAlaIleAsnAsnThrCysIleThrAsnGly 80
DB 241 TGCATTATGCTCAGGACACTGCCAGATGACGCTATTAATAACACATGCATTAATGGC 300
QY 81 HisCysPheAlaIleGluGluAspGlnGlyGluThrThrLeuThrSerGlyCys 100
DB 301 CATTCGTTTGGCATTATAGAGAAGATGATCAGGAGAAACACCGTTTCTGGGTG 360
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QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
DB 421 ACAATAGAAATGTTGTCGACCAATTTGTGCAACCAATATTTGCAGCCTACACTGCCCT 480
QY 141 ValValIleGlyProPhePheAspGlySerValArgTTPLeuAlaValIleIleSerMet 160
DB 481 GTCGTTATAGGCCCATTCCTTGATGGCAGCGTCCGATGGCTGGCTCACTCTATG 540
QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrIysHisTyrCys 180
DB 541 GCTGCTGTATTGTCGCCATGATCGCTTTCTCCAGCTGCTTCTGTTACAAACATTACTGT 600
QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
DB 601 AAGAGTATCTCAAGCAGAGGTCGTTACAAACCGTGAATTCGGAACAGGATGAAGCATTTAT 660
QY 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
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QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
DB 721 GGATTACCTTTATTGTTTCAGCGAACTATTGCAAAACAGATTTCAGATGTTTCGGCAGGTT 780
QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
DB 781 GGTAAAGGCGCGTATGGAGAAGTATGGATGGGTAATGGCGTGAAGGTAAGTGGCTGTC 840
QY 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280

DB 841 AAAGTATTTTACCACCTGAAGAAGCTAGCTGGTTTAGAGAAACAGAAATCTACCAGACG 900
QY 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
DB 901 GTGTTAATGCGTCATGAAATATATACTTGGTTTTATAGCTGCAGACATTAAAGCCCGGT 960
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QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
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QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
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DB 1441 GTGCTAGTAGCCCATCTTATGAAGACATGCTGAGGTGCTGTGTGTGAACCGTTGCGG 1500
QY 481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValIleLysLeuMet 500
DB 1501 CCAATCGCTCTAACCCGCTGGAACAGTATGAATGTCTTCGAGCCGTTTGAAGCTGATG 1560
QY 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
DB 1561 TCAGAAATGCTGGGCCCATTAATCCAGCATCCAGACTCAGAGCTTGGAGAAATCAAGAAGACG 1620
QY 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
DB 1621 CTCGAAAGATGGTTGAATCCAGGATGTAAGATT 1656
RESULT 4
QY986812 3003 bp DNA linear PAT 25-JAN-2005
LOCUS Sequence 121 from Patent WO2005003158.
DEFINITION QY986812
ACCESSION QY986812
VERSION QY986812.1 GI:58194651
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1
AUTHORS Brunkow, M.E., Galas, D.J., Kovacevich, B., Mulligan, J.T.,
Paepke, B.W., van Ness, J., and Winkler, D.G.
TITLE Compositions and methods for increasing bone mineralization
JOURNAL Patent: WO 2005003158-A 121 13-JAN-2005;
Celltech R & D, Inc. (US)
FEATURES Location/Qualifiers


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Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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US-10-600-645-2 (1-532) x CQ986812 (1-3003)

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ACCESSION CS027157
VERSION CS027157.1 GI:60496971
KEYWORDS Rattus norvegicus (Norway rat)
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
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REFERENCE Winkler,D.G., Shi,J. and Latham,J.
AUTHORS Antibodies specific for sclerostin and methods for increasing bone
.TITLE mineralization
JOURNAL Patent: WO 2005014650-A 90 17-FEB-2005;
CELLTECH R & D, Inc. (US)
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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DEFINITION Rat mRNA for bone morphogenetic protein type IA receptor, complete cds.

ACCESSION D38082
VERSION D38082.1 GI:1398909
KEYWORDS rALK-3; bone morphogenetic protein type IA receptor; bone morphogenetic protein receptor; BMP receptor; serine/threonine kinase; transmembrane protein.

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REFERENCE 1 (bases 1 to 3003)
AUTHORS Takeda,K., Oida,S., Ichijo,H., Iimura,T., Maruoka,Y., Amagasa,T. and Sasaki,S.

TITLE Molecular cloning of rat bone morphogenetic protein (BMP) type IA receptor and its expression during ectopic bone formation induced by BMP

JOURNAL Biochem. Biophys. Res. Commun. 204 (1), 203-209 (1994)
PUBMED 7945360
REFERENCE 2 (bases 1 to 3003)
AUTHORS Oida,S.

TITLE Direct Submission
JOURNAL Submitted (26-AUG-1994) Shinichiro Oida, Faculty of Dent., Tokyo Medical and Dental University, Department of Biochemistry, 1-5-45 Yushima, Bunkyo-ku, Tokyo 113, Japan (Tel:03-3813-6111(ex.5126), Fax:03-5684-8047)
COMMENT On Jun 29, 1996 this sequence version replaced gi:599585.
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Sciurognathi; Muridae; Murinae; Rattus.
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REFERENCE Brunkow,M.E., Galas,D.J., Kovacevich,B., Mulligan,J.T.,
AUTHORS Paepker,B.W., van Ness,J. and Winkler,D.G.
TITLE Compositions and methods for increasing bone mineralization
JOURNAL Patent: WO 2005003158-A 119 13-JAN-2005;
Celltech R & D, Inc. (US)
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Db 466 CATTGCTTTGCCATTATAGAAGAAGATGATCAGGAGAAACACCGTTAACTTCTGGGTGT 525
QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArg 120
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Qy      521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
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RESULT 8
CO986811
LOCUS      CO986811          3167 bp      DNA      linear      PAT 25-JAN-2005
DEFINITION Sequence 120 from Patent WO2005003158.
ACCESSION CO986811
VERSION   CO986811.1  GI:58194650
KEYWORDS
SOURCE    Rattus norvegicus (Norway rat)
ORGANISM  Rattus norvegicus
REFERENCE 1
AUTHORS   Brunkow M.E., Galas,D.J., Kovacevich,B., Mulligan,J.T.,
          Paepers,W., van Ness,J. and Winkler,D.G.
TITLE     Compositions and methods for increasing bone mineralization
JOURNAL   Patent: WO 2005003158-A 120 13-JAN-2005;
          Celltech R & D, Inc. (US)
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Score:          2838.00      Matches:      532
Percent Similarity: 100.00%      Conservative: 0
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DB:             6      Gaps:      0

US-10-600-645-2 (1-532) x CO986811 (1-3167)

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Db      706 GCTGCTCTGTATTTGTGCCCATGATCGTCTTCTCCAGCTGCTTCTGTTACAAACATTTACTGT 765
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RESULT 9
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LOCUS CS027155
DEFINITION Sequence 88 from Patent WO2005014650.
ACCESSION CS027155
VERSION CS027155.1 GI:60496969

KEYWORDS
SOURCE Rattus sp.
ORGANISM Rattus sp.

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE
1 Winkler,D.G., Shi,J. and Latham,J.
Antibodies specific for sclerostin and methods for increasing bone
mineralization
JOURNAL Patent: WO 2005014650-A 88 17-FEB-2005;
Celltech R & D, Inc. (US)

FEATURES
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Location/Qualifiers

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ORIGIN

Alignment Scores:
Pred. No.: 9,156-271 Length: 3167
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-600-645-2 (1-532) x CS027155 (1-3167)

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DEFINITION Sequence 89 from Patent WO2005014650.
ACCESSION CS027156
VERSION CS027156.1 GI:60496970
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.

1
REFERENCE Winkler,D.G., Shi,J. and Latham,J.
AUTHORS Antibodies specific for sclerostin and methods for increasing bone
TITLE mineralization
JOURNAL Patent: WO 2005014650-A 89 17-FEB-2005;
Celltech R & D, Inc. (US)
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Alignment Scores:
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US-10-600-645-2 (1-532) x CS027156 (1-3167)

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RESULT 12

AY365062

LOCUS

DEFINITION Mus musculus bone morphogenetic protein receptor type 1a (Bmpr1a)
 mRNA, complete cds.

ACCESSION

AY365062

VERSION

AY365062.1 GI:34334005

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

ORGANISM

REFERENCE 1 (bases 1 to 1599)
 Shalamanov P.D., Morty, R.E. and Eickelberg, O.
 Expression of bone morphogenic protein receptor 1a in the mouse
 Unpublished
 2 (bases 1 to 1599)
 Shalamanov P.D., Morty, R.E. and Eickelberg, O.
 Direct Submission
 Submitted (11-AUG-2003) Internal Medicine, University of Giessen
 Medical Centre, Aulweg 123 (Rooms 6-11), Giessen, Hessen 35392,
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FEATURES

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ORIGIN

Alignment Scores:
 Pred. No.: 1,19e-269 Length: 1599
 Score: 2823.00 Matches: 526
 Percent Similarity: 99.81% Conservative: 5
 Best Local Similarity: 98.87% Mismatches: 1
 Query Match: 99.47% Indels: 0
 DB: Gaps: 0

US-10-600-645-2 (1-532) x AY365062 (1-1599)

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RESULT 13

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DEFINITION M.musculus ALK-3 mRNA, complete CDS.
ACCESSION Z23154
VERSION Z23154.1 GI:437868
KEYWORDS ALK-3 gene; serine/threonine kinase receptor.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
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            Sciurognathi; Muridae; Murinae; Mus.
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REFERENCE 1 (bases 1 to 1599)
AUTHORS Dewulf,N., Verschueren,K., Lonnoy,O., Moren,A., Grimsby,S., Vande
        Spiegie,K., Miyazono,K., Huybreoek,D. and Ten Dijke,P.
TITLE Distinct spatial and temporal expression patterns of two type I
        receptors for bone morphogenetic proteins during mouse
        embryogenesis
JOURNAL Endocrinology 136 (6), 2652-2663 (1995)
PUBMED 7750489
REFERENCE 2 (bases 1 to 1599)
AUTHORS Miyazono,K.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-1993) Kohei Miyazono, Ludwig Institute for Cancer
        Research, Biomedical, Center, Uppsala, S-751 24, Sweden
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mat_peptide

ORIGIN

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Alignment Scores:
Pred. No.: 1,19e-269 Length: 1599
Score: 2823.00 Matches: 526
Percent Similarity: 99.81% Conservative: 5
Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
Db: 9 Gaps: 0
US-10-600-645-2 (1-532) x MMALK3A (1-1599)
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QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
Db 1 ATGACTCAGCTATACACTTACATCAGATTACTGGAGGCTGTCTGTTTCATCATTTCTCAT 60
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RESULT 14
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LOCUS A38817 2070 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 13 from Patent WO9411502.
ACCESSION A38817
VERSION A38817.1 GI:2295247
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 2070)
Miyazono,K., Djike,P.T., Franzen,P., Yamashita,H. and Heldin,C.
ACTIVIN RECEPTOR-LIKE KINASES, PROTEINS HAVING SERINE THREONINE
KINASE DOMAINS AND THEIR USE
Patent: WO 9411502-A 13 26-MAY-1994;
LUDWIG INST CANCER RES (GB)
COMMENT
Other publication CA 2149441 940526
Other publication AU 5432094 940608
Other publication NZ 257631 960326
Other publication JP 8505049T 960604.
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Alignment Scores:
Pred. No.: 1,65e-269 Length: 2070
Score: 2823.00 Matches: 526
Percent Similarity: 99.81% Conservative: 5
Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 6 Gaps: 0

US-10-600-645-2 (1-532) x A38817 (1-2070)
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RESULT 15
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LOCUS AR140650 Sequence 13 from patent US 6207814.
DEFINITION AR140650
ACCESSION AR140650
VERSION AR140650.1 GI:14483146
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2070)
AUTHORS Miyazono,K., ten Dijke,P., Franzen,P., Yamashita,H. and
Heidin,C.-H.
TITLE Activin receptor-like kinases, ALK-3 and ALK-6, and nucleic acids
encoding them
JOURNAL Patent: US 6207814-A 13 27-MAR-2001;
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ORIGIN
Alignment Scores:
Pred. No.: 1.65e-269 Length: 2070
Score: 2823.00 Matches: 526
Percent Similarity: 99.81% Conservative: 5
Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 6 Gaps: 0
US-10-600-645-2 (1-532) x AR140650 (1-2070)

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QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
DB 337 CAGAAGAACCAGAAATAGAGTGACTTTAGCACCAGAGGATACCTTGCTTTCTTAAG 396
QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
DB 397 TGTCTATTGCTCAGGACACTGCCAGATGATGCTATTATPAACACATGCAATAACTAATGGC 456
QY 81 HisCysPheAlaIleIleGluAspAspGlnGlyThrThrLeuThrSerGlyCys 100
DB 457 CATTGCTTTGCCATTATAGAAGAAGATGATCAGGGAGAAACACATTAACTTCTGGGTGT 516
QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
DB 517 ATCAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCGAAAGCCAGCTACGCAGG 576
QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
DB 577 ACATAGATGTTGTCGGACCAATTTGTGCAACCCAGTATTTGCAGCTTACACTGCCCTCT 636
QY 141 ValValIleGlyProPhePheAspGlySerValArgTyrLeuAlaValLeuIleSerMet 160
DB 637 GTTGTATATAGTTCGTTCTTGTATGCGACATCCGATGCTGTTGTGCTCATTTCCATG 696
QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrIleHisTyrCys 180
DB 697 GCTGTCTGTATAGTGTCTATGATCATCTTCTCCAGCTGCTTTTGTCTAAAGCATTTATTGT 756
QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
DB 757 AGAGTATCTCAAGCAGGGGTGTTACAAACCGTGATTTGGAAACAGATGAAGCATTTATT 816
QY 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
DB 817 CCAGTAGGAGAAATCATTGAAGACCTGATTGACCAGTCCCAAGCTCTGGGAGTGGATCT 876
QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
DB 877 GGATTTGCCCTTTATGTTGTTCCAGCGAACTATTGCAAAACAGATTTCAGATGGTTCCGCAGGTT 936
QY 241 GlyLysGlyArgTyrGlyGluValTyrMetGlyLysTyrArgGlyGluLysValAlaVal 260
DB 937 GGTAAAGCCGCTATGGAGAAGTATGGATGGGTAAATGGCGTGGTGAATAAGTGGCTGTG 996
QY 261 LysValPhePheThrThrGluGluAlaSerTyrPheArgGluThrGluIleTyrGlnThr 280
DB 997 AAAGTGTTTTTTACCACCTGAAGAAGCTACTGTTTATAGAGAACAGAAATCTACCAGAGC 1056
QY 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
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QY 301 SerTyrThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrArgPhe 320
DB 1117 TCTTGACTCAGCTGATTATTGATTCTGATTACCATGAAATGGATCTCTCTATGACTTC 1176
QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
DB 1177 CTGAATGTGCCACACTACAGACCAGAGCCCTACTCAAGTTAGCTTATTCTGCTGCTTGT 1236
QY 341 GlyLeuCysHisIleuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
DB 1237 GGTCTGTGCCACCTCCACACAGAAATTTATGTTAGTACCCAGGGAAGCCTGCAATTGCTCAT 1296
QY 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
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Db 277 GTTCAAGGCGAAGTCTAGATAGTATGCTCCATGGCACTGGTATGAATCAGACTGGAC 336
Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
Db 337 CAGAAGAACCCAGAAATGGAGTGNCTTTAGCACCAGAGGATACCTTGCCTTTCTTAAG 396
Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaLeuAsnThrCysIleThrAsnGly 80
Db 397 TGTATTGCTCAGGACACTGCCAGATGATGCTATTATAACACATGCATAAATGTC 456
Qy 81 HisCysPheAlaIleIleGluGluAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 457 CATTCCTTTGTCATTTATAGAGAGATGATCAGGAGAAACACATTAACCTTCGGGTG 516
Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 517 ATGAAGTATGAAGCTCTGATTTCAATGCAAGGATTCACGAAAGCCAGCTACGAGG 576
Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 577 ACAATAGAAATGTTGCGACCAATTTGTGCAACAGTATTTGCGAGCTTACACTGCCCT 636
Qy 141 ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
Db 637 GTTGTATAGTCCGTTCTTTGATGGCAGCATCCGATGGCTGGTGTGCTCATTTCCATG 696
Qy 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
Db 697 GCTGTCTGTATAGTTGTATGATCATCTTCCAGCTGCTTTTGTCTATAAGCATTTATGT 756
Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
Db 757 AAGAGTATCTCAAGCAGGGTCTGTACAAACCGTGATTTGGAACAGGATGAAGCATTTATT 816
Qy 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
Db 817 CCAGTAGAGAAATCATTTGAAAGACCTGATTTGACCAGTCCCAAGCTCTGGAGTGGATCT 876
Qy 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 877 GGATTGCTTTATTTGGTTACGCACTATTTGCCAAACAGATTCAGATGGTTTCGCGAGGTT 936
Qy 241 GlyLysGlyArgTyrGlyValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
Db 937 GGTAAAGCCGCTATGAGAGATGATGATGGTAAATGGCGTGTGTAAGTGGCTGTC 996
Qy 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
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Qy 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAspIleLysGlyThrGly 300
Db 1057 GTGTTAATGGCTCATGAAATATATCTTGGTTTATAGCTGAGACATTAAGGCACCTGGT 1116
Qy 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 1117 TCCTGGACTCAGCTGATTTGATTACTGATTTACCATGAATGGATCTCTATGACTTC 1176
Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 1177 CTGAAATGTGCACACTAGACACACAGAGCCCTACTCAAGTTAGCTTATTCTGCTGCTGT 1236
Qy 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1237 GGTCTGTGCCACCTCCACACAGAAATTTATGGTACCAGGGAAGCCCTGCAATTTGCTCAT 1296
Qy 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
Db 1297 CGAGACCTGAAGAGACAAACATCTCTATTAGAAATAATGGAAGTTGCTGTATTGCTGAC 1356
Qy 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1357 CTGGGCTAGCTGTAAATTTCAACAGTGATACAAATGAAGTTGACATACCTTTGAATACC 1416

Qy 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db 1417 AGGTTGGGCACCAAGCGGTATCATGGCTCCAGAGTGTGGATGAAGCCTGAATAAAAC 1476
Qy 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
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Qy 441 AlaArgArgCysIleThrGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1537 GCTCGTCTGTATTACAGGAGGAATCGTGAGGAATATCAATTTACCATATTACAACATG 1596
Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysAtgLeuArg 480
Db 1597 GTGCCCCAGTACCCATCTATGAGGATGCGTGAGGTTGTGTGTGTAACACGCTTGGG 1656
Qy 481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1657 CCAATCGTGTCTAACCGCTGGAACAGCGATGAATGTCTTCGAGCAGTTTTTGAAGCTAATG 1716
Qy 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
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Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1777 CTTGCAAAAAATGGTTGATCCAGGATGTAAAGATT 1812

Search completed: December 9, 2005, 21:16:28

Job time : 5300 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 9, 2005, 17:20:39 ; Search time 614 Seconds
(without alignments)

5774.620 Million cell updates/sec

Title: US-10-600-645-2

Perfect score: 2838

Sequence: 1 MTQLTYTIRLGLACLFIIH.....TALRIKTKLAKMVESQDVKI 532

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=N_Geneseq -QMT=fascap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_21.*

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4: Geneseqn2001as.*
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13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2838	100.0	1813	2	AAQ83530
2	2838	100.0	3003	14	Adw28817 Rat bone
3	2838	100.0	3003	14	Adx97430 Rat bone
4	2838	100.0	3167	14	Adw28816 Rat bone

5	2838	100.0	3167	14	Adw28815 Rat bone
6	2838	100.0	3167	14	Adx97428 Rat bone
7	2838	100.0	3167	14	Adx97429 Rat bone
8	2823	99.5	2070	2	AAQ66640 Mouse Act
9	2823	99.5	2070	2	Aaz059847 Human mAL
10	2823	99.5	2070	14	Ady51875 Murine AL
11	2823	99.5	2402	2	AAQ90184 BRK-1 DNA
12	2823	99.5	2402	2	Aat27228 Bone mOrp
13	2823	99.5	2402	2	Aat28021 Mouse BMP
14	2823	99.5	2402	2	Aav71972 Mouse BMP
15	2798	98.6	2056	2	AAQ90183 Truncated
16	2769	97.6	1599	13	AdQ89877 Antagonis
17	2769	97.6	1599	13	AdR73164 Human bon
18	2769	97.6	2623	8	AdS3821 DNA used
19	2769	97.6	2932	2	AAQ66636 Human Act
20	2769	97.6	2932	2	Aat06031 Human ALK
21	2769	97.6	2932	2	Aaz09843 Human HAL
22	2769	97.6	2932	5	Aas87057 DNA encod
23	2769	97.6	2932	10	ACF05952 Human bon
24	2769	97.6	2932	14	Adw28812 Human bon
25	2769	97.6	2932	14	AdX07490 Cyclin-de
26	2769	97.6	2932	14	Adx97425 Human bon
27	2769	97.6	2932	14	Ady51867 Human ALK
28	2769	97.6	2932	14	Aec02077 Nuclcotid
29	2763	97.4	3631	14	AdY81406 Human act
30	2635.5	92.9	1743	10	AdE07106 Novel cod
31	2635.5	92.9	1743	14	AdU40263 Novel hum
32	2604.5	91.8	1929	10	AdE07107 Novel cod
33	2604.5	91.8	1929	14	AdU40264 Novel hum
34	2601	91.6	2730	5	AAS87064 DNA encod
35	2129.5	75.0	1695	5	AAS87063 DNA encod
36	2011	70.9	1185	12	ACH87174 Human Gen
37	1972	69.5	1612	5	AdH11871 Wild-type
38	1968	69.3	1612	5	AdH11872 Booroola
39	1952	68.8	1575	8	ACD13394 Human DNA
40	1952	68.8	1575	14	Adw28813 Human bon
41	1952	68.8	1575	14	AdX97426 Human bon
42	1952	68.8	2032	6	ABK92206 Prostate
43	1952	68.8	2032	6	ABT07695 Breast ca
44	1952	68.8	2032	6	ABK90314 DNA encod
45	1952	68.8	2032	8	ABT17075 Androgen-

ALIGNMENTS

RESULT 1
AAQ83530
ID AAQ83530 standard; DNA; 1813 BP.
XX
AC AAQ83530;
XX
DT 25-MAR-2003 (revised)
DT 28-SEP-1995 (first entry)
XX
Sequence encoding bone morphogenic protein receptor CPK1-23a.
XX
Bone morphogenic protein; receptor; serine/threonine kinase; BMP; bone;
cartilage; injury; treatment; inhibition; ss.
XX
Rattus rattus.
XX
FH Key Location/Qualifiers
FT CDS 61..1659
FT /*tag= a
FT /product= "Bone morphogenic protein receptor."
XX
PN WO9507982-A1.
XX
PD 23-MAR-1995.
XX
PF 07-SEP-1994; 94WO-US010080.
XX
PR 17-SEP-1993; 93US-00123934.

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XX PA (GEMY ) GENETICS INST INC.
XX PI Wozney JM, Celeste AJ, Thies RS, Yamaji N;
XX DR DR
XX DR WPI; 1995-131350/17.
XX DR P-PSDB; AAR70237.
XX PT Truncated BMP and serine/threonine kinase receptor proteins - used to
XX PT inhibit the effects of BMP-2 and/or BMP-4.
XX PS Claim 2; Page 48-50; 83pp; English.
XX PS
XX CC Truncated bone morphogenic protein (BMP) receptors and serine/threonine
XX CC kinase receptors may be used in compositions to inhibit the effects of
XX CC BMP's such as BMP-2 and BMP-4. The truncated receptors pref. comprise the
XX CC ligand binding domain, but not the serine/threonine kinase and
XX CC transmembrane domains. The truncated proteins are soluble and will be
XX CC excreted into supernatant by recombinant mammalian cells expressing them.
XX CC Such cells can be delivered in a medium or matrix which partially impedes
XX CC their mobility, thereby localising the cells to a site of bone or
XX CC cartilage injury. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 1813 BP; 506 A; 397 C; 439 G; 471 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4,36e-294 Length: 1813
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-600-645-2 (1-532) x AAQ83530 (1-1813)
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DB 61 ATGACTCAGCTATACACTTACATCAGATTACTGGGAGCCTGCTGTTCATCTCTCAT 120
QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
DB 121 GTTCAAGGCGAGAATCTAGATAGTATGCTCCATGGTACTGGTATGAATCAGACGTGGAC 180
QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
DB 181 CAGAAGAAGCCGAAATGGAGTGACGTTAGCACCAGAGGACACCTTACTCTTTCTTAA 240
QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
DB 241 TGTATTGCTCAGGACACTGCCAGATGACGCTATTATTAACACATGCATACTAATGGC 300
QY 81 HisCysPheAlaIleIleGluGluAspAspGlnGlyThrThrLeuThrSerGlyCys 100
DB 301 CATTTGCTTTGCCATTATAGAAGAAGATGATCAGGAGAGAAACACCGTTAACTTCTGGTGT 360
QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
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QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
DB 421 ACNATAGATGTTGTTCGACCAATTTGTGCAACCAATATTTGCAGCTACACTGCCCTCT 480
QY 141 ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
DB 481 GTCGTTATAGGCCCATTTCTTTGATGGCAGCGTCCGATGGCTGGCTGTCTATCTCTATG 540
QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
DB 541 GCTGCTGTATTGTGCCCATGATCGCTTCTTCAGCTGCTTCTGTGTACAAACATTACTGT 600
QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGluAspGluAlaPheIle 200
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RESULT 2
ADW28817
ID ADW28817 standard; DNA; 3003 BP.

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DB 601 AAGAGTATCTCAAGCAGAGGTCGTTACAAACCGTGACTTTGGAACAGAGTGAAGCATTTATT 660
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QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTyrPArgGlyGluLysValAlaVal 260
DB 781 GGTAAAGGCCCGGTATGGAGAGTAGTATGGATGGTAAATGGCGTGGTGAANAAGTGGCTGTC 840
QY 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
DB 841 AAAGTATTTTATTTTACCACTGAAGAAGTAGCTGGTATTAGAGAAACAGAAATCTACCAGAG 900
QY 281 ValLeuMetArgHisGlnAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
DB 901 GTGTTAAATGCGTCATGAAAAATATATCTGGTTTTATAGCTGCAGACATTTAAAGGCCCGGT 960
QY 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
DB 961 TCCTGGACTCAGCTGATTTGATTACTGATTACCATGAGAAATGGTCTCTCTATGACTTC 1020
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DB 1021 CTGAAATGTGCCACCTCGACACAGAGCCCTACTCAAGTTAGCTTATTTCTGCTGCTGT 1080
QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlnLysProAlaIleAlaHis 360
DB 1081 GGTCTGTGCCACCTCCACACAGAAATTTATGGCAGCAAGGCAAGCCCTGCAATTTGCTCAT 1140
QY 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
DB 1141 CGAGACCTGAAGAGCAAAAACATCTTATTAAAGAAAATGGTAGTTGCTGTTATGCTGAC 1200
QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
DB 1201 CTGGGCCCTAGCTGTTAAATTTCAACAGTGACACAAATGAAGTTGACATACCTTTGAACACC 1260
QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLysLysAsn 420
DB 1261 AGGTGGGCACACAGCGGTACATGGCTCCAGAAGTGTGGAGAGAGCTGAGTAAAAAC 1320
QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
DB 1321 CATTTCCAGCCCTACATCATGGCTGACATCTACAGCTTTGGTTTTCATCATTTGGGAGATG 1380
QY 441 AlaArgArgCysIleThrGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
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DB 1441 GTGCCCTAGTACCCCATCTTATGAAGACATGCGTGAGGTGCTGTGTGTGAACCGCTTGGCG 1500
QY 481 ProfileValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
DB 1501 CCAATCGTCTTAACCGCTGGNACAGTGTGATGATGCTCTTCGAGCCGTTTTGAAGCTGATG 1560
QY 501 SerGluCysTyrTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
DB 1561 TCAGAATGCTGGGCCCATAAATCCAGACTCCAGACTCACAGCTTTTGAAGATCAAGAAGACG 1620
QY 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
DB 1621 CTCGAAAAGAGTGTGTTGAATCCAGGATGTAAAGATT 1656
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XX AC ADW28817;
XX XX
XX DT 07-APR-2005 (first entry)
XX DE
XX XX Rat bone morphogenetic protein (BMP) receptor type 1 DNA Seq 121.
XX KW receptor; bone morphogenetic protein; bone injury; antibody production;
XX KW TGF beta antagonist; BMP-antagonist; osteopathic; osteopenias;
XX KW osteoporosis; gene; ds.
XX OS Rattus norvegicus.
XX XX
XX FH Key Location/Qualifiers
XX FT CDS 83..1681
XX FT /*tag= a
XX FT /product= "BMP receptor type 1 protein"
XX XX
XX PN WO2005003158-A2.
XX XX
XX PD 13-JAN-2005.
XX XX
XX PF 15-JUN-2004; 2004WO-US018910.
XX XX
XX PR 16-JUN-2003; 2003US-00463190.
XX XX
XX PA (CLLT) CELLTECH R & D INC.
XX XX
XX PI Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepers BW;
XX PI Van Ness J, Winkler DG;
XX DR WPI: 2005-081936/09.
XX DR P-PSDB; ADW28803.
XX XX
XX PT New antibody or antigen-binding fragment that binds specifically to
XX PT sclerostin polypeptide and which inhibits binding of sclerostin
XX PT polypeptide to a bone morphogenic protein, useful for increasing bone
XX PT mineral content or density.
XX XX
XX PS Disclosure; SEQ ID NO 121; 205pp; English.
XX XX
XX CC This invention relates to a novel antibody or antigen-binding fragment
XX CC that binds specifically to a sclerostin (SOST) polypeptide and impairs
XX CC formation of a sclerostin homodimer. Specifically, it refers to an
XX CC antibody that competitively inhibits binding of the sclerostin
XX CC polypeptide to a bone morphogenic protein (BMP) type I receptor binding
XX CC site or a BMP type II receptor binding site. The present invention
XX CC describes a hybridoma cell capable of producing the antibody and a host
XX CC cell for antibody expression. Furthermore, it provides a nucleic acid
XX CC molecule encoding a transforming growth factor-beta (TGF-beta) binding
XX CC protein known as SOST (and also BEER) and methods for detection thereof.
XX CC Accordingly, such antibodies and osteopathic compositions of the
XX CC invention can be used for treating osteopenia, osteoporosis, fractures
XX CC and other disorders related to low bone mineral content and density. As
XX CC such, these compositions improve bone mineralization and can be described
XX CC as TGF-beta antagonists and/or BMP-antagonists. This polynucleotide is a
XX CC bone morphogenetic protein receptor type 1 DNA sequence given in an
XX CC exemplification of the invention.
XX XX
XX SQ Sequence 3003 BP; 840 A; 626 C; 654 G; 883 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9,236-294 Length: 3003
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-600-645-2 (1-532) x ADW28817 (1-3003)

QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyValaCysLeuPheIleSerHis 20
|||||

Db 83 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCCTGTCTGTTCATCTTCTCAT 142
QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetIysSerAspValasp 40
Db 143 GTTCAAGGGCAGAACTAGATAGTATGCTCCATGGTACTGGTATGAAATCAGACGTGGAC 202
QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
Db 203 CAGAGAAGCCGGAAATGGAGTGAGTTCAGCCAGAGGACACCTTACTCTTTTAAAA 262
QY 61 CysTyrCysSerGlyHisCysProAspAlaIleAsnAsnThrCysIleThrAsnGly 80
Db 263 TGTATTGCTCAGGACACTGCCAGATGACGCTATTATAACACATGCATAACTAATGGC 322
QY 81 HisCysPheAlaIleIleGluGluAspAspGlnGlyThrThrLeuThrSerGlyCys 100
Db 323 CATTTGCTTTGCCATTATAGAAGAAGATGATCAGGGAGAACCCAGTTAACTTCTGGGTGT 382
QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 383 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCAAAAGCCAGCTACGCAGG 442
QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 443 ACAATAGAATGTTTGTCCGACCAATTTGTCAACCAATATTTGCAGGCTACACTGCCCCCT 502
QY 141 ValValIleGlyProphePheAspGlySerValArgTrrLeuAlaValLeuIleSerMet 160
Db 503 GTTCGTTATAGGCCCATTTCTTGTGTCAGCGTCCGATGGCTGGCTGTCTCTCTATG 562
QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
Db 563 GCTGTCTGTATTGTGCCCATGATCGTCTTCTCCAGCTGCTTCTGTTCACAACTACTGT 622
QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
Db 623 AAGAGTATCTCAAGCAGAGGTCGTTACAACCGTGACTTGGAAACAGGATGAAGCATTTATT 682
QY 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
Db 683 CAGTAGGAGAAATCACTGAAGACCTGATTGACCAGTCACAAAGCTCTGGTAGTGATCT 742
QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 743 GGATTACCTTTATTGTTTCAGCGAATATTTGCCAAACAGATTCAGATGGTTCGCGAGTT 802
QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrrPArgGlyGluLysValAlaVal 260
Db 803 GGTAAAGGCCGGTATGGAGAAAGTATGGATGGGTAAATGGGTGGTGAAGGCTGCTGTC 862
QY 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db 863 AAAGTATTTTTCACCATGAAGAGCTAGCTGGTTTAGAGAAACAGAAATCTACCCAGCG 922
QY 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db 923 GTGTTAATGCGTCATGAANAATATCTTGGTTTTATAGCTGCAGACATTAAGGCACCGGT 982
QY 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 983 TCCTGGACTCAGCTGTATTGATTGATTACTGATTACCATGAGAAATGGGTCTCTCTATGACTTC 1042
QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAaCys 340
Db 1043 CTGAAATGTGCCACCTCGACACCCAGAGCCCTACTCAAGTTAGCTTATTCTGTGCTGCTGT 1102
QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1103 GGTCTGTGCCACTCCACACANATTTATGCGACGCAAGGCAAGGCTGCAATGCTCAT 1162
QY 361 ArgAspLeuLysSerIysAsnIleLeuIleLysLysAsnGlySerCysIleAlaApp 380
Db 1163 CGAGACCTGAGAGAGCAAAACATCCTTATTAAAGAAAAATGGTAGTTGCTGTATTGCTGAC 1222

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QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db 1283 AGGTTGGGACACAGCGGTACATGGCTCCAGAAGTGCTGGACGAGAGCTGTAGTAAAC 1342
QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTyrPGLuMet 440
Db 1343 CATTTCCAGCCCTACATCATGCTGACATCTACAGCTTTGGTTTGATCATTTGGGAGATG 1402
QY 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1403 GCCCGCTGCTGTATTACAGGAGGAATCGTGGAGGAATATCAATTACCATATTTACAAACATG 1462
QY 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1463 GTGCTAGTGACCCATCTTATGAGACATCGCTGAGCTGCTGTGTGTGAAACGCTTGGCG 1522
QY 481 ProfileValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1523 CCAATCGTCTCTAACCGCTGGAACAGTGATGAATGTCTTCGAGCGCTTTTGAAGCTGATG 1582
QY 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db 1583 TCAGAAATGCTGGGCCCATTAATCCAGCATCCAGACTCACAGCTTTTGAGAAATCAAGAAGACG 1642
QY 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1643 CTCGCAAGATGCTGTGAATCCAGGATGTAAAGATT 1678
```

RESULT 3

```
ADX97430
ID ADX97430 standard; DNA; 3003 BP.
XX
AC ADX97430;
XX
DT 05-MAY-2005 (first entry)
XX
DE Rat bone morphogenic protein type I receptor encoding DNA, SEQ ID 90.
KW antibody; sclerostin; SOST; bone morphogenic protein receptor;
KW Transforming Growth Factor; osteopathic; gene therapy; bone repair;
KW osteopenia; osteoporosis; bone injury; gene; ds.
XX
OS Rattus norvegicus.
XX
FH Key Location/Qualifiers
FT CDS 83..1681
FT /*tag= a
FT /product= "Rat bone morphogenic protein type I receptor"
XX
XX WO2005014650-A2.
XX
XX 17-FEB-2005.
XX
XX 15-JUN-2004; 2004WO-US018912.
XX
XX 16-JUN-2003; 2003US-0478977P.
XX
XX (CLL) CELLTECH R & D INC.
XX
XX Winkler DG, Shi J, Latham J;
XX
XX WPI: 2005-163219/17.
XX
XX P-PSDB; ADX97416.
XX
XX New isolated antibody specific for a sclerostin polypeptide, useful for
XX increasing bone mineralization or for treating or preventing conditions
XX associated with low bone mineral density, e.g. osteoporosis or
XX osteopenia.
```

```
XX
PS Disclosure; SEQ ID NO 90; 157pp; English.
XX
CC The invention relates to a novel isolated antibody, or its antigen-
CC binding fragment, which binds specifically to a sclerostin (SOST)
CC polypeptide. The SOST polypeptide comprises any of 6 sequences having 190
CC or 213 amino acids, fully defined in the specification (ADX97341,
CC ADX97360, ADX97398, ADX97400, ADX97402 or ADX97408). The antibody
CC competitively inhibits binding of the SOST polypeptide to a bone
CC morphogenic protein (BMP) Type I Receptor binding site and a BMP Type II
CC capable of binding to a BMP Type I Receptor polypeptide. The invention
CC further comprises a hybridoma cell producing the new antibody; a host
CC cell that is capable of expressing the new antibody; a composition
CC comprising the new antibody, or its antigen-binding fragment, and a
CC physiological carrier; an immunogen comprising a peptide comprising 6, 7,
CC 8, 9, 10, 11, 12, or at least 21-50 or 20-75 consecutive amino acids of
CC the SOST polypeptide; methods for producing an antibody that specifically
CC binds to the SOST polypeptide, and methods for identifying an antibody
CC that modulates a Transforming Growth Factor (TGF)-beta signaling pathway,
CC that impairs binding of a BMP to the SOST polypeptide, that impairs SOST
CC homodimer formation, or that increases bone mineral content. The novel
CC antibody and compositions have osteopathic activity. The SOST nucleic
CC acids may be used in gene therapy. The composition and methods are useful
CC for increasing bone mineralization, which may treat or prevent diseases
CC or conditions associated with low bone mineral density, such as
CC osteopenia, osteoporosis or bone fractures. This polynucleotide sequence
CC represents a rat bone morphogenic protein type I receptor encoding DNA of
CC the invention.
XX
SQ Sequence 3003 BP; 840 A; 626 C; 654 G; 883 T; 0 U; 0 Other;
```

Alignment Scores:

```
Pred. No.: 9.23e-294 Length: 3003
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
```

US-10-600-645-2 (1-532) x ADX97430 (1-3003)

```
QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
Db 83 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCGCTGCTGTTTCATCATTTCTCAT 142
QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db 143 GTTCAAGGCGAGAATCTAGATAGTAGTATGCTCCTGTTGTTATGAAATCAGACGTGGAC 202
QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
Db 203 CAGAAGAAGCGGAAATGGAGTGACGTAGCAGTACACAGAGGACACCTTACCTTTCTTAAAA 262
QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
Db 263 TGCTATTGCTCAGGACACTGCCACAGATGACCTATTATAACACATGATCACTAATGCG 322
QY 81 HisCysPheAlaIleIleGluGluAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 323 CATTTGCTTTGCCATTATAGAACAGATGATCAGGAGAAACACAGTTTAACTTCTGGGTGT 382
QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 383 ATGAAGTATGAAGCTCTGATTTTCAATGCAAGGATTCCACCAAAAGCCAGCTACGCAGG 442
QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 443 ACAATAGAATGTTTTCGGACCAATTTGTGCAACCAATATTTTGCAGCTTACACTGCCCCCT 502
QY 141 ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
Db 503 GTCGTTATAGGCCCATTTCTTTGATGGCAGCGCTCGATGGCTGGCTGCTCATCTCTATG 562
```

Qy 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrIleLysHisTyrCys 180
Db 563 GCTGCTGTATTGTCGCGCATGATGCTCTCTCCAGCTGCTCTCTGTACAAACATTACTGT 622

Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGlnAspGluAlaPheIle 200
Db 623 AAGAGTATCTCAAGCAGAGGTCGTTACAAACCGTGACTTGGAAACAGGATGAAGCATTTATT 682

Qy 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
Db 683 CCAGTAGAGAGATCACTGAAAGACCTGATTGACCAGTCACAAAGCTCTGGTAGTGATCT 742

Qy 221 GlyLeuProLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 743 GGATTACCTTTATTGGTTCAGCAACTATTGCCAAACAGATTACAGTGGTTCGCCAGGTT 802

Qy 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
Db 803 GGTAAAGGCCGCTATGAGAGAGTATGATGGGTAAATGGCGTGGTGAAGATGGCTGTC 862

Qy 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db 863 AAAGTATTTTACCCTGGAAGAGCTAGCTGGTTTAGAGAAACAGAAATCTACCCAGACG 922

Qy 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db 923 GTCTTAATGCTCATGAAATATATCTGGTTTTATAGCTGCAGACATTAAGACACCGGT 982

Qy 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 983 TCCTGGACTCAGCTGATTTGATTACTGATTACCATGAGAATGGTCTCTCTATGACTTC 1042

Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 1043 CTGAATGTGCCACCTGGACACAGAGCCCTACTCAAGTTAGCTTTATTCTGCTGCTGT 1102

Qy 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1103 GGTCTGTGCCACCTCCACAGAAATTTATGGCAGCGAAGCAAGCTGCAATGCTCAT 1162

Qy 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
Db 1163 CGAGACCTGAAGACGAAAAACATCCTATTAAAGAAAAATGGTAGTTGCTGTATTGCTGAC 1222

Qy 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1223 CTGGGCTAGCTGTTAAATTCACAGTGACACAAATGAAGTTGACATACCCCTTGAACACC 1282

Qy 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db 1283 AGGTTGGGACCAAGCGGTACATGGCTCCAGAAAGTCTCGACGAGAGCTGAGTAAAC 1342

Qy 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
Db 1343 CAITTCAGCCCTACATCATGCTGACATCTACAGCTTTGGTTTGATCATTTGGGAGATG 1402

Qy 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1403 GCCCGTCGCTGATTACAGAGGAATCGTGGAGGAATATCAATTACCATATTACACATG 1462

Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1463 GTGCCGTAGTACCCATCTTATGAAGACATCGGTGAGGTGCTGTGTGTGAACCGCTTGGCG 1522

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Db 1523 CCAATCGTCTCTAACCGCTGGACAGTGATGATGATGCTTCGAGCCGTTTTGAAGCTGATG 1582

Qy 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db 1583 TCAGAAATGTGGGCCCAATAATCCAGCATCCAGACTCACAGCTTTCAGAAATCAAGAAGACG 1642

Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1643 CTCGCCAAGATGGTTGANTCCAGGATGTAAGATT 1678

RESULT 4
ADM28816
ID ADM28816 standard; DNA; 3167 BP.
XX
AC ADM28816;
XX
DT 07-APR-2005 (first entry)
XX
DE Rat bone morphogenetic protein (BMP) receptor type 1 DNA Seq 120.
XX
KW receptor; bone morphogenetic protein; bone injury; antibody production;
KW TGF beta antagonist; BMP-antagonist; osteopathic; osteopenias;
XX
OS osteoporosis; gene; ds.
XX
OS Rattus norvegicus.
XX
FH Key Location/Qualifiers
FT CDS 226..1824
FT /*tag= a
FT /product= "BMP receptor type 1 protein"
XX
XX WO2005003158-A2.
XX
XX 13-JAN-2005.
XX
XX 15-JUN-2004; 2004WO-US018910.
XX
XX 16-JUN-2003; 2003US-00463190.
XX
XX (CLLT) CELLTECH R & D INC.
XX
XX Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepers BW;
PI Van Ness J, Winkler DG;
XX
XX WPI: 2005-081936/09.
XX
XX P-PSDB; ADM28802.
XX
XX New antibody or antigen-binding fragment that binds specifically to
XX sclerostin polypeptide and which inhibits binding of sclerostin
XX polypeptide to a bone morphogenic protein, useful for increasing bone
XX mineral content or density.
XX
XX Disclosure; SEQ ID NO 120; 205pp; English.
XX
XX This invention relates to a novel antibody or antigen-binding fragment
XX that binds specifically to a sclerostin (SOST) polypeptide and impairs
XX formation of a sclerostin homodimer. Specifically, it refers to an
XX antibody that competitively inhibits binding of the sclerostin
XX polypeptide to a bone morphogenic protein (BMP) Type I receptor binding
XX site or a BMP Type II receptor binding site. The present invention
XX describes a hybridoma cell capable of producing the antibody and a host
XX cell for antibody expression. Furthermore, it provides a nucleic acid
XX molecule encoding a transforming growth factor-beta (TGF-beta) binding
XX protein known as SOST (and also BEER) and methods for detection thereof.
XX Accordingly, such antibodies and osteopathic compositions of the
XX invention can be used for treating osteopenia, osteoporosis, fractures
XX and other disorders related to low bone mineral content and density. As
XX such, these compositions improve bone mineralization and can be described
XX as TGF-beta antagonists and/or BMP-antagonists. This polynucleotide is a
XX bone morphogenetic protein receptor type 1 DNA sequence given in an
XX exemplification of the invention.
XX
XX Sequence 3167 BP; 908 A; 647 C; 688 G; 924 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9,99e-294 Length: 3167
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0
US-10-600-645-2 (1-532) x ADW28816 (1-3167)			
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Db	226	ATGACTCAGCTATACACTTACATCAGATTACTGGAGGCTGCTCTGTTTCATCATTTCTCAT	285
Qy	21	ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp	40
Db	286	GTTCAGGCGCAGAACTTAGATAGTATGCTCCATGCTACTGGTATGAAATCAGACGTGGAC	345
Qy	41	GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys	60
Db	346	CAGAAAGACCGGAAATAGGATGACGTTAGCACGAGGACACCTTACCTTTCTTAAAA	405
Qy	61	CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly	80
Db	406	TGCTATTGCTCAGGACACTGCCACATGACGCTATTATACACATGATTAACCTAATGCG	465
Qy	81	HisCysPheAlaIleIleGluAspAspGlnGlyThrLeuThrSerGlyCys	100
Db	466	CATTGCTTGGCATTATAGAAGATGATCAGGAGAAACACCGTTAACTTCTGGGTGT	525
Qy	101	MetLysTyrGluClySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArg	120
Db	526	ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCAAAAGCCGACGTACGCAGG	585
Qy	121	ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro	140
Db	586	ACAAATAGATGTTGTTCGACCAATTTGTGCAACCAATATTTGCAGCCTACACTGCCCCCT	645
Qy	141	ValValIleGlyProPhePheAspGlySerValArgTyrLeuAlaValLeuIleSerMet	160
Db	646	GTGCTTATAGGCCCATCTTTGATGCGAGCGTCCGATGGCTGGCTGCTCATCTCTATG	705
Qy	161	AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys	180
Db	706	GCTGTCTGTATTGTGCCATGATGCTCTTCTCCAGCTGCTTCTGTACAAAACATTACTGT	765
Qy	181	LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle	200
Db	766	AAGAGTATCTCAAGCAGAGGTCGTTACAAACCGTGACTTGGAAACAGGATGAAGCATTTAT	825
Qy	201	ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySer	220
Db	826	CCAGTAGGAGAAATCACTGAAGACCTGATTGACCAAGTCACAAAGCTCTGGTAGTGTCT	885
Qy	221	GlyLeuProLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal	240
Db	886	GGATTACCTTTATTGGTTTCAGCGAACTATTGCAAAACAGATTTCAGATGGTTCCGCGAGTT	945
Qy	241	GlyLysGlyArgTyrGlyGluValTyrMetGlyLysTyrArgGlyGluLysValAlaVal	260
Db	946	GGTAAAGCCGGTATGGAGAGTATGGATGGTAAATGCGTGGTGAAGAAAGTGGCTGTC	1005
Qy	261	LysValPhePheThrThrGluGluAlaSerTyrPheArgGluThrGluIleTyrGlnThr	280
Db	1006	AAAGTATTTTTTACCACCTGAAGAAGCTAGCTGGTTTTAGAGAAACAGAAATCTACCAGACG	1065
Qy	281	ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly	300
Db	1066	GTGTTTAAATGCGTCATGAAATATACTTGGTTTTTATAGCTGCAGACATTTAAAGGCGCCGGT	1125
Qy	301	SerTyrThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe	320
Db	1126	TCCTGGACTCAGCTGATTGTGATTAATGATTAACCATGAGATGGGTCTCTCTATGACTTC	1185
Qy	321	LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys	340
Db	1186	CTGAAATGTGCCACCTGGACACACAGGCCCTTACTCAAGTTAGCTTATTCTGCTGCTGT	1245

Qy	341	GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis	360
Db	1246	GGTCTGTGCCACCTCCACAGAAATTTATGGCAGCAAGGCAAGCCTGCAATTTGCTCAT	1305
Qy	361	ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp	380
Db	1306	CGAGACCTGAGAGCNAAAAACATCTTTATTAAAGAAAATGGTAGTTGCTGTTGCTGAC	1365
Qy	381	LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAlaAspIleProLeuAsnThr	400
Db	1366	CTGGCCCTAGCTGTATAATTCAACAGTCACACAAATGAAGTTGACATACCTTGAACACC	1425
Qy	401	ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn	420
Db	1426	AGGTGGGCACACAGCGGTACATGGCTCCAGAAAGTCTGGACGAGCCTGAGTAAAAAC	1485
Qy	421	HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTyrGluMet	440
Db	1486	CATTTCCAGCCCTACATCATCGCTGACATCTACAGCTTTGGTTTGATCATTTGGGAGATG	1545
Qy	441	AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet	460
Db	1546	CCCCGTGCTGTATTACAGGAGGAATCGTGAGGAATATCAATTACCATATTTACAACATG	1605
Qy	461	ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg	480
Db	1606	GTGCTTAGTGACCATCTTATGAAGACATGCTGAGGTCGTGTGTGAAAACGCTTGGCG	1665
Qy	481	ProIleValSerAsnArgTyrAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet	500
Db	1666	CCAATCGTCTTAACCCGCTGGAAACAGTGATGAATGCTCTCGAGCCGTTTGAAGCTGATG	1725
Qy	501	SerGluCysTyrAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr	520
Db	1726	TCAGAAATGCTGGGCCCATAAATCCAGACTCCAGACTCACAGCTTTGAGAATCAAGAAGACG	1785
Qy	521	LeuAlaLysMetValGluSerGlnAspValLysIle	532
Db	1786	CTCGAAAGATGGTTGAATCCAGGATGTAAGATTT	1821
RESULT 5			
ID	ADW28815	standard; DNA; 3167 BP.	
XX	ADW28815;		
AC	ADW28815;		
DT	07-APR-2005	(first entry)	
XX			
DE	Rat bone morphogenetic protein (BMP) receptor type 1 DNA Seq 119.		
XX			
KW	receptor; bone morphogenetic protein; bone injury; antibody production;		
KW	TGF beta antagonist; BMP-antagonist; osteopathic; osteopenias;		
KW	osteoporosis; gene; ds.		
XX			
OS	Rattus sp.		
XX			
FH	Key	Location/Qualifiers	
FT	226..1824		
FT	/tag= a		
FT	/product= "BMP receptor type 1 protein"		
XX			
PN	WO2005003158-A2.		
XX			
PD	13-JAN-2005.		
XX			
PF	15-JUN-2004; 2004WO-US018910.		
XX			
PR	16-JUN-2003; 2003US-00463190.		
XX			
PA	(CLLT) CELLTECH R & D INC.		
XX			
PI	Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepfer BW;		
PI	Van Ness J, Winkler DG;		

XX WPI; 2005-081936/09.
 DR P-PSDB; ADM28801.
 XX
 PT New antibody or antigen-binding fragment that binds specifically to
 PT sclerostin polypeptide and which inhibits binding of sclerostin
 PT polypeptide to a bone morphogenic protein, useful for increasing bone
 PT mineral content or density.
 XX
 XX Disclosure; SEQ ID NO 119; 205pp; English.
 XX
 CC This invention relates to a novel antibody or antigen-binding fragment
 CC that binds specifically to a sclerostin (SOST) polypeptide and impairs
 CC formation of a sclerostin homodimer. Specifically, it refers to an
 CC antibody that competitively inhibits binding of the sclerostin
 CC polypeptide to a bone morphogenic protein (BMP) Type I receptor binding
 CC site or a BMP Type II receptor binding site. The present invention
 CC describes a hybridoma cell capable of producing the antibody and a host
 CC cell for antibody expression. Furthermore, it provides a nucleic acid
 CC molecule encoding a transforming growth factor-beta (TGF-beta) binding
 CC protein known as SOST (and also BEER) and methods for detection thereof.
 CC Accordingly, such antibodies and osteopathic compositions of the
 CC invention can be used for treating osteopenia, osteoporosis, fractures
 CC and other disorders related to low bone mineral content and density. As
 CC such, these compositions improve bone mineralization and can be described
 CC as TGF-beta antagonists and/ or BMP-antagonists. This polynucleotide is a
 CC bone morphogenetic protein receptor type 1 DNA sequence given in an
 CC exemplification of the invention.
 XX
 SQ Sequence 3167 BP; 908 A; 647 C; 688 G; 924 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	9,99e-294	Length:	3167
Score:	2838.00	Matches:	532
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-10-600-645-2 (1-532) x ADM28815 (1-3167)

QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleSerHis 20
 DB
 226 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCGCTGCTGTTTCATCTCAT 285
 QY 21 ValGlnGlyClnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
 DB 286 GTTCAAGGGCAGAACTCTAGATAGTATGCTCCATGGTACTGGTATGAATCAGACGTGGAC 345
 QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
 DB 346 CAGAAAGCCGGAAATGGAGTGACGTGTAGCACCAGAGACACCTTACCTTTCTTAAAA 405
 QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
 DB 406 TGCTATTGCTCAGACACTGCCAGATGACGCTATTAAACACATGCACTAATATGCG 465
 QY 81 HisCysPheAlaIleIleGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
 DB 466 CATTTGCTTTGCCATTATAGAAGAAGATGATCAGGGAGAAACACACGTTAACTCTGGGTGT 525
 QY 101 MetLysTyrGluGlySerPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
 DB 526 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGATTCACAAAGCCAGCTACGACGG 585
 QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrIleGlnProThrLeuProPro 140
 DB 586 ACAATAGATGTTGTGCGACCAATTTGTGCAACCAATATTTGCAGCTACACTGCCCTCT 645
 QY 141 ValValIleGlyProPheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
 DB 646 GTCGTTATAGGCCCAATCTTTGTATGGCAGCGTCCGATGGCTGGCTGCTCTCTATG 705

QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
 DB 706 GCTGTCTGTATTGTCGCCCATGATCGTCTTCTCCAGCTGCTTCTGTACAAACATTACTGT 765
 QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
 DB 766 AAGAGTATCTCAAGCAGAGGTCGTTACAACCGTGACTTGGAAACAGGATGAAGCATTTATT 825
 QY 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
 DB 826 CCAGTAGAGAGATCACTGAAAGACCTGATTGACCACTCACAAGCTCTGGTAGTGGATCT 885
 QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
 DB 886 GGATTACCTTTATTGGTTCCAGCAACTATTGCCAAACAGATTCCAGATGGTTCCGCGAGTT 945
 QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTyrArgGlyGlnLysValAlaVal 260
 DB 946 GGTAAAGGCCGCTATGGAGAAGTATGGATGGGTAAATGGCGTGGTGAAGGTGGCTGTC 1005
 QY 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
 DB 1006 AAGATTATTTTACCCTGAAAGAGCTAGTGGTTTAGAGAAACAGAAATCTACCAAGC 1065
 QY 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
 DB 1066 GTGTTAATCGGTCATGAAATATATCTTGGTTTTATAGCTGCAGACATTAAGGCCCGGT 1125
 QY 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
 DB 1126 TCCTGGACTCAGCTGTATTGATTACTGATTACCATGAGATGGGTCTCTATGACTTC 1185
 QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
 DB 1186 CTGAAATGTCACCCCTGACACACAGAGCCCTACTCAAGTTAGCTTATTCTGCTGCTGT 1245
 QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
 DB 1246 GGTCTGTGCACCTCCACACAGAAATTTATGGCAGCAGGCGAGCTGCAATTTGCTCAT 1305
 QY 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
 DB 1306 CGAGACCTGAGAGCAAAACATCCTTATTAAGAAAAATGGTAGTTGCTGTATTGCTGAC 1365
 QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
 DB 1366 CTGGGCTAGCTGTGTTAAATTCAACAGTGCACAAATGAAGTTGCATACCTTTGAACACC 1425
 QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
 DB 1426 AGGGTGGGACCCAGCGGTACATGGCTCCAGAAAGTGTGGAGAGAGCCCTGAGTAAANAC 1485
 QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
 DB 1486 CATTTCCAGCCCTACATCATGCTGCATCTCAGCTTGGTGGTGGTGGTGGTGGTGGT 1545
 QY 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
 DB 1546 GCCCGCTGCTGTATTACAGGAGAAATCGTGGAGGAATATCAATATACCATATTACAAATG 1605
 QY 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
 DB 1606 GTGGCTAGTGACCCATCTTATGAAGACATCGCTGAGGTGCTGTGTGTGTAAGCGCTTGGCG 1665
 QY 481 ProfileValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
 DB 1666 CCAATCGTCTCTAACCGCTGGAAACAGTGAATGATGCTTCGAGCCGCTTTTGAAGCTGATG 1725
 QY 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysThr 520
 DB 1726 TCAGAAATGTGGGCCCATAAATCCAGCATCCAGACTCACAGCTTTTGAGAAATCAAGAAGC 1785
 QY 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532

Db 1786 CTCGCAAGATGTTGATCCCGAGGTAAAGATT 1821
|||||
RESULT 6
ADX97428
ID ADX97428 standard; DNA; 3167 BP.
XX
AC ADX97428;
XX
DT 05-MAY-2005 (first entry)
XX
DE Rat bone morphogenic protein type I receptor encoding DNA, SEQ ID 88.
XX
KW antibody; sclerostin; SOST; bone morphogenic protein receptor;
KW Transforming Growth Factor; osteopathic; gene therapy; bone repair;
KW osteopenia; osteoporosis; bone injury; gene; ds.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT 226..1824
FT /*tag= a
FT /product= "Rat bone morphogenic protein type I receptor"
XX
PN WO2005014650-A2.
XX
XX 17-FEB-2005.
XX
XX 15-JUN-2004; 2004WO-US018912.
XX
XX 16-JUN-2003; 2003US-0478977P.
XX
XX (CLLT) CELLTech R & D INC.
XX
XX Winkler DG, Shi J, Latham J;
XX
XX WPI: 2005-163219/17.
XX
XX P-PSDB; ADX97414.
XX
XX New isolated antibody specific for a sclerostin polypeptide, useful for
XX increasing bone mineralization or for treating or preventing conditions
XX associated with low bone mineral density, e.g. osteoporosis or
XX osteopenia.
XX
XX Disclosure; SEQ ID NO 88; 157pp; English.
XX
XX The invention relates to a novel isolated antibody, or its antigen-
XX binding fragment, which binds specifically to a sclerostin (SOST)
XX polypeptide. The SOST polypeptide comprises any of 6 sequences having 190
XX or 213 amino acids, fully defined in the specification (ADX97341,
XX ADX97360, ADX97398, ADX97400, ADX97402 or ADX97408). The antibody
XX competitively inhibits binding of the SOST polypeptide to a bone
XX morphogenic protein (BMP) Type I Receptor binding site and a BMP Type II
XX Receptor binding site, where the BMP Type I Receptor binding site is
XX capable of binding to a BMP Type I Receptor polypeptide. The invention
XX further comprises: a hybridoma cell producing the new antibody; a host
XX cell that is capable of expressing the new antibody; a composition
XX comprising the new antibody, or its antigen-binding fragment, and a
XX physiological carrier; an immunogen comprising a peptide comprising 6, 7,
XX 8, 9, 10, 11, 12, or at least 21-50 or 20-75 consecutive amino acids of
XX the SOST polypeptide; methods for producing an antibody that specifically
XX binds to the SOST polypeptide; and methods for identifying an antibody
XX that modulates a Transforming Growth Factor (TGF)-beta signaling pathway,
XX that impairs binding of a BMP to the SOST polypeptide, that impairs SOST
XX homodimer formation, or that increases bone mineral content. The novel
XX antibody and compositions have osteopathic activity. The SOST nucleic
XX acids may be used in gene therapy. The composition and methods are useful
XX for increasing bone mineralization, which may treat or prevent diseases
XX or conditions associated with low bone mineral density, such as
XX osteopenia, osteoporosis or bone fractures. This polynucleotide sequence
XX represents a rat bone morphogenic protein type I receptor encoding DNA of
XX the invention.

SQ Sequence 3167 BP; 908 A; 647 C; 688 G; 924 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 9.99e-294 Length: 3167
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
US-10-600-645-2 (1-532) x ADX97428 (1-3167)
QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleSerHis 20
DB 226 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCCTGCTGTTCATTTCTCAT 285
QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
DB 286 GTTCAGGGCAGAAATCTAGATAGTATGCTCCATGGTACTGGTATGAATCAGACGTGGAC 345
QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
DB 346 CAGAAAGACCGGAAATGGAGTGCAGTTAGCAGTACAGAGGACACCTTACCTTTCTAAAA 405
QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
DB 406 TGCTATTGCTCAGGACACTGCCAGATGACCTATTATAACACATGCATTAATATGGC 465
QY 81 HisCysPheAlaIleLeuGluAspGlnGlyGluThrThrLeuThrSerGlyCys 100
DB 466 CATTTGCTTTGCCATTATAGAAAGAGATGATCAGGGAGNAACACGTTAACTTCTGGGTGT 525
QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
DB 526 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGATTCCACAAAGCCAGCTACGCAGG 585
QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
DB 586 ACAATAGAAATGTTGTCGAGCAATTTGTGCAACCAATATTTGCAGCCTTACACTGCCCT 645
QY 141 ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
DB 646 GTCGTTATAGCCCATCTTTGATGGCAGCGTCCGATGGCTGGCTGCTCATCTCTATG 705
QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
DB 706 GCTGCTGTATTGTCGCAATGATCGTCTTCTCCAGCTGCTTCTGTACAAACATTACTGT 765
QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
DB 766 AAGAGTATCTCAAGCAGAGGTCGTTACAAACCGTACTTGGAAACAGGATGAAGCATTTAT 825
QY 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
DB 826 CCAGTAGAGAAATCCTGAAAGACCTGATTGACCACTGACAAAGCTCTGGTAGTGATCT 885
QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
DB 886 GGATTACCTTTATTTGGTTTCAGCGAACTATTGCCAAACAGATTTCAGATGGTTCGGCAGGTT 945
QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
DB 946 GGTAAAGCCCGGTATGGAGAAAGTATGATGGTAAATGGCTGGTGGTGAAGAGTGGCTGTC 1005
QY 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
DB 1006 AAGATATTTTACCTGAGAAAGCTAGCTGGTTTAGAGAAAACAGAAATCTACAGACG 1065
QY 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
DB 1066 GTGTTAATGCGTCATGAAATATATCTTGGTTTTATAGCTGCAGACATTTAAAGGCCAGCT 1125
QY 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320

Db 1126 TCCTGGACTCAGCTGTATTTGATTACTCAATTAACCATGAGAAATGGTCTCTCTATGACTTC 1185
Qy LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 1186 CTGAAATGTGCCACCTCGGACACAGAGCCCTACTCAAGTTAGCTTATTCTGCTGCCTGT 1245
Qy 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1246 GGTCTGTGCCACCTCCACACAGAAATTTATGGCAGCAAGCAAGCTGCAATTGCTCAT 1305
Qy 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
Db 1306 CGAGACCTGAAGAGCAAAAACATCTTATTAAAGAAAAATGGTAGTTGCTGTATTGCTGAC 1365
Qy 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1366 CTGGCCCTAGCTGTAAATTAACAGTGCACAAATGAAGTTGACATACCCTTTGAACACC 1425
Qy 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db 1426 AGGTTGGCCACCGGCGGTACATGGCTCCAGAGTGTCTGGCAGAGAGCTGAGTAAAAAC 1485
Qy 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTyrGluMet 440
Db 1486 CATTTCCAGCCCTACATCATGGCTGACATCTACAGCTTTTGGTTTGATCATTTGGGAGATG 1545
Qy 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1546 GCCCGTCGCTGTATTACAGAGGAATCGTGGAGGAATATCAATTACCATAATTAACAATG 1605
Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1606 GTCCCTAGTGACCCATCTTATGAAGACATCGGTGAGTCTGTGTGTGAACCTTGGCG 1665
Qy 481 ProIleValSerAsnArgTyrAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1666 CCAATGCTCTTAACCGCTGAACAGTGAATGCTTCCAGCCGCTTTTGAAGCTGATG 1725
Qy 501 SerGluCysTrpIleHisAsnProIleAsnArgLeuThrAlaLeuArgIleLysThr 520
Db 1726 TCAGATGTCTGGGCCCAATATCCAGCATCCAGACTCACAGCTTTGAGAAATCAAGAAGACG 1785
Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1786 CTCGCAAGATGTTGAATCCAGGATGTAAGATT 1821

RESULT 7

ADX97429
ID ADX97429 standard; DNA; 3167 BP.
XX
AC ADX97429;
XX
DT 05-MAY-2005 (first entry)
XX
DE Rat bone morphogenic protein type I receptor encoding DNA, SEQ ID 89.
XX
KW antibody; sclerostin; SOST; bone morphogenic protein receptor;
KW Transforming Growth Factor; osteopathic; gene therapy; bone repair;
KW osteopenia; osteoporosis; bone injury; gene; ds.
XX
OS Rattus norvegicus.
XX
FH Key Location/Qualifiers
FT CDS 226..1824
FT /*tag= a
FT /product= "Rat bone morphogenic protein type I receptor"
XX
PN W02005014650-A2.
XX
PD 17-FEB-2005.
XX
PF 15-JUN-2004; 2004WO-US018912.

XX
PR 16-JUN-2003; 2003US-0478977P.
XX (CLLT) CELLTECH R & D INC.
PA
XX Winkler DG, Shi J, Latham J;
PI
XX WPI; 2005-163219/17.
DR P-PSDB; ADX97415.
DR
XX
XX
PT New isolated antibody specific for a sclerostin polypeptide, useful for
PT increasing bone mineralization or for treating or preventing conditions
PT associated with low bone mineral density, e.g. osteoporosis or
PT osteopenia.
XX
PS Disclosure; SEQ ID NO 89; 157pp; English.
XX
CC The invention relates to a novel isolated antibody, or its antigen-
CC binding fragment, which binds specifically to a sclerostin (SOST)
CC polypeptide. The SOST polypeptide comprises any of 6 sequences having 190
CC or 213 amino acids, fully defined in the specification (ADX97341,
CC ADX97360, ADX97398, ADX97400, ADX97402 or ADX97408). The antibody
CC competitively inhibits binding of the SOST polypeptide to a bone
CC morphogenic protein (BMP) Type I Receptor binding site and a BMP Type II
CC Receptor binding site, where the BMP Type I Receptor binding site is
CC capable of binding to a BMP Type I Receptor polypeptide. The invention
CC further comprises a hybridoma cell producing the new antibody; a host
CC cell that is capable of expressing the new antibody; a composition
CC comprising the new antibody, or its antigen-binding fragment, and a
CC physiological carrier; an immunogen comprising a peptide comprising 6, 7,
CC 8, 9, 10, 11, 12, or at least 21-50 or 20-75 consecutive amino acids of
CC the SOST polypeptide; methods for producing an antibody that specifically
CC binds to the SOST polypeptide; and methods for identifying an antibody
CC that modulates a transforming growth factor (TGF)-beta signaling pathway,
CC that impairs binding of a BMP to the SOST polypeptide, that impairs SOST
CC homodimer formation, or that increases bone mineral content. The novel
CC antibody and compositions have osteopathic activity. The SOST nucleic
CC acids may be used in gene therapy. The composition and methods are useful
CC for increasing bone mineralization, which may treat or prevent diseases
CC or conditions associated with low bone mineral density, such as
CC osteopenia, osteoporosis or bone fractures. This polynucleotide sequence
CC represents a rat bone morphogenic protein type I receptor encoding DNA of
CC the invention.
XX
SQ Sequence 3167 BP; 908 A; 647 C; 688 G; 924 T; 0 U; 0 Other;

Alignment Scores:
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Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-600-645-2 (1-532) x ADX97429 (1-3167)

Qy 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleSerHis 20
Db 226 ATGACTACGCTATACACTTACATCAGATTACTGGGAGCCTGTCTGTTCATCTTCTCAT 285
Qy 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db 286 GTTCAAGGGCAGAAATCTAGATAGTAGTATGCTCCATGGTACTGGTATGAAATCAGACGTGGAC 345
Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
Db 346 CAGAGAAGCCGGAATAATGGAGTACGTTAGCACAGAGGACACCTTACCTTCTTTAAAAA 405
Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
Db 406 TGCTATTGCTCAGGACACTGCCCGCAGATGACGCTATTATTAACACATGCAATAATAATGCG 465
Qy 81 HisCysPheAlaIleIleGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100

Db ||||| 466 CATTGCTTGCCATTATAGAACAGATGATCAGGAGAAACACAGTTAACTTCTGGGTG 525
Qy ||||| 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db ||||| 526 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCAAAAAGCCAGCTACGCAGG 585
Qy ||||| 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db ||||| 586 ACAATAGAAATGTTGTCGGACCAATTTGTGCAACCAATATTTGCAGCCTACACTGCCCCCT 645
Qy ||||| 141 ValValIleGlyProPhePheAspGlySerValArgTTPLeuAlaValLeuIleSerMet 160
Db ||||| 646 GTCTGTATAGGCCCATTTCTTGATGGCAGCGTCCGATGGCTGGCTGCTCATCTCTATG 705
Qy ||||| 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrIleHisTyrCys 180
Db ||||| 706 GCTGTCTGTATTGTCGCCATGATCGTCTTCTCAGCTGCTTCTGTTTACAAACATTACTGT 765
Qy ||||| 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
Db ||||| 766 AAGAGTATCTCAAGCAGAGGTGTTTACAAACCGTGACTTGGAAACAGGATGAAGCATTTATT 825
Qy ||||| 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySer 220
Db ||||| 826 CCAGTAGGAGATCACTGAAAGACCTGATTGACCAAGTACCAAGAGCTTGGTAGTGATCT 885
Qy ||||| 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db ||||| 886 GGATTACCTTTATTGTTTCCAGCGAATATTGCAAAACAGATTTCAGATGGTTCCGCAGGTT 945
Qy ||||| 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
Db ||||| 946 GGTAAAGCCGCTATGGGAAAGTATGGATGGGTAAATGGCGTGGTGAATAAGTGGCTGTC 1005
Qy ||||| 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db ||||| 1006 AAGATATTTTTTACCCTGAAGAGCTAGCTGTTTGTAGAGAAACAGAAATCTACCAAGC 1065
Qy ||||| 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db ||||| 1066 GTGTTAATGCGTCATGAAATATATCTTGGTTTTATAGCTGCAGACATTAAGGCCACCGT 1125
Qy ||||| 301 SerTrpThrGlnLeuTyrIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db ||||| 1126 TCTCGACTCAGCTGATTGTTGATTACTGATTACCATGAAATGGGTCTCTCTATGACTTC 1185
Qy ||||| 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db ||||| 1186 CTGAATGTGCCACCTGGACACCAAGCCCTACTCAAGTTAGCTTATTCTGCTGCCCTGT 1245
Qy ||||| 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db ||||| 1246 GTCTGTGCCACCTCCACACAGAAATTTATGSCACGCAAGGCAAGCCTGCAATTCCTCAT 1305
Qy ||||| 361 ArgAspLeuLysSerIleAsnIleLeuLysLysAsnGlySerCysCysIleAlaAsp 380
Db ||||| 1306 CGAGACCTGAGAGCAAAACATCCTTATTAGAAAAATGGTGTGTTGCTGATTGCTGAC 1365
Qy ||||| 381 LeuGlyLeuAlaValIlePheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db ||||| 1366 CTGGCCCTAGCTGTGTTAAATTTCAACAGTGACACAAATGAAGTTGACATACCTTTGAACACC 1425
Qy ||||| 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db ||||| 1426 AGGGTGGGACCCAGCGGTACATGGCTCCAGAAGTGTGGACGAGAGCCTGAGTAAACAC 1485
Qy ||||| 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
Db ||||| 1486 CATTTCCAGCCCTACATATGCTGACATCTACAGCTTTGGTTTGTATCATTTGGGAGATG 1545
Qy ||||| 441 AlaArgArgCysIleThrGlyIleValGluTyrGlnLeuProTyrTrpAsnMet 460

Db ||||| 1546 GCCCGTCGCTGTATTACAGGAGGAATCGTGAGGAATATCAATTACCATATTTACAACATG 1605
Qy ||||| 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db ||||| 1606 GTGCTTAGTACCCATCTTATGAAGACATGCGTGAGGTCTGTGTGTGTAACGCTTGCGG 1665
Qy ||||| 481 ProIleValSerAsnArgTTPAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db ||||| 1666 CCAATCGTCTCTAACCGCTGGAAACAGTGAATGTCTTCGAGCGCTTTGAGCTGATG 1725
Qy ||||| 501 SerGluCysTTPAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db ||||| 1726 TCAGAACTCTGGCCCATTAATCCAGCATCCAGACTCACAGCTTTGAGAATCAAGAAGACG 1785
Qy ||||| 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db ||||| 1786 CTCGCAAGATGTTGAATCCAGGATGTAAGATT 1821
RESULT 8
AAQ66640
ID AAQ66640 standard; cDNA; 2070 BP.
XX
AC AAQ66640;
XX
XX 25-MAR-2003 (revised)
DT 20-JAN-1995 (first entry)
XX
DE Mouse Activin receptor-like kinase 3 (mALK-3) cDNA.
KW serine threonine kinases; activin receptors; Act-R; superfamily;
KW transforming growth factor; TGF; diagnostics; detection; therapy;
KW rheumatoid arthritis; glomerular nephritis; fibrosis; ss.
XX
OS Mus musculus.
XX
PH Key Location/Qualifiers
FT 5'UTR 1..216
FT /*tag= a
FT CDS 217..1815
FT /*tag= b
FT /*product= "activin receptor-like kinase 3"
FT 3'UTR 1816..2070
FT /*tag= c
XX
PN WO9411502-A2.
XX
PD 26-MAY-1994.
XX
XX 17-NOV-1993; 93WO-GB002367.
XX
PR 17-NOV-1992; 92GB-00024057.
PR 08-MAR-1993; 93GB-00004677.
PR 08-MAR-1993; 93GB-00004680.
PR 28-MAY-1993; 93GB-00011047.
PR 02-JUL-1993; 93GB-00013763.
PR 03-AUG-1993; 93GB-00016099.
PR 15-OCT-1993; 93GB-00021344.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
XX Miyazono K, Dijke P, Franzen P, Yamashita H, Heldin C;
XX
XX WPI; 1994-183503/22.
DR P-PSDB; AAR55372.
XX
XX Activin receptor-like kinase(s) with serine/threonine kinase domains -
PT have activin/TGF beta-type I receptor function and can be used in
PT diagnosis or therapy or rheumatoid arthritis, glomerular nephritis,
PT fibrosis, etc.
XX
PS Claim 21; Page 65-67; 97pp; English.
XX
XX The inventors have identified a new family of receptor kinases called

CC activin receptor-like kinases (ALK). Their discovery was based on the
 CC realisation that receptor serine/threonine kinases form a new receptor
 CC family, which may include the type II receptors for other proteins in the
 CC transforming growth factor (TGF) beta superfamily. The activin receptor
 CC type II sequences from mouse and the daf1 gene product of C.elegans have
 CC high sequence similarity and were used to design degenerate primers to
 CC clone related cDNA's (see AA06643-49). Six distinct putative receptor
 CC serine/threonine kinases (ALK 1-6, of which human ALK 1-5 are AA06634-38
 CC respectively, and the mouse ALK-1,3,4, and 6 are AA06639-42 respectively)
 CC were identified. mALK-3 was obtained from a mouse lambdaEX 10x cDNA
 CC library using hALK-3 cDNA as a probe. Two overlapping clones were
 CC identified that together covered the complete sequence of mALK-3.
 CC Products of the invention can be used in therapy, eg. to modulate
 CC conditions associated with activin or TGF beta activity. These conditions
 CC include fibrosis, eg. liver cirrhosis and pulmonary fibrosis, cancer,
 CC rheumatoid arthritis and glomeronephritis. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX

SQ Sequence 2070 BP; 592 A; 415 C; 479 G; 583 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 2.17e-292 Length: 2070
 Score: 2823.00 Matches: 526
 Percent Similarity: 99.81% Conservative: 5
 Best Local Similarity: 98.87% Mismatches: 1
 Query Match: 99.47% Indels: 0
 DB: 2 Gaps: 0

US-10-600-645-2 (1-532) x AA066640 (1-2070)

QY 1 MetThrGlnLeuTyrThrTrpIleArgLeuLeuGlyAlaCysLeuPheIleSerHis 20
 DB 217 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCCTGTCTGTTTCATCTTCTCAT 276
 QY 21 ValGlnGlyClnAsnLeuAspSerMetLeuHisGlyThrGlyMetIysSerAspValAsp 40
 DB 277 GTTCAAGGGCAGAACTTAGATAGTATGCTCCATGGCACCTGGTATGAATCAGACTTGGAC 336
 QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
 DB 337 CAGAGNAGCCAGAAATGGAGTGACTTTAGCACCCAGAGGATACCTTGGCTTTCTTAAAG 396
 QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
 DB 397 TGTATTGTCTCAGGACACTGCCCCAGATGATGCTATTATAACACATGCATCAATATGGC 456
 QY 81 HisCysPheAlaIleIleGluGluAspAsnGlnGlyGluThrThrLeuThrSerGlyCys 100
 DB 457 CATTTGCTTTGCCATTATAGAAAGATGATCAGGGAGAAACCAATTAACCTTCGGGTGT 516
 QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
 DB 517 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCGAAACCCAGCTACCGAGG 576
 QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
 DB 577 ACAATAGATGTTGTTCGGACCAATTTGTCAACACAGTATTTCAGGCTACACTGCCCTCT 636
 QY 141 ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
 DB 637 GTTGTATAGTCCGTTCTTTGATGGCAGCATCCGATGGCTGGTGTGCTCATTTTCCATG 696
 QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrIysHisTyrCys 180
 DB 697 GCTGTCTGTATAGTGTATGATCATCTTCTCAGCTGCTTTGCTATAGCAATTATGT 756
 QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
 DB 757 AAGAGTATCTCAAGCAGGGGTCTTTACACCGTGATTTTGAACAGGATGAGCAATTATT 816
 QY 201 ProValGlyClnSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySer 220
 DB 817 CCAGTAGGAGAAATCATTTAAAGACCTGATTGACCACTCCCAAGCTCTGGAGTGGATCT 876

QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
 DB 877 GGATTCCTCTTATTTGGTTTTCAGCGAATATTGCCAAACAGANTTCAGATGGTTCCGCGAGTT 936
 QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
 DB 937 GGTAAAGGCGCTTATGGAGAAGTATGCATGGGTAAATGGCTGGTGAATAAGTGGCTGTC 996
 QY 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
 DB 997 AAGTGTGTTTTTACCCTGAAAGAAGCTAGCTGGTTTAGAGAAAACAGAAATCTACACAGCG 1056
 QY 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
 DB 1057 GTGTTAATGGCTCATGAAATAATATCTGGTTTTATAGCTGCAGACATTAAGAAGCAGCTGGT 1116
 QY 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
 DB 1117 TCTGGACTCAGCTGTATTTGATTACTGATTACCATGAAATGGATCTCTCTATGACTTC 1176
 QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
 DB 1177 CTGAAATGTGCCACACTAGACACACAGAGCCCTACTCAAGTTAGCTTATTTCGGCTGCTGT 1236
 QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
 DB 1237 GGTGTGTGCACCTCCACACAGAAATTTATGTACCAAGGAGGAGCTGCAATTTGCTCAT 1296
 QY 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
 DB 1297 CGAGACCTCAGAGCAGCAAAACATCCTTTAAGAAAAATGGAAGTTGCTGTATTGCTGAC 1356
 QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
 DB 1357 CTGGGCTAGCTGTAAATTCACAGTGTATACAAATGAAAGTTGACATACCTTTGAATACC 1416
 QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
 DB 1417 AGGTTGGGACCAACAGCGGTACATGGCTCCAGAAAGTCTGGATGAAGCCTGAAATAAACA 1476
 QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
 DB 1477 CATTTCCAGCCCTACATCATGCTGACATCTATAGCTTTGTTGTTGATCATTTTGGGAAATG 1536
 QY 441 AlaArgArgCysIleThrGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
 DB 1537 GCTCGTGTGTATTACAGGAGGAATCGTGGAGGAATATCAATTTACCATATTACCAACATG 1596
 QY 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
 DB 1597 GTGCCAGTGACCCCTCTATGAGGACATCGCTGAGGTTGTGTGTGAAACCTTTGCGG 1656
 QY 481 ProfileValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
 DB 1657 CCAATCGTGTCTAACCGCTGGAACAGCGATGAATGCTTCGAGCAGCTTTTGAAGCTAATG 1716
 QY 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
 DB 1717 TCAGAAATGTTGGGCCCATAAATCCAGCTCCAGACTCACAGCTTTTGAGATCAAGAAGACA 1776
 QY 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
 DB 1777 CTTGCAAAATGGTTGAATCCCGAGGATGTAAGATT 1812

RESULT 9

AAZ09847

ID AAZ09847 standard; cDNA; 2070 BP.

XX AAZ09847;

XX 26-NOV-1999 (first entry)

XX

DE Human mALK-3 from clone ME-7 and ME-D CDNA.
 XX mALK-3; activin receptor-like kinase; therapy; activin; TGF-beta; cancer;
 KW fibrosis; liver cirrhosis; pulmonary fibrosis; glomerulonephritis; mouse;
 KW rheumatoid arthritis; detection; diagnosis; drug screening; ds.
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 217..1815
 FT /*tag= a
 FT /product= "mALK-3"
 XX
 XX WO9946386-A1.
 PN
 XX
 XX 16-SEP-1999.
 PD
 XX
 XX 12-MAR-1999; 99WO-US055735.
 PF
 XX
 XX 13-MAR-1998; 98US-00039177.
 PR
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA
 XX
 XX Miyazono K, Imamura T, Ten Dijke P;
 PI
 XX
 XX WPI; 1999-551413/46.
 DR
 XX P-PSDB; AAY33305.
 DR
 XX
 PT New isolated activin receptor-like kinases, used to develop products for
 PT treating e.g. fibrosis, cancer, rheumatoid arthritis and
 PT glomerulonephritis.
 PT
 PT
 PS Disclosure; Page 88-91; 110pp; English.
 XX
 CC This invention describes novel human and murine activin receptor-like
 CC kinases (ALK's). The novel ALK products can be used in therapy, e.g. to
 CC modulate conditions associated with activin or TGF-beta activity, such as
 CC fibrosis, e.g. liver cirrhosis and pulmonary fibrosis, cancer, rheumatoid
 CC arthritis and glomerulonephritis. The products can also be used for
 CC detection, diagnosis and drug screening. This sequence encodes the murine
 CC mALK-3 protein isolated from clones ME-7 and ME-D
 XX
 SQ Sequence 2070 BP; 592 A; 414 C; 480 G; 584 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,17e-292 Length: 2070
 Score: 2823.00 Matches: 526
 Percent Similarity: 99.81% Conservative: 5
 Best Local Similarity: 98.87% Mismatches: 1
 Query Match: 99.47% Indels: 0
 DB: 2 Gaps: 0

US-10-600-645-2 (1-532) x AAZ09847 (1-2070)

QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
 DB 217 ATGACTCAGCTATACACTTACATCAGATTACTGGGAGCCCTGTGTTCATCTTCTCAT 276
 QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetIysSerAspValAsp 40
 DB 277 GTTCAAGGGCAGAACTCTAGATAGTAGTCTCCATGGCAGCTGGTATGAAATCAGACTTGGAC 336
 QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
 DB 337 CAGAGAAGCCAGAAATGGAGTGAATTTAGCACCAGAGGATACCTTGCCTTCTCTAAAG 396
 QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
 DB 397 TGTATTGTCTCAGGACACTGCCACAGATGATGCTATTATTAACACATGACATAACTAATGGC 456
 QY 81 HisCysPheAlaIleIleGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
 DB 457 CATTGCTTTGCCATTATAGAGAAGATGATCAGGGGAGAAACCCACATTAACTTCTGGGTCT 516

QY 101 MetLysTyrGluGlySerAspPheGlnCysIysAspSerProLysAlaGlnLeuArgArg 120
 DB 517 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCCACGAAAGCCAGCTAGCGAGG 576
 QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
 DB 577 ACATATAGAAATGTTGTGGAGCCAAATTTGTGCAACCAAGTATTTGCGACCTACACTGCCCT 636
 QY 141 ValValIleGlyProPhePheAspGlySerValArgTyrPheLeuAlaValLeuIleSerMet 160
 DB 637 GTTGTATATAGTCCGTTCTTTGATGGCAGCATCCGATGGCTGGTGTGCTCATTTCCATG 696
 QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
 DB 697 GCTGTCTGTATAGTTGCTATCATCTTCTCCAGCTCTTTCGATTAAGCATTTATTGT 756
 QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
 DB 757 AAGAGTATCTCAGCAGGGGTCTGTACAACTGATTTGGAAACAGGATGAGCATTTATT 816
 QY 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
 DB 817 CCAGTAGGAGAAATCATTTGAAAGACCTGATTGACCACTCCCAAGCTCTGGAGTGGATCT 876
 QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
 DB 877 GGATTTGCCCTTTATTTGGTTTTCAGCGAACTATTCCCAACAGATTTTCAGATGGTTTCGGCAGGTT 936
 QY 241 GlyLysGlyArgTyrGlyGluValTyrMetGlyLysTyrArgGlyGlyLysValAlaVal 260
 DB 937 GGTAAAGGCCCTCTATGGAGAAAGTATGGATGGGTAAATGGCGTGTGCAAAAGTGGCTGTC 996
 QY 261 LysValPhePheThrThrGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
 DB 997 AAAGTGTGTTTTCACCACTGAAGAAGCTAGCTGGTTTAGAGAAAACAGAAATCTTACCAGACG 1056
 QY 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
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 QY 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
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 QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
 DB 1177 CTGAAATGTGCCACACACTAGACACAGAGCCCTACTCAAGTTAGCTTATTTCTGCTGCTGT 1236
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 DB 1237 GGTCTGTGCCACCTCCACACAGAAATTTATGGTACCCAGAGGAGCCCTGCAATTCGCTCAT 1296
 QY 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
 DB 1297 CGAGACCTGAAGAGCAAAACATCTTATTAAAGAAAATGGAAGTTGCTGTATTGCTGAC 1356
 QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
 DB 1357 CTGGCCCTAGCTGTATAATTCAACAGTCATACAAATGAAGTTTGACATACCTTGAATACC 1416
 QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLysSerLysAsn 420
 DB 1417 AGGTGGGCACCAACGGGTACATGGCTCCAGAAGTGTGGATGGAAGCTTGAATAAAAAC 1476
 QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleIleIleIle 440
 DB 1477 CATTTCAGCCCTACATCATGCTGACATCTATAGCTTTGGTTGGTTCATTTGGGAAATG 1536
 QY 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
 DB 1537 GCTCGTCTGTATTATACAGGAGGAATCGTGAGGAATATCAATTACCATATTTACAACATG 1596

Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
 Db 1597 GTGCCAGTACCCATCTATGAGGACATGCTGAGGTGTGTGTGTGAAACGCTTCGG 1656
 Qy 481 ProIleValSerAsnArgTTPAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
 Db 1657 CCAATCGTGTCTAACCGCTGGAACAGCGATGAATGTCTTCGAGCAGTTCCTGAAAGCTAATG 1716
 Qy 501 SerGluCysTTPAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
 Db 1717 TCAGATGTTGGGCCCAATAATCCAGCTCCAGACTCAGCGTTTGAGATCAAGACACA 1776
 Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
 Db 1777 CTTGCAAAAATGGTTGAATCCAGGATGTTAAAGATT 1812

RESULT 10

ADY51875

ID ADY51875 standard; cDNA; 2070 BP.

XX

AC ADY51875;

XX

DT 19-MAY-2005 (first entry)

XX

DE Murine ALK-3 cDNA (clones ME-7 & ME-D) Seq 13.

XX

KW gene; ss; antibody production; serine-threonine kinase receptor;
 KW activin like kinase; transforming growth factor beta; liver cirrhosis;
 KW pulmonary fibrosis; cancer; rheumatoid arthritis; glomerulonephritis;
 KW hepatocytic; antiinflammatory; respiratory-gen.; cytostatic;
 KW antirheumatic; antiarthritic; nephrotropic.

XX

OS Mus musculus.

XX

FH Key Location/Qualifiers

FT CDS 217..1815

FT /*tag= a

FT /product= "ALK-3 protein"

XX

PN US2005048607-A1.

XX

PD 03-MAR-2005.

XX

PF 19-DEC-2003; 2003US-00739413.

XX

PR 17-NOV-1992; 92GB-00024057.

XX

PR 08-MAR-1993; 93GB-00004677.

XX

PR 08-MAR-1993; 93GB-00004680.

XX

PR 28-MAY-1993; 93GB-00011047.

XX

PR 02-JUL-1993; 93GB-00013763.

XX

PR 03-AUG-1993; 91GB-00036099.

XX

PR 15-OCT-1993; 93GB-00021344.

XX

PR 17-NOV-1993; 93WO-GB002367.

XX

PR 30-OCT-1995; 95US-00436265.

XX

PR 13-MAR-1998; 98US-00039177.

XX

PR 12-MAR-1999; 99US-00267963.

XX

PA (MIYA/) MIYAZONO K.

XX

PA (IMAM/) IMAMURA T.

XX

PA (TDIG/) TEN DIJKE P.

XX

PI Miyazono K, Imamura T, Ten Dijke P;

XX

DR WPI; 2005-195280/20.

XX

DR P-PSDB; ADY51876.

CC acids and the encoded proteins thereof. Specifically, it refers to
 CC receptor kinases identified as activin receptor like kinases (Alks) that
 CC are members of the transforming growth factor beta (TGF-beta)
 CC superfamily. The present invention describes a method for identifying TGF
 CC -beta inhibitors by determining whether a substance inhibits binding of
 CC TGF-beta to Alk-1, in particular where that substance is an antibody that
 CC binds to TGF-beta or the extracellular domain of Alk-1. The proteins
 CC having specific serine/threonine receptor kinase activity can be used in
 CC therapy to modulate activin or TGF-beta activity and as such can be used
 CC to treat liver cirrhosis and pulmonary fibrosis, cancer, rheumatoid
 CC arthritis or glomerulonephritis. Accordingly, they exhibit hepatotropic,
 CC antiinflammatory, respiratory-gen, cytostatic, antirheumatic,
 CC antiarthritic and nephrotropic activities. This polynucleotide is the
 CC murine ALK cDNA sequence of the invention.
 XX

SQ Sequence 2070 BP; 592 A; 414 C; 480 G; 584 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,17e-292 Length: 2070
 Score: 2823.00 Matches: 526
 Percent Similarity: 99.81% Conservative: 5
 Best Local Similarity: 98.87% Mismatches: 1
 Query Match: 99.47% Indels: 0
 DB: 14 Gaps: 0

US-10-600-645-2 (1-532) x ADY51875 (1-2070)

Qy 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleSerHis 20
 Db 217 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCCCTGTCTGTTCATTCATTCAT 276
 Qy 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
 Db 277 GTTCAAGGGCAGAACTCTAGATAGTATGCTCCATGGCAGCTGGTATGAATCAGACTTGGAC 336
 Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
 Db 337 CAGAAGAAGCCAGAAATGGAGTGACTTTTAGCACCAGAGAGATACCTTGCCTTTCTTAAAG 396
 Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
 Db 397 TGTATTGTCTCAGGACACTGCCAGATGATGCTATTATTAACACACATGCATTAATGGC 456
 Qy 81 HisCysPheAlaIleIleGluGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
 Db 457 CATTTGCTTTGCCATTATAGAAGAAGATGATCAGGGAGAACCCACATTAACTTCGGGTGT 516
 Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
 Db 517 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCGAAAGCCAGCTACGAGG 576
 Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
 Db 577 ACAATAGAAATGTTGTGGGACCAATTTGTGCAACACAGTATTTCGAGGCTACACTGCCCCCT 636
 Qy 141 ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
 Db 637 GTTGTATAGTCCGCTCTTTGATGCGACATCCGATGGCTGGTGTGCTCATTTCCATG 696
 Qy 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
 Db 697 GCTGCTGTATAGTTGCTATGATCATCTTCTCAGCTGCTTTTGCTATAAGCATATTGT 756
 Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
 Db 757 AAGAGTATCTCAAGCAGGGGTGCTTACACCGTGATTTGGAACAGGATGAAGCATTTATT 816
 Qy 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
 Db 817 CCAGTAGGAGAAATCATTTGAAAGACCTGATTGACCAAGTCCCAAGGCTCTGGGAGTGATCT 876
 Qy 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240

Determining if a substance inhibits binding of transforming growth
 factor(TGF)-beta to Alk-1 comprises contacting a cell expressing an Alk-1
 with the substance in the presence of TGF-beta.

PS Disclosure; SEQ ID NO 13; 59pp; English.

XX This invention relates to novel serine/ threonine receptor kinase nucleic

```
Db      877  GGATTGCGCTTTATTGGTTTCAGCGAACTATTGCGAAACAGATTTCAGATGGTTTCGGCAGGTT 936
Qy      241  GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTyrPheArgGlyGluLysValAlaVal 260
Db      937  GGTAAAGGCGCTATGCGAAGATGATGGATGGGTAAATGGGTGCGTGAAGAAAGTGGCTGTC 996
Qy      261  LysValPhePheThrThrGluGluAlaSerTyrPheArgGluThrGluLeuTyrGlnThr 280
Db      997  AAAGTGTTTTTACCCTGAAGAGCTAGCTGTTTAGAGAAACAGAAATCACCAGAG 1056
Qy      281  ValLeuMetArgHisGluAsnLeuLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db      1057  GTGTTAATGCGTCATGAAATATACTTGGTTTTATAGCTGCAGACATTAAAGGCCTGGT 1116
Qy      301  SerTyrThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db      1117  TCCTGGACTCAGCTGATTTGATTTACTGATTACCATGAAATGGATCTCTATGACTTC 1176
Qy      321  LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db      1177  CTGAAATGTCCACACTACAGACCAGAGCCCTACTCAAGTTAGCTTAITCTGCTGTGT 1236
Qy      341  GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db      1237  GGTCTGTGCCACTCCACACAGAAATTTATGTACCCAGGAGGCTGCAATGCTCAT 1296
Qy      361  ArgAspLeuLysSerLysAsnIleLeuLysLysAsnGlySerCysCysIleAlaAsp 380
Db      1297  CGAGACCTGAAGAGCAAAACATCCTTATTAAAGAAAATGGAAGTTGCTGTATTGCTGAC 1356
Qy      381  LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db      1357  CTGGGCTAGCTGTGTTAAATTCACAGTGATACAAATGAAAGTTGACATCCCTTGAATACC 1416
Qy      401  ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db      1417  AGSGTGGGCACCAAGCGGTACATGGCTCCAGAAGTCTGATGAAGGCTGGAATAAAC 1476
Qy      421  HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
Db      1477  CATTTCCAGCCCTACATCATCGCTGACATCTATAGCTTTGGTTTGATCATTTGGGAAATG 1536
Qy      441  AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db      1537  GCTCGTGTGTGTTATACAGAGGAATCGTGGAGGAATATCAATTACCATATTACAACTG 1596
Qy      461  ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db      1597  GTGCCAGTGACCCATCCTATGAGGACATGCGTGAGGTTGTGTGTGTAAGCGCTTGGCG 1656
Qy      481  ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db      1657  CCAATCGTGTCTAAACCGCTGGAACAGCGATGAATGCTTCGAGCAGTTTTTGAAGCTAATG 1716
Qy      501  SerGluCysTyrAlaHisProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db      1717  TCAGAAATGTGGGCCCATTAATCCAGCCTCCAGACTCACAGCTTTGAGAATCAAGAAGACA 1776
Qy      521  LeuAlaLysMetValGluSerGlnAspValLysIle 532
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RESULT 11

```
AAQ90184
ID AAQ90184 standard; DNA; 2402 BP.
XX
AC AAQ90184;
XX
DT 25-MAR-2003 (revised)
DT 01-NOV-1995 (first entry)
XX
DE BRK-1 DNA.
XX
```

```
KW BRK-1; BMP receptor kinase protein-1; bone morphogenetic protein; ds.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
CDS 11..1609
FT /*tag= a
FT sig_peptide 11..79
FT /*tag= b
FT mat_peptide 80..1606
FT /*tag= c
XX
PN W09514778-A2.
XX
XX 01-JUN-1995.
XX
XX 23-NOV-1994; 94WO-US013534.
XX
XX 24-NOV-1993; 93US-00158735.
XX
XX (PROC ) PROCTER & GAMBLE CO.
XX
XX Cook JS, Correa PE, Koenig BB, Rosenbaum JS, Ting J;
XX
XX WPI; 1995-206935/27.
XX
XX P-PSDB; AAR74343.
XX
XX New bone morphogenetic protein receptor kinase protein - used for
XX identifying cpds. capable of binding it and for developing therapeutic
XX cpds. and detection system(s).
XX
XX Claim 3; Page 29-32; 49pp; English.
XX
XX A cDNA library prepared from NIH3T3 poly-A RNA was screened with J159 PCR
XX fragment to isolate clone BRK-1 (sequence given in AAQ90184) encoding
XX full-length BMP receptor kinase protein (AAR74343). Vectors including the
XX cDNA were used to express recombinant BRK-1 in CHO and COS-7 hosts.
XX (Updated on 25-MAR-2003 to correct FN field.)
XX
XX Sequence 2402 BP; 676 A; 482 C; 540 G; 704 T; 0 U; 0 Other;
```

Alignment Scores:

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Pred. No.: 2 71e-292 Length: 2402
Score: 2823.00 Matches: 526
Percent Similarity: 99.81% Conservative: 5
Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 2 Gaps: 0
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US-10-600-645-2 (1-532) x AAQ90184 (1-2402)

```
Qy 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
Db 11 ATGACTCAGCTATACACTTACATCAGATTCTGGAGCCTGTCTTTCATCATTTCTCAT 70
Qy 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValasp 40
Db 71 GTTCAAGGGCGAGAATCTAGATAGTAGTATGCTCCATGGCACTGGTATGAAATCAGACTTGGAC 130
Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
Db 131 CAGAAAGAGCCAGAAAATGGAGTGACTTTAGCACAGAGGATACCTTGCCTTTCTTAAG 190
Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
Db 191 TGTATTGCTCAGGACACTGCCAGATGATGCTATTATAACACATGCATACTAATGTC 250
Qy 81 HisCysPheAlaIleIleGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 251 CATTGCTTTGCCATTATAGAAGAGATGATCAGGGAGAAACACACATTAACTTCTCGGTGT 310
Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
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Db 311 ATGAAGTATGAAGCTCTGATTTTCAATGCAAGGATTCACCGAAGCCAGCTACGCAGG 370
Qy 121 ThrileGluCysCysArgThrAsnLeuCysAsnGlnThrLeuGlnProThrLeuProPro 140
Db 371 ACAATAGATGTTGTCGACCAATTTGTGCAACAGTATTTGCAAGCTTACACTGCCCCCT 430
Qy 141 ValValileGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuileSerMet 160
Db 431 GTTGTTATAGTCCGTTCTTTGATGGCAGCATCCGATGGCTGGTGTGCTCAITTTCCATG 490
Qy 161 AlaValCysileValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
Db 491 GCTGTCGTATAGTGTATGATCATCTCTCCAGCTGCTTTTCTATAAGCATTTATGT 550
Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
Db 551 AAGGTATCTCAAGCAGGGTCTGTACACCGTGATTTGGAACAGGATGAAGCATTTATT 610
Qy 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
Db 611 CCAGTAGGAGAAATCATTTGAAAGACCTGATTGACCAGTCCCAAGCTCTGGAGTGGATCT 670
Qy 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 671 GGATTCCTTTTATTGGTTTCAGCGAACTATTGCCAAACAGATTCAGATGGTTCCGCAAGTT 730
Qy 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
Db 731 GGTAAAGCCGCTATGGAGAAGTATGATGGTAAATGGCGTGTGAAAAGTGGCTGTC 790
Qy 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db 791 AAAGTGTTTTTTACCACCTGAAGAAGCTAGCTGGTTTAGAGAAACAGAAATCTACCAAGC 850
Qy 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db 851 GTGTTAATGCTCATGAAATATATCTTGGTTTTATAGCTGCAGACATTTAAAGCACTGGT 910
Qy 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 911 TCTTGACTCAGCTGTATTGATTACTGATTACCATGAAATGGATCTCTCTATGACTTC 970
Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 971 CTGAATGTCACACACTAGACACAGAGCCCTACTCAAGTTAGCTTATTCTGCTGTTGT 1030
Qy 341 GlyLeuCysHisIleHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1031 GGTCTGTGCCACCTCCACACAGAAATTTATGGTACCACAGGAAGCTGCAATGGCTCAT 1090
Qy 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
Db 1091 CGAGACTGAAGAGCAAAACATCTCTATTAAAGAAATGGAAGTGGCTGTATTGCTGAC 1150
Qy 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1151 CTGGCCCTAGCTGTAAATTCACAGTGATACAAATGAAGTTGACATACCTTGAATACC 1210
Qy 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db 1211 AGGGTGGGACCAACGGGTACATGGGTCCAGAGTGTGATGAAAGCCCTGAAATAAAAAC 1270
Qy 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
Db 1271 CATTTCCAGCCCTACATCATGGCTGACATCTATAGCTTTGGTTTGTATCATTTGGGAAATG 1330
Qy 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1331 GCTCGTGTGTATTACAGAGAGGATCGTGGAGGATATCAATTACCATATTACACATG 1390
Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1391 GTGCCAGTGACCCATCCTATGAGGACATCGGTGAGGTTGTGTGTGAAACCGTTGCGG 1450

Qy 481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1451 CCNATCGTGTCTAACCGCTGGAAACAGCATGAATGCTTCGACGAGTTTTTGAAGCTAATG 1510
Qy 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db 1511 TCAGAATGTTGGCCCAATAATCCAGCTCCAGACTCACAGCTTTGAGAATCAAGAAGACA 1570
Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1571 CTTGCCAAAAATGGTTGAATCCCAAGGATGTAAGATT 1606
RESULT 12
AAT27228
ID AAT27228 standard; cDNA; 2402 BP.
XX
AC AAT27228;
XX
DT 22-AUG-1996 (first entry)
XX
DE Bone morphogenetic protein type-I receptor kinase-1 gene.
XX
KW Mouse; bone morphogenetic protein receptor kinase-1;
KW bone morphogenetic protein receptor kinase-3; antibody; diagnostic;
KW bone disorder; osteogenic; bone morphogenetic protein-agonist;
KW drug screening; reporter gene; bone morphogenetic protein-antagonist;
KW hormone-responsive element; ds.
XX
OS Mus musculus.
XX
FH Key
CDS 11..1609
FT /*tag= a
FT /product= "Bone morphogenetic protein receptor kinase-1"
XX
PN W09614412-A2.
XX
PD 17-MAY-1996.
XX
PF 30-OCT-1995; 95WO-US014085.
XX
PR 04-NOV-1994; 94US-00334179.
XX
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Rosenbaum JS, Nohno T;
XX
DR WPI; 1996-251762/25.
DR P-PSDB; AAR96201.
XX
PT Isolated bone morphogenic protein receptor kinase protein - used to
determine if a test cpd. is capable of binding to, or is (ant)agonist of
BMP receptor kinase protein transcription.
XX
PS Example 4; Page 61-63; 87pp; English.
XX
CC The sequence encodes mouse bone morphogenetic protein (BMP) receptor type
-I kinase-1 (BRK-1), which induces cellular differentiation in response
to BMP. The gene may be inserted in plasmid pJT4, to form plasmid pJT4-
J159F, and co-expressed with a type-II BRK-3 gene to study complex
formation between the 2 receptor types. The BRK-3 receptor and antibodies
against it may be used in diagnostic assays for BMP disorders, or in
therapy to bind or scavenge BMPs. In addition, expression of the BRK-3
gene along with a reporter gene under the control of a hormone-
responsive element in a cell culture may be used to screen compounds for
BRK-agonist or -antagonist activity, by monitoring reporter gene
expression
XX
SQ Sequence 2402 BP; 676 A; 482 C; 540 G; 704 T; 0 U; 0 Other;
Alignment Scores: 2.71e-292 Length: 2402
Pred. No.:

Score: 2823.00 Matches: 526
Percent Similarity: 99.81% Conservative: 5
Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 2 Gaps: 0
US-10-600-645-2 (1-532) x AAT27228 (1-2402)
QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
DB 11 ATGACTCAGCTATACACTTACATCAGATTACTGGGAGCGTCTGTTCATCTCAT 70
QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetIleSerAspValAsp 40
DB 71 GTTCAAGGGCAGAATCTAGATAGTATGCTCCATGGCAGCTGGTATGAAATCAGACTTGGAC 130
QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
DB 131 CAGAAGAGCCAGAAATGGAGTGACTTTAGCACCAGAGGATACCTTGGCTTTCTTAAAG 190
QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
DB 191 TGTATTGTCTCAGGACACTGCCAGATGATGCTATTATTAACACATGCATACTAATGGC 250
QY 81 HisCysPheAlaIleIleGluAspGlnGlyGluThrThrLeuThrSerGlyCys 100
DB 251 CATTTGCTTTGCCATTATAGAAAGATGATCAGGGAGAAACACACTTAATCTCTGGGTGT 310
QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
DB 311 ATGAAGTATGAGGCTCTGATTTTCAATGCAAGGATTACCCAGAGCCAGCTAGCGAGG 370
QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
DB 371 ACAATAGAATGTTGTCGACCAATTTGTCAACACAGTATTTGCAGCCTACACTGCCCCCT 430
QY 141 ValValIleGlyProPhePheAspGlySerValArgTyrPheAlaValLeuIleSerMet 160
DB 431 GTTGTTATAGGTCGTTCTTGTATGGCAGCATCCGATGGCTGGTGTGCTCATTTTCCATG 490
QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
DB 491 GCTGTCTGTATAGTGTATGATCATCTTCTCAGCTGCTTTTGTCTATAGGATATTATGT 550
QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
DB 551 AAGAGTATCTCAAGCAGGGGTGTTACAACCGTGATTTTGGAAACAGGATGAAGCAATTTATT 610
QY 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerCysGlySer 220
DB 611 CCAGTAGGAGAATCATTTGAAGACCTTGATTTGACCAAGCTCCCAAGCTCTGGGAGTGGATCT 670
QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
DB 671 GAATTCCTTTATTTGTTTTCAGGAACTATTGTCGAAACAGATTTCAGATGGTTCGGCAGGTT 730
QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTyrArgGlyGluLysValAlaVal 260
DB 731 GGTAAAGGCCGCTATGGAGAAGTATGGATGGGTAAATGGCGTGGTGAAGAGTGGCTGTC 790
QY 261 LysValPhePheThrThrGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
DB 791 AAAGTGTTTTTTACCCTCAAGAAAGCTAGCTGGTTTAGAGAAACAGAAATCTTACCAGAGC 850
QY 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
DB 851 GTGTTAATCGCTCATGAAATATATCTTGGTTTTTATAGCTGCAGACATTAAGCGCACTGGT 910
QY 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
DB 911 TCTGGACTCAGCTGTATTGATTACTGATTACCATGAAATGGATCTCTCTATGACTTC 970
QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340

DB 971 CTGAAATGTGCACACTAGACACCAGACCCCTACTCAAGTTAGCTTATTCTGCTCTGT 1030
QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
DB 1031 GGTCTGTGCCACCTCCACACAGAAATTTATGTTACCCCAAGGAGCCTGCAATTGCTCAT 1090
QY 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysIleAlaAsp 380
DB 1091 CGAGACCTGGAAGAGCAGCAAAACATCTTATTAAAGAAAAATGGAAGTTGCTTATTGCTGAC 1150
QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
DB 1151 CTGGCCCTAGCTGTAAATTTCAACAGTGATCAAAATGAAGTTGACATACCTTTGAATACC 1210
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DB 1211 AGGGTGGGCACCAAGCGGTACATGGCTCCAGAAAGTGTGGATGAAAGCCTGAATAAAAC 1270
QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
DB 1271 CATTTCCAGCCCTACATCATGGCTGACATCTATAGCTTTGGTTTTCATTTGGGAAATG 1330
QY 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
DB 1331 GCTGCTGCTGTATTACAGAGGAATCTGTGAGGAATATCAATTACCATATTACAACTG 1390
QY 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValIleArgLeuArg 480
DB 1391 GTGCCCACTGACCATCTATGAGGACATCGTGAGGTTGTGTGTGTAACGCTTGGCG 1450
QY 481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
DB 1451 CCAATCGTGTCTAAACCGCTGGAACAGCGATCAATGCTTCTCGAGCAGTTTGAAGCTAATG 1510
QY 501 SerGluCysTyrAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
DB 1511 TCAGAATGTTGGGCCCATTAATCCAGCTCCAGACTCCAGCTTTGAGAATCAAGAAGACA 1570
QY 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
DB 1571 CTTGCAAAATGTTGAATCCAGGATGTAAGATT 1606
RESULT 13
AAT28021
ID AAT28021 standard; cDNA; 2402 BP.
XX
AC AAT28021;
XX 31-DEC-1996 (first entry)
DE Mouse BMP type I receptor kinase (BRK-1) cDNA.
XX
XX BMP type II receptor kinase-3; BRK-3; bone morphogenetic protein;
KW BMP type I receptor kinase; BRK-1; BMP receptor; ds.
XX
OS Mus sp.
XX
XX Key Location/Qualifiers
CDS 11..1609
FT /*tag= a
XX
XX WO9614579-A1.
XX 17-MAY-1996.
XX
PF 30-OCT-1995; 95WO-US014027.
XX
PR 04-NOV-1994; 94US-00334178.
PR 05-JUN-1995; 95US-00462467.
XX
PA (PROC) PROCTER & GAMBLE CO.
XX

PI Rosenbaum JS;
XX WPI; 1996-251887/25.
DR P-PSDB; AAR95225.
XX
XX Assays for bone morphogenetic protein activities - using complex of BMP
PT type I receptor kinase protein and BMP receptor kinase protein BRK-3.
XX
XX Claim 5; Page 64-66; 101pp; English.
XX
XX A cDNA clone (AAT28021) codes for full-length mouse bone morphogenetic
CC protein (BMP) type I receptor kinase protein-1 (BRK-1) (AAR95225), a
CC receptor capable of binding BMP and transducing a signal initiated by the
CC binding. Host cells co-transfected with vectors carrying full-length,
CC incomplete or soluble BMP type I receptor kinase protein cDNA and full-
CC length, incomplete, soluble or truncated BMP type II receptor kinase
CC protein-3 (BRK-3) cDNA (see also AAT28018-20 and AAT28022-30) express a
CC BMP receptor complex useful for screening cpds. for BMP receptor affinity
CC or for determining the concentration of a BMP receptor ligand in a
CC clinical sample
XX
SQ Sequence 2402 BP; 676 A; 482 C; 540 G; 704 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 2,71e-292 Length: 2402
Score: 2823.00 Matches: 526
Percent Similarity: 99.81% Conservative: 5
Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 2 Gaps: 0
US-10-600-645-2 (1-532) x AAT28021 (1-2402)
QY 1 MetThrClnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
DB 11 ATGACTCAGTATACACTTACATCAGATTACTGGAGCCCTGTCTGTTCATCATTTCTCAT 70
QY 21 ValGlnGlyGlnAenLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
DB 71 GTTCAAGGGCAGAAATCTAGATAGTATGCTTCATGGCAGCTGGTATGAATCAGACTTGGAC 130
QY 41 GlnLysLysProGluAenGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
DB 131 CAGAAGAAGCCAGAAATGGAGTGACTTTAGCACCAGAGGATACCTTGGCTTTCTTAAAG 190
QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAenAsnThrCysIleThrAsnGly 80
DB 191 TGCTATTTGCTCAGGACACTGCCCAGATGATGCTATTAAATAACACATGCACTAAATGGC 250
QY 81 HisCysPheAlaIleIleGluGluAspGlnGlyGluThrThrLeuThrSerGlyCys 100
DB 251 CATTGCTTTGCCATTATAGAGAAGATGATCAGGGAGAAACCATTAATCTTCGGTGT 310
QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
DB 311 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCGAAAGCCAGCTACGCAGG 370
QY 121 ThrIleGluCysCysArgThrAenLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
DB 371 ACAATAGAATGTTGTTCGGACCAATTTGTGCAACAGTATTTGCAGGCTACACTGCCCCCT 430
QY 141 ValValIleGlyProPhePheAspGlySerValArgTyrLeuAlaValLeuIleSerMet 160
DB 431 GTTGTTATAGTCCGTCCTTTGTATGGCAGCATCCGATGGCTGGTGTGCTCATTTCCATG 490
QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
DB 491 GCTGTCTGTATAGTGTGCTATGATCATCTTCTCCAGCTGCTTTTGTCTATAAGCATTTATCT 550
QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluClnAspGluAlaPheIle 200
DB 551 AAGAGTATCTCAAGAGGGGTCGTTACAACCGGTGATTTGGAAACAGGATGAAGCATTTATT 610

RESULT 14
AAV71972
ID AAV71972 standard; cDNA; 2402 BP.
XX
AC AAV71972;

QY 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
DB 611 CCAGTAGGAGAAATCATTTGAAAGACCTGATTGACCACTCCCAAGCTCTGGAGTGGATCT 670
QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
DB 671 GGATGCTCTTATTTGGTTTCAGCGAACTATTGCGCAACAGATTAGATGGTTCGGCAGGTT 730
QY 241 GlyLysGlyArgTyrGlyGluValTyrMetGlyThrTrpArgGlyGluLysValAlaVal 260
DB 731 GGTAAAGGCCCGCTATGGAGAAAGTATGGATGGGTAAATGGCGTGGTGAAGAAGTGGCTGTC 790
QY 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
DB 791 AAGTGTGTTTACCCTGAAGAAGCTAGCTGGTTAGAGAAACAGAAATCTACCAACAGC 850
QY 281 ValLeuMetArgHisGluAenIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
DB 851 GTGTTAATGGCTCATGAAATATATCTGTTTATAGCTGCAGACATTAAGGCACCTGGT 910
QY 301 SerTrpThrClnLeuTyrIleThrAspTyrHisGluAenGlySerLeuTyrAspPhe 320
DB 911 TCCTGGACTCAGCTGATTGTTGATTACCATGAAATGGATCTCTCTATGACTTC 970
QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLysLeuAlaTyrSerAlaAlaCys 340
DB 971 CTGAAATGTGCCACACTAGACACAGGCCCTACTCAAGTTAGCTTATTCTGCTGCTTGT 1030
QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
DB 1031 GGTCTGTGCCACCTCCACACAGAAATTTATGGTACCAAGGGAAGCGCTCAATTTGCTCAT 1090
QY 361 ArgAspLeuLysSerLysAsnIleLeuLysLysAsnGlySerCysCysIleAlaAsp 380
DB 1091 CGAGACCTGAGAGCAAAACATCTCTTATTAGAAAAATGGAAGTTGCTGTTATTTGCTGAC 1150
QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
DB 1151 CTGGGCTAGCTGTTTAAATTTCAACAGTGATACAAATGAAGTTGACATACCTTTGAATACC 1210
QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
DB 1211 AGGGTGGGCACCAAGCGGTACATGGCTCCAGAAAGTCTGGATGAAAGCCTGAATAAAAC 1270
QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTyrGluMet 440
DB 1271 CATTTCCAGCCCTACATCATCTGCTGACATCTATAGCTTTGGTTGTATCAATTTGGGAAATG 1330
QY 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
DB 1331 GCTGCTGTTGTATTACAGAGGAATCGTGGAGGAATATCAATTACCATATTACACATG 1390
QY 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
DB 1391 GTGCCAGTGACCCCTCTATCAGGACATGCGTGGAGTGTGTGTGTGTAACCGCTTGGCG 1450
QY 481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
DB 1451 CCAATCGTGTCTAAACCGCTGGAACAGCGATGAATGTCTTCGAGCAGTTTTTGAAGCTAATG 1510
QY 501 SerGluCysTyrAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
DB 1511 TCAGAAATGTTGGGCCCATTAATCCAGCTCCAGACTCACAGCTTTGAGATTTGAAGAAGACA 1570
QY 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
DB 1571 CTTGCAAAAATGTTGTAATCCCGAGGATGTAAGATT 1606

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XX 16-FEB-1999 (first entry)
DT
XX Mouse BMP receptor kinase protein (BRK)-1 encoding cDNA.
DE
XX Bone morphogenetic protein; BMP; BMP receptor kinase; ActRIIB receptor;
KW BRK; receptor ligand; drug; ds.
XX
XX Mus sp.
OS
XX Key Location/Qualifiers
FH 11.1609
FT /*tag= a
FT /product= "mouse BRK-1 protein"
XX
PN WO9852038-A1.
XX
XX 19-NOV-1998.
XX
XX 13-MAY-1998; 98WO-US009519.
XX
XX 16-MAY-1997; 97US-0046768P.
XX (PROC ) PROCTER & GAMBLE CO.
XX
XX Rosenbaum JS;
PI
XX
XX WPI; 1999-009930/01.
DR P-PSDB; AAW86248.
XX
XX Screening method using bone morphogenetic protein receptor complex -
PT which binds to potential drugs, and ActRIIB receptor used in the complex,
PT also host cells transfected with DNA encoding the complex.
XX
XX Claim 2; Page 88-91; 110pp; English.
XX
XX This cDNA encodes a mouse BMP receptor kinase protein (BRK)-1. This can
CC be used in the method of the invention of determining whether a compound
CC can bind to a bone morphogenetic protein (BMP) receptor kinase protein
CC complex. The method comprises allowing a compound in a sample to bind to
CC the complex, where the complex is comprised of (i) a BMP; (ii) a BRK
CC protein; (iii) an ActRIIB receptor. The method can be used to determine
CC the concentration of a BMP receptor ligand in a sample by comparing the
CC binding to a standard curve prepared with known concentrations of BMP
CC ligand. The method can also be used to determine whether a test compound
CC produces a signal on binding to a BMP receptor protein complex. The
CC method is useful for determining whether a ligand, such as a known or
CC putative drug, can bind to and/or activate the receptors
XX
SQ Sequence 2402 BP; 676 A; 482 C; 540 G; 704 T; 0 U; 0 Other;

```

```

Alignment Scores:
Pred. No.: 2,71e-292 Length: 2402
Score: 2823.00 Matches: 526
Percent Similarity: 99.81% Conservative: 5
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Query Match: 99.47% Indels: 0
DB: 2 Gaps: 0

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US-10-600-645-2 (1-532) x AAV71972 (1-2402)

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QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleSerHis 20
DB 11 ATGACTCAGCTATACACTTACATCAGATTACTGGGAGCGCTGCTGTTTCATCTTCAT 70
QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
DB 71 GTTCAAGGCGAAGTCTAGATAGTAGTCCATGGCAGCTGGTATGAAATCAGACTTGGAC 130
QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
DB 131 CAGAGAAGCCAGAAATGGAGTACTTTAGCACCAGAGGATACCTTGCCTTCTTAAAG 190

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QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
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QY 81 HisCysPheAlaIleIleGluGluAspGlnGlyGluThrThrLeuThrSerGlyCys 100
DB 251 CATGCTTTGCTATATAGAGAGATGATCAGGGAGAAACCCACATTAACTTCGGGTGT 310
QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
DB 311 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCAACGAAAGCCAGCTAGCAGG 370
QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
DB 371 ACAATAGAAATGTTGCGAGCAAAATTTGCAACCAAGTATTTGCAGCCCTACACTGCCCT 430
QY 141 ValValIleGlyProPhePheAspGlySerValArgTyrPheLeuAlaValIleSerMet 160
DB 431 GTTGTATAGTCCGTTCTTTGATGGCAGCATCCGATGGCTGGTGTGCTCATTTCCATG 490
QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
DB 491 GCTGCTCTATAGTTGCTATGATCATCTTCTCCAGCTGCTTTTGTCTATAAGCATATTCT 550
QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
DB 551 AAGAGTATCTCAAGCAGGGGTCGTTTACAACCGTGATTTGGAAACAGGATGAAGCATTTAT 610
QY 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
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QY 221 GlyLeuProLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
DB 671 GGATTCCTTTATGTTTTCAGCGAACTATTGCCAAACAGATTTCAGATGGTTCGGCAGGTT 730
QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
DB 731 GGTAAAGCCCTATGGAGAAAGTATGGATGGTAAATGGCGTGGTGAAGAGTGGCTGTC 790
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Db	1311	GGTCTGTGCCACCTCCACACAGAAATTTATGTTAGTACCCACAGGAAGCTGCAATTGCTCAT	1370
Qy	361	ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp	380
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Qy	401	ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn	420
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Qy	511	ArgLeuThrAlaLeuArgIleLysLysThrLeuAlaLysMetValGluSerGlnAspVal	530
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Qy	531	LysIle	532
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Job time : 662 secs

GenCore version 5.1.1.6
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Run on: December 9, 2005, 19:34:50 ; Search time 203 Seconds
(without alignments)
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Ygapop 10.0 , Ygapext 0.5
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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	2823	99.5	2070	3	US-09-395-115-13
6	2823	99.5	2070	3	US-08-436-265-13
7	2823	99.5	2070	3	US-09-679-187-13
8	2823	99.5	2070	3	US-09-267-963D-13
9	2823	99.5	2402	3	US-08-462-467B-11

10	2823	99.5	2402	3	US-08-158-735A-3	Sequence 3, Appli
11	2823	99.5	2402	3	US-08-334-179A-11	Sequence 11, Appl
12	2798	98.6	2056	3	US-08-158-735A-1	Sequence 1, Appl
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17	2769	97.6	2932	3	US-09-679-187-5	Sequence 5, Appli
18	2769	97.6	2932	3	US-08-448-371A-5	Sequence 5, Appli
19	2769	97.6	2932	3	US-09-267-963D-5	Sequence 5, Appli
20	2769	97.6	2932	3	US-09-949-016-604	Sequence 604, App
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26	1942	68.4	1952	3	US-09-382-256-17	Sequence 17, Appl
27	1942	68.4	1952	3	US-09-395-115-17	Sequence 17, Appl
28	1942	68.4	1952	3	US-08-436-265-17	Sequence 17, Appl
29	1942	68.4	1952	3	US-09-679-187-17	Sequence 17, Appl
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42	1268	44.7	2227	3	US-09-949-016-3895	Sequence 3895, Ap
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44	1268	44.7	2308	3	US-09-395-115-9	Sequence 9, Appli
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ALIGNMENTS

RESULT 1
US-08-123-934A-1
; Sequence 1, Application US/08123934A
; Patent No. 6291206
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; APPLICANT: CELESTE, Anthony J.
; APPLICANT: THIES, R. Scott
; APPLICANT: YAMAJI, No. 6291206oru
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute Inc. - Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,934A
; FILING DATE: 17-SEP-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 876 1170

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; TELEFAX: 617 876 5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: CFK1-23a
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 61..1656
US-08-123-934A-1

Alignment Scores:
Pred. No.: 1
Score: 1.28e-317 Length: 1813
Matches: 2838.00
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US-10-600-645-2 (1-532) x US-08-123-934A-1 (1-1813)

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QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLysSerLysAsn 420
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RESULT 2

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; Patent No. 6610513
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; CELESTE, Anthony J.
; THIES, R. Scott
; YAMAJI, No. 6610513oru
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute Inc.- Legal Affairs
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STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/874,628
FILING DATE: 05-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,934
FILING DATE: 17-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5203
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 876 1170
TELEFAX: 617 876 5851

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1813 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

IMMEDIATE SOURCE:

CLONE: CPM1-23a

NAME/KEY: CDS

LOCATION: 61..1656

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-874-628-1

Alignment Scores:

Pred. No.:	1.28e-317	Length:	1813
Score:	2838.00	Matches:	532
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

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QY	21	ValGlnGlyClnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValasp	40
DB	121	GTTCAAGGGCAGAACTAGATAGTATGCTCCATGGTACTGTTATGAAATCAGACGTTGGAC	180
QY	41	GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys	60
DB	181	CAGAAGAAGCCGGAATGGAGTGACGTTAGCACCCAGAGGACACCTTACCTTTCTTAA	240
QY	61	CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly	80
DB	241	TGCTATTGCTCAGACACATGCCAGATGACGCTATTAAATACACATGATCACTAATG	300
QY	81	HisCysPheAlaIleIleGluGluAspGlnGlyThrThrLeuThrSerGlyCys	100
DB	301	CATTGCTTTGCCATTATAGAAGAAGATGATCAGGAGAAACACCGTTTAACTTCTGG	360
QY	101	MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg	120
DB	361	ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTACCAAAAGCCAGCTACGAG	420

QY	121	ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro	140
DB	421	ACAATAGATGTTGTCGACCAATTTGTGCAACCAATATTTGCAGCCTACACTGCCCT	480
QY	141	ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet	160
DB	481	GTGCTTATAGGCCCATTTCTTTGATGCGCAGCGTCGATGGCTGGCTGCTCATCTCTAT	540
QY	161	AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys	180
DB	541	GCTGTCTGTATTGTGCGCATGATCGTCTTCTCAGCTGCTTCTGTTACAAACATTACT	600
QY	181	LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle	200
DB	601	AAGAGTATCTCAAGCAGAGGTCGTACAAACCGTGACTTGGACAGGATGAAGCATTTAT	660
QY	201	ProValGlyClnSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer	220
DB	661	CCAGTAGGAGAACTCACTGAAAGACCTGATTGACAGTCAAAAGCTCTGGTAGTGATCT	720
QY	221	GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal	240
DB	721	GGATTACCTTTTATGGTTGAGCAACTATTGCCAAACAGATTGAGTGGTTCGCGAGCT	780
QY	241	GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal	260
DB	781	GGTAAGGGCGGTATCGAGAAGTATCGATGGGTAAATGGCTGGTGAANAAGTGGCTGTC	840
QY	261	LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr	280
DB	841	AAAGTATTTTACCACCTGAAGAAGCTAGCTGGTTTAGAGAAACAGAAATCTACACAGC	900
QY	281	ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly	300
DB	901	GTGTTAATGCTCATGAAATATATCTGGTTTTATAGTCGACAGACATTAAGGACCGGT	960
QY	301	SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe	320
DB	961	TCCTGGACTCAGCTGATTGTTGATTACTGATTACCATGAGATGGGTCTCTCTATGACTTC	1020
QY	321	LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys	340
DB	1021	CTGAAATGTGCCACCTCGACACCCAGAGCCCTACTCAAGTTAGTATTCTGCTGCTGCT	1080
QY	341	GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis	360
DB	1081	GGTCTGTGCCACCTCCACACAGAAATTTATGGCAGCAAGGCAAGGCTGCAATTTGCTCAT	1140
QY	361	ArgAspLeuLysSerLysAsnIleLeuLysLysAsnGlySerCysCysIleAlaAsp	380
DB	1141	CGAGACCTGAGAGCAGCAAAACATCTTATTAGAAAAATGGTAGTTGCTGTTATGCTGAC	1200
QY	381	LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr	400
DB	1201	CTGGGCTAGCTGTTAAATTTCAACAGTGACACAAATGAAGTTGACATACCTTTGAACACC	1260
QY	401	ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn	420
DB	1261	AGGGTGGGCGCCAGCGGTTACATGGCTCCAGAAGTCTCGAGAGAGCCCTGAGTAAAC	1320
QY	421	HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet	440
DB	1321	CATTTCAGCCCTACATCATGCTGCATCTACAGCTTTGGTTTGTATCATTTTGGGAGATG	1380
QY	441	AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet	460
DB	1381	GCCCGCTCGTGTATTACAGAGGAATCGTGGAGGAATCAATTAACATATTACAACATG	1440
QY	461	ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg	480
DB	1441	GTGCTAGTAGCCCATCTTTATGAAGACATGCGGTGAGTCTGCTGTGTAAGCGCTTGGC	1500
QY	481	ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet	500

Db 1501 CCAATGCTCTTAACCGCTGGACAGTGAATGCTTCGAGCCGCTTTGAAGCTGATG 1560
QY 501 SerGluCysTyrAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db 1561 TCAGAAATGCTGGGCCCAATAATCCAGCATCCAGACTCCAGCTTTGAGAAATCAAGAAGACG 1620
QY 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1621 CTCGAAAGATGTTGAATCCAGGATGTAAGATT 1656

RESULT 3

PCT-US94-10080-1
; Sequence 1, Application PC/TUS9410080
; GENERAL INFORMATION:
; APPLICANT: GENETICS INSTITUTE, INC.
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute Inc. - Legal Affairs
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10080
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,934
; FILING DATE: 17-SEP-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, Steven R
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5203-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8260
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: CFK1-23a
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 61..1656
PCT-US94-10080-1

Alignment Scores:

Pred. No.:	1,28e-317	Length:	1813
Score:	2838.00	Matches:	532
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-600-645-2 (1-532) x PCT-US94-10080-1 (1-1813)

QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuGlyAlaCysLeuPheIleIleSerHis 20
Db 61 ATGACTCAGCTATACACTTACATCAGATTACTGGGAGCCGCTGCTGTTCATCATTTCTCAT 120

QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db 121 GTTCAAGGCGCAGAAATCTAGATAGTATGCTCTCCATGTGTTGAAATCAGACGCGGAC 180
QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
Db 181 CAGAGAAGCCGCAAAATGGAGTACGTTAGCACCAGAGGACACCTTACCTTTCTTAAA 240
QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
Db 241 TGTATTGCTCAGGACACTGCCAGATGACGCTATTATAACACATGATGATGATGATGATG 300
QY 81 HisCysPheAlaIleLeuGluAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 301 CATTCCTTTGCCATTATAGAAAGATGATCAGGAGAAACACCGTTAACTTCTGCGGTG 360
QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 361 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCAAAAGCCAGCTACGACG 420
QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 421 ACAATAGAAATGTTGCGGACCAATTTGTCAACCAATATTTGCAGCCTACACTGCCCC 480
QY 141 ValValIleGlyProPheAspGlySerValArgTyrLeuAlaValLeuIleSerMet 160
Db 481 GTCGTTATAGGCCCAATCTTTGATGGCAGCGTCCGATGGCTGGCTGCTCATCTATG 540
QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrIleHisTyrCys 180
Db 541 GCTGCTGTATTTGTCGCCATGATCGCTTCTCCAGCTGCTTCTGTACAAAACATTACTGT 600
QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
Db 601 AAGAGTATCTCAAGCAGAGGTCGTTACAAACGTCGCTTGGAAACAGGATGAAGCATTT 660
QY 201 ProValGlyGluSerLeuLysAspLeuLeuAspGlnSerGlnSerSerGlySerGlySer 220
Db 661 CCAGTAGGAGAAATCACTGAAAGACCTGATTGACCAGTCAAAAGCTCTGGTAGTGATCT 720
QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 721 GGATTACCTTTATTTGTTTTCAGGAACTATTTGCCAAACAGATTTCAGTGGTTCGGCAG 780
QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTyrArgGlyGluLysValAlaVal 260
Db 781 GGTAAAGGCGCGTATGGAGAAAGTATGGATGGTAAATGGCGTGTGTAAGGAGTGGCTGC 840
QY 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db 841 AAAGTATTTTTCACCACTGAAAGAGCTAGCTGGTTTAGAGAAACAGAAATCTACCAGCG 900
QY 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db 901 GTGTTAATGCGTCATGAAATAATATCTGTTTTATAGCTGTCAGACATTTAAAGGCCCG 960
QY 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 961 TCCTGGACTCAGCTGATTGATTACTGATTACCATGAGATGGGTCTCTCTATGACTTC 1020
QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 1021 CTGAAATGTGCCACCTGGACACCGACCCCTACTCAAGTTAGCTTATTCTCTGCGCTGT 1080
QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1081 GGTCTGTGCCACCTCCACAGAAATTTATGGCAGCAAGGACGCTGCAATTTGCTCAT 1140
QY 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
Db 1141 CGAGACCTGAAGAGAGCAAAACATCTTTATTAAGAAAAATGGTAGTTGCTGTTATGCTGAC 1200
QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400

Db 1201 CTGGCCCTAGCTGTAAATTCAACAGTGCACAAATGAAGTTGACATACCTTTGAACACC 1260

Qy 401 ArgValGlyThrArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420

Db 1261 AGGTGGCCACCGCGTACATGGCTCCAGAGTGTGGACGAGACCTGAGTAAAC 1320

Qy 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTyrGluMet 440

Db 1321 CATTTCCAGCCCTACATCATGGCTGACATCTACAGCTTTGGTTTGATCATTTGGGAGATG 1380

Qy 441 AlaArgArgCysIleThrGlyGlyValValGluGluTyrGlnLeuProTyrTyrAsnMet 460

Db 1381 GCCCGTGCCTGTATTACAGGAGGAATCGTGGAGGAATATCAATTTACCATATTCAACATG 1440

Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480

Db 1441 GTCCCTAGTAGCCCATCTTATGAAGACATGCGTGAGGTGCTGTGTGAACCGCTTGGCG 1500

Qy 481 ProIleValSerAsnArgTyrAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500

Db 1501 CCAATCGTCTCTAACCGCTGAACAGTGTGATGATGCTTCGAGCGCTTTGAAGCTGATG 1560

Qy 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520

Db 1561 TCAGATGCTGGGCCCAATAATCCAGCATCCAGACTCCAGACTTGAGACTTGAAGAGACG 1620

Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532

Db 1621 CTCGCAAGATGTTGAATCCAGGATGTAAGATT 1656

RESULT 4

US-09-382-256-13

Sequence 13, Application US/09382256A

Patent No. 6207814

GENERAL INFORMATION:

APPLICANT: MIYAZONO, Kohei

TEN DIJKE, Peter

FRANZEN, Petra

YAMASHITA, Hidetoshi

HELDIN, Carl-Henrik

TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS

HAVING SERINE THREONINE KINASE DOMAINS,

AND THEIR USE

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fulbright & Jaworski L.L.P.

STREET: 666 Fifth Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10103

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/382,256A

FILING DATE: 24-Aug-1999

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB93/02367

FILING DATE: No. 6207814ember 17, 1993

APPLICATION NUMBER: GB 9224057.1

FILING DATE: No. 6207814ember 17, 1992

APPLICATION NUMBER: GB 9304677.9

FILING DATE: March 8, 1993

APPLICATION NUMBER: GB 9304680.3

FILING DATE: March 8, 1993

APPLICATION NUMBER: 9311047.6

FILING DATE: May 28, 1993

APPLICATION NUMBER: 9313763.6

FILING DATE: July 2, 1993

APPLICATION NUMBER: 9316099.2

FILING DATE: August 3, 1993

APPLICATION NUMBER: 321344.5

FILING DATE: October 15, 1993

ATTORNEY/AGENT INFORMATION:

NAME: No. 6207814man D. Hanson

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5298.1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 318-3000

TELEFAX: (212) 752-5958

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 2070 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ANTI-SENSE: NO

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

ORGANISM: Mouse

FEATURE:

NAME/KEY: CDS

LOCATION: 217..1812

SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-382-256-13

Alignment Scores:

Pred. No.: 1,2e-315

Score: 2823.00

Percent Similarity: 99.81%

Best Local Similarity: 98.87%

Query Match: 99.47%

DB: 3

Length: 2070

Matches: 526

Conservative: 1

Mismatches: 5

Indels: 0

Gaps: 0

US-10-600-645-2 (1-532) x US-09-382-256-13 (1-2070)

Qy 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleSerHis 20

Db 217 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCCCTGCTGTTTCATCTTCAT 276

Qy 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrClyMetLysSerAspValAsp 40

Db 277 GTTCAAGGGCAGAACTAGATAGTCTCCATGGCAGCTGGTATGAATCAGACTTGGAC 336

Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60

Db 337 CAGAAGAGCCAGAAATGGAGTGACTTTAGCACAGAGAGATACCTTGCCTTTCTTAAG 396

Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80

Db 397 TGCTATTGCTCAGGACACTGCCAGATGATGCTATTATAAACACATGCACTAATATGGC 456

Qy 81 HisCysPheAlaIleIleGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100

Db 457 CATTTGCTTTGCCATTATGAAGAAGATGATCAGGGAGAAACCCACATTAACTTTGGGTGT 516

Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120

Db 517 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCGAAGCCAGCTACGAGG 576

Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrIleLeuGlnProThrLeuProPro 140

Db 577 ACAATAGAATGTTGTCCGACCAATTTGTGCAACACAGTATTTGCGAGCTACACATGCCCCCT 636

Qy 141 ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValIleSerMet 160

Db 637 GTTGTATAGGTCCTGTTTGTATGTCAGCATCCGATGGCTGGTGTGCTCATTTCCATG 696

Qy 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180

Db 697 GCTGCTCTGATAGTCTGCTATGATCATCTCTCCAGCTGCTTTGCTATAGCATATTGT 756
QY LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
Db 757 AAGAGTATCTCAAGCAGGGGTGCTTACAAACCGTGATTTGGAAACAGGATCAAGCATTTATT 816
QY ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
Db 817 CCAGTAGGAGAAATCATTTGAAAGACCTGATTCAGACAGTCCCAAGCTCTGGGAGTGATCT 876
QY GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 877 GGATTCGCTTTATGTTGTCAGCGAACTATTGCCAAACAGATTGATGGTTGGCAGGTT 936
QY GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
Db 937 GGTAAAGGCCGCTATGGAGAAGTATGGATGGGTAAATGGGTGCGTGAAGGCTGTC 996
QY LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db 997 AAGTGTGTTTTTACCACCTGAAGAAGCTAGCTGGTTTAGAGAAACAGAAATCTACCAGACG 1056
QY ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db 1057 GTGTTAATGCGTCATGAAATATATCTTGTTTTATAGCTGCAGACATTAAAGCACTGTT 1116
QY SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 1117 TCCTGGACTCAGCTGATTTGATTGATTACTGATTACCATGAAATGGATCTCTCTATGACTTC 1176
QY LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 1177 CTGAAATGTGCCACACTAGACACAGAGCCCTACTCAAGTTAGCTTTATTCTGCTGCTGT 1236
QY GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1237 GGTCTGTGCACCTCCACACAGAAATTTATGTACCAGGGAAGCTCGAAATGCTCAT 1296
QY ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysIleAlaAsp 380
Db 1297 CGAGACCTGAAGAGCAAAACATCCCTATTAAAGAAAAATGGAAGTTGCTGTATTGCTGAC 1356
QY LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1357 CTGGGCTAGCTGTTAAATTCACACGTGATACAAATGAAAGTTGACATACCCTTGAATACC 1416
QY ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db 1417 AGGTTGGGCACCAGCGGTACATGGCTCCAGAAAGTCTGGATGAAAGCCTGAATAAAAC 1476
QY HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
Db 1477 CATTTCCAGCCCTACATCATGGCTGACATCATAGCTTTGGTTTGATCATTTGGGAAATG 1536
QY AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1537 GCTCGTGTGTATTACAGAGGAATCGTGGAGGAATATCAATTACATATTACACATG 1596
QY ValProSerAspProSerTyrGluAspMetAtqGluValValCysValLysArgLeuArg 480
Db 1597 GTGCCAGTGACCCATCTTATAGGACATCGGTGAGGTTGTGTGTGGAACGCTTGGCG 1656
QY ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1657 CCAATCGTGTCTAACCGCTGGACAGCGATGAATGCTTCGAGCACTTTTGAAGCTAATG 1716
QY SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db 1717 TCAGAATGTTGGGCCCATATATCCAGCCTCCAGACTCCAGACTTTGAGAAATCAAGAAGACA 1776
QY LeuAlaLysMetValGluSerGlnAspValLysIle 532

Db 1777 CTTGCCAAAATGGTTGAATCCCGAGTGTAAAGATT 1812
RESULT 5
US-09-395-115-13
; Sequence 13, Application US/09395115
; Patent No. 6271365
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
; APPLICANT: Fransen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/395,115
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,265
; FILING DATE: 30-October-1995
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: 17-No. 6271365ember-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9224057.1
; FILING DATE: 17-No. 6271365ember-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304677.9
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304680.3
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9311047.6
; FILING DATE: 28-May-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9313763.6
; FILING DATE: 2-July-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9136099.2
; FILING DATE: 3-August-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9321344.5
; FILING DATE: 15-October-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohlei, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2070 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; FEATURE:

NAME/KEY: CDS
LOCATION: 217..1812
US-09-395-115-13

Alignment Scores:

Pred. No.: 1,26-315 Length: 2070
Score: 2823.00 Matches: 526
Percent Similarity: 99.81% Conservative: 5
Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 3 Gaps: 0

US-10-600-645-2 (1-532) x US-09-395-115-13 (1-2070)

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QY 1 MetThrGlnLeuTyrThrIleArgLeuLeuGlyAlaCysLeuPheIleSerHis 20
DB 217 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCCCTGCTGTTTCATCTTCAT 276
QY 21 ValGlnGlnAenLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
DB 277 GTTCAAGGGCAGAAATCAGATGATGCTCCATGGCACTGGTATGAATCAGACTTGGAC 336
QY 41 GlnLysLysProGluAenGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
DB 337 CAGAAGAAGCCAGAAATGGAGTGACTTTAGCACCAGAGGATACCTTGGCCTTCTTAAAG 396
QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAenAenThrCysIleThrAsnGly 80
DB 397 TGCTATTGCTCAGGACACTGCCAGATGATGCTTAATAACACATGCACTAACTAATGGC 456
QY 81 HisCysPheAlaIleIleGluGluAspGlnGlyGluThrThrLeuThrSerGlyCys 100
DB 457 CATTTGCTTTGCCATTATAGAAGAGATGATCAGGAGAAACCACTTAATCTCTGGGTGT 516
QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
DB 517 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCGAAAGCCAGCTACGCAGG 576
QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
DB 577 ACAATAGATGTTGTCGGACCAATTTGTGCAACAGATATTTGCGAGCCCTACACTGCCCCCT 636
QY 141 ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
DB 637 GTTGTATAGTTCGTTCTTTGATGGCAGCATCCGATGGCTGGTGTGCTCAITTTCCATG 696
QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
DB 697 GCTGTCTGTATAGTTGCTATGATCATCTTCTCAGCTGCTTTTGTCTATAAGCATTTATGT 756
QY 181 LysSerIleSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
DB 757 AAGAGTATCTCAGCAGGGGTGCTTACACCGGATTTGGAACAGGATGAAGCATTTATT 816
QY 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
DB 817 CCAGTAGGAGAAATCATTGAAGACCTGATTGACCACTCCCAAGACTCTGGAGTGGATCT 876
QY 221 GlyLeuProLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
DB 877 GGATTGCTTTATTGTTTTCAGCAACTATTGCCAAACAGATTCAGATGGTTCCGCGAGTT 936
QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
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QY 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
DB 997 AAGTGTGTTTTTACCCTGGAAGAGCTAGCTGTTTAGAGAAACAGAAATCTACACAGC 1056
QY 281 ValLeuMetArgHisGluAenIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
DB 1057 GTGTTAATGCTCATGAAAAATATACTTGGTTTTTATAGCTGCAGACATTAAGGCACTGGT 1116
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QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
DB 1177 CTGAAATGTGCCACACTAGACACAGAGCCCTACTCAAGTTAGCTTATTTCTGCTGCTGT 1236
QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
DB 1237 GGTCTGTGCCACCTCCACACAGAAATTTATGGTATGCCAAGGAGCCCTGCAATTTGCTCAT 1296
QY 361 ArgAspLeuLysSerLysAenIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
DB 1297 CGAGACTGGAAGAGCAAAACATCTTATTAGAAAAAATGGAAGTTGCTGTATTGCTGAC 1356
QY 381 LeuGlyLeuAlaValLysPheAenSerAspThrAsnGluValAspIleProLeuAsnThr 400
DB 1357 CTGGGCTAGCTGTAAATTTCAACAGTGATACAAATGAAAGTTGACATACCTTGAATACC 1416
QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
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QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
DB 1477 CATTTCCAGCCCTACATCATGGCTGACATCTATAGCTTTGGTTGATCATTTGGGAANT 1536
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QY 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
DB 1597 GTGCCAGTGACCCATCTCTATGAGGACATCGCTGAGGTTGTGTGTGTGAACCGCTTCGG 1656
QY 481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
DB 1657 CCANTCGTGTCTNACCGCTGGAAACAGCATGAATGCTTCGAGCAGTTTTTGAAGCTAATG 1716
QY 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
DB 1717 TCAGATGTTGGGCCCATTAATCCAGCTCCAGACTCCAGCTTTGAGATCAAGAGACA 1776
QY 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
DB 1777 CTTGCAAAAATGGTTGAATCCCGAGGATGTAAGATT 1812
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RESULT 6

US-08-436-265-13
Sequence 13, Application US/08436265
Patent No. 6316217

GENERAL INFORMATION:

APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins And Their Use
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: 17-NO. 6316217ember-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9224057.1
; FILING DATE: 17-NO. 6316217ember-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304677.9
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304680.3
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9311047.6
; FILING DATE: 28-May-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9313763.6
; FILING DATE: 2-July-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9136099.2
; FILING DATE: 3-August-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9321344.5
; FILING DATE: 15-October-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohlei, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2070 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 217..1812
; US-08-436-265-13

Alignment Scores:
Pred. No.: 1.2e-315 Length: 2070
Score: 2823.00 Matches: 526
Percent Similarity: 99.81% Conservative: 5
Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 3 Gaps: 0

US-10-600-645-2 (1-532) x US-08-436-265-13 (1-2070)

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DB 217 ATGACTCAGCTATACACTTACATCAGATTACTGGGAGCCTGCTGTTCATCATTTCTCAT 276
QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
DB 277 GTTCAAGGCGAGAACTAGATAGTATGCTCCATGGCAGCTGGTATGAAATCAGACTTGGAC 336
QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
DB 337 CAGAGAAGCCAGAAATCGAGTACTTTAGCACCAGAGGATACCTTGCCTTTCTTAAAG 396
QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
DB 1477 CATTTCCAGCCCTACATCATGGTCACATCTATACCTTTGGTTTGCATCATTTGGGAAATG 1536
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QY 81 HisCysPheAlaIleIleGluAspAspGlnGlyThrThrLeuThrSerGlyCys 100
DB 457 CATTCCTTTGCCATTATAGAAGAGATGATCAGGGAGAAACCCACATTAACTTCTGGGTGT 516
QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArg 120
DB 517 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCGAAAGCCAGCTAGCAGG 576
QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
DB 577 ACAATAGAAATGTTGTCGACCAATTTGTGCAACAGATATTTGCAGCCTACACTGCCCT 636
QY 141 ValValIleGlyProPhePheAspGlySerValArgTyrLeuAlaValLeuIleSerMet 160
DB 637 GTTGTATAGGTCCGTTCTTGTATGGCAGCATCCGATGGCTGGTGTGTCTCATTTCCATG 696
QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrIleHisTyrCys 180
DB 697 GCTGTCTGTATAGTTGCTATATCATCTTCTCCAGCTGCTTTTGTATTAAGCATATTGT 756
QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspAlaPheIle 200
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DB 817 CCAGTAGGAGAATCATTTGAAAGACCTGATTGACCAGTCCCAAGCTCTGGGAGTGGATCT 876
QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
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DB 1357 CTGGCCCTAGCTGTTAAATTCACACAGTGATACAAATGAAGTTGACATACCTTGAATACC 1416
QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
DB 1417 AGGGTGGGCACCAACCGGTACATGGCTCCAGAAGTGGCTGGATGAAGCCCTGAATAAAAAC 1476
QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTyrPheGluMet 440
DB 1477 CATTTCCAGCCCTACATCATGGTCACATCTATACCTTTGGTTTGCATCATTTGGGAAATG 1536

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Qy 481 ProfileValSerAsnArgTTPAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1657 CCAATCGTGCTAACCCCTGGAACAGCGATGAATGTCTTCGAGCAGTTTGAAGCTAATG 1716
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Db 1717 TCAGATGTTGGGCCCCATAATCCAGCTCCAGCTCCAGCTTCAGACTTCAGACTTTGAGACAC 1776
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Db 1777 CTTGCAAAAATGGTTGAATCCAGGATGTTAAAGATT 1812

RESULT 7
US-09-679-187-13
; Sequence 13, Application US/09679187
; Patent No. 6331621
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohsei, Dijke, Peter Ten;
; APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
; TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/679,187
; FILING DATE: 03-OCT-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,265
; FILING DATE: 30-October-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: 17-No. 6331621ember-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9224057.1
; FILING DATE: 17-No. 6331621ember-1992
; APPLICATION DATA:
; APPLICATION NUMBER: 9304677.9
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304680.3
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9311047.6
; FILING DATE: 28-May-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9313763.6
; FILING DATE: 2-July-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9136099.2
; FILING DATE: 3-August-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9321344.5
; FILING DATE: 15-October-1993
; ATTORNEY/AGENT INFORMATION:
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; NAME: Kohlei, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-3200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2070 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 217..1812
; US-09-679-187-13

Alignment Scores:
Pred. No.: 1,2e-315 Length: 2070
Score: 2823.00 Matches: 526
Percent Similarity: 99.81% Conservative: 5
Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 3 Gaps: 0

US-10-600-645-2 (1-532) x US-09-679-187-13 (1-2070)

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Db 277 GTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGGCAGCTGGTATGAATCAGACTTGGAC 336
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Db 337 CAGAAGAAGCCAGAAATGGAGTGTCTTTAGCACCAGAGAGATACCTTGCCTTTCTTAAAG 396
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Db 397 TGTATTGTCTCAGGACACTGCCACAGATGATGCTATTATTAATAACACATGCATAAATGGC 456
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Db 517 ATGAAGTATGAAGGCTCTGATTTTCAATCAAGAGATTCACCGAAAGCCAGCTACGCAGG 576
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Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGlnAspGluAlaPheIle 200
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QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db 1417 AGSGTGGCCACCAAGCGGTACATGGCTCCAGAAGTCTCGATGAAGCCCTGAATAAACC 1476
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QY 481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1657 CCAATCGTCTCAACCGCTGGAACAGCGATGAATGCTTCGAGCAGTTTTGAAGCTAATG 1716
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Db 1717 TCAGAAATGTGGGCCCATTAATCCAGCCTCCAGACTCACAGCTTTTGAGATCAAGAAGACA 1776
QY 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1777 CTTGCAAAATGGTTGAATCCCGAGGATGTAAGATT 1812
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RESULT 8

US-09-267-963D-13

; Sequence 13, Application US/09267963D

; Patent No. 6692925

; GENERAL INFORMATION:

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; APPLICANT: MIYAZONO, Kohei
; APPLICANT: IMAMURA, Takeshe
; APPLICANT: DEN DIJKE, Peter
; TITLE OF INVENTION: PROTEINS HAVING SERINE/THREONINE KINASE DOMAINS, CORRESPONDING
; FILE REFERENCE: NUCLEIC ACID MOLECULES AND THEIR USE
; CURRENT APPLICATION NUMBER: US/09/267,963D
; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/GB93/02367
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: US 09/039,177
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-267-963D-13
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Alignment Scores:

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Pred. No.: 1.2e-315 Length: 2070
Score: 2823.00 Matches: 526
Percent Similarity: 99.81% Conservative: 5
Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 3 Gaps: 0
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US-10-600-645-2 (1-532) x US-09-267-963D-13 (1-2070)

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QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
Db 217 ATGACTCAGCTATACACTTACATCAGATTACTGGGAGCCTGTCTTTCATCATTTCTCAT 276
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Db 277 GTTCAAGGCGCAGAAATCTAGATAGTAGTCTCCATGCGCACTGGTATGAAATCAGACTTGGAC 336
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Db 337 CAGAGAAGCCAGCAAAATGGAGTGACTTTAGCACCAGAGGATACCTTGCTTTCTTAAAG 396
QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
Db 397 TCGTATTGCTCAGGACACTGCCAGATGATGCTATTATAACACATGATACATACTAATGTC 456
QY 81 HisCysPheAlaIleIleGluGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 457 CATTTGCTTTGCCATTATAGAAGAGATGATCAGGGAGAAACCCACATTAACTTCTGGGTGT 516
QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 517 ATGAAGTATGAAGGCTCTGATTTTCAATCCAAGGATTCCACGAAAGCCAGCTACGCAGG 576
QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 577 ACAATAGAAATGTGTGCGGACCAATTTGCAACCAAGTATTTGCAGCCTACACTGCCCTCT 636
QY 141 ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
Db 637 GTTGTATTAGTCCGTTCTTTGATGGCAGCATCCGATGGCTGGTTGTGCTCATTTCCATG 696
QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
Db 697 GCTGTCTGTATAGTTGCTATGATCATCTTCTCCAGCTGCTTTTGTGCTAATAAGCATTTGT 756
QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGlnAspGluAlaPheIle 200
Db 757 AAGATATCTCAAGCAGGGGTGTTTACAAACCGTGATTTGGAAACAGAGTGAAGCATTTAT 816
QY 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
Db 817 CCAGTAGGAGAAATCATTTGAAAGACCTGATTGACCAAGTCCCAAGGCTCTGGGAGTGCATCT 876
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Qy 221 GlyLeuProLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 877 GGATTGGCTTTATTGGTTACGCAACTATTGCCAAACAGATTACAGATGGTTCCGACGTT 936
Qy 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
Db 937 GGTAAAGCCCGCTATGGAGAAGTATGGATGGGTAAATGGCGTGTGAAAAAGTGGCTGTC 996
Qy 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db 997 AAAGTGTGTTTACCACTGAAGAAGCTAGCTGGTTTAGAGAAACAGAAATCTACACAGC 1056
Qy 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db 1057 GTGTTAATGGCTCATGAAATATATCTTGGTTTATAGCTGCAGACATTAAGGCACTGGT 1116
Qy 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 1117 TCCTGGACTCAGCTGTATTTGATTACTGATTTACCATGAAATGGATCTCTCTATGACTTC 1176
Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 1177 CTGAATGTGCCACTAGACACAGAGCCCTACTCAAGTTAGCTTATTCTGCTGCTGT 1236
Qy 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1237 GGCTGTGGCCCTCCACAGAAATTTATGGTACCCAGGAAGCCTGCAATGCTCAT 1296
Qy 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysIleAlaAsp 380
Db 1297 CGAGACCTGAAGAGCAAAACATCTTATTAAAGAAAAATGGAAGTTGCTGTATTGCTGAC 1356
Qy 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1357 CTGGCCCTAGCTGTATAATTAACAGAGTACATAAAATGAAGTTGACATACCTTGAATACC 1416
Qy 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuLysAsn 420
Db 1417 AGGGTGGCCACCAAGCGGTACATGGCTCCAGAGAGTGTGGATGAAGCCTGAATAAACC 1476
Qy 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
Db 1477 CATTTCCAGCCCTACATCATGGCTGACATCTATAGCTTTGGTTTGATCTTTGGGAAATG 1536
Qy 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1537 GCTCGCTGTTGTATTACAGAGGAATCGTGGAGGAATATCAATTTACCATATTACAACATG 1596
Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1597 GTGCCCGTACCCATCTTATGAGGACATCGGTAGGTTGTGTGTGAACCCCTTCCGG 1656
Qy 481 ProfileValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1657 CCAATCGTGTCTAACCGCTGAAACAGCGATGAATGCTTCGACGAGTTTGAAGCTAATG 1716
Qy 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysThr 520
Db 1717 TCAGAATGTTGGGCCCAATAATCCAGCCCTCAGACTCAGACTTTTGAAGATCAAGAAGACA 1776
Qy 521 LeuAlaLysMetValGluSerGlnAspValIleIle 532
Db 1777 CTTTGCAAAAAATGTTTGATCCAGGATGTAAAGATT 1812

RESULT 9
US-08-462-467B-11
; Sequence 11, Application US/08462467B
; Patent No. 6210899
; GENERAL INFORMATION:
; APPLICANT: Rosenbaum, Jan S
; TITLE OF INVENTION: The Use of a BMP Protein Receptor
; TITLE OF INVENTION: Complex for Screening Bone Metabolism Actives and Cells
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; TITLE OF INVENTION: Co-Transfected With a Type II BMP Receptor and a Type I
; TITLE OF INVENTION: BMP Receptor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Procter & Gamble Company
; STREET: 11810 East Miami River Road
; CITY: Ross
; STATE: OH
; COUNTRY: USA
; ZIP: 45061
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,467B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hersko, Bart S.
; REGISTRATION NUMBER: 32,572
; REFERENCE/DOCKET NUMBER: 5474R
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 627-0633
; TELEFAX: (513) 627-0260
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2402 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-462-467B-11

Alignment Scores:
Pred. No.: 1,54e-315 Length: 2402
Score: 2823.00 Matches: 526
Percent Similarity: 99.81% Conservative: 5
Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 3 Gaps: 0

US-10-600-645-2 (1-532) x US-08-462-467B-11 (1-2402)

Qy 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
Db 11 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCCTGTCTGTTTCATCTTCAT 70
Qy 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db 71 GTTCAAGGGCAGAATCTAGATAGTATGCTCCATGGCAGCTGGTATGAATCAGACTTGGAC 130
Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
Db 131 CAGAGAAGCCAGAAATCGAGTGACTTTAGCACCAGAGATACCTTGCCTTTCTTAAG 190
Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
Db 191 TGTATTGCTCAGGACACTGCCAGATGATGCTATTATAACACATGATCACTAATAATGTC 250
Qy 81 HisCysPheAlaIleIleGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 251 CATTTGCTTTGCCATTATAGAAGAAAGATGATCAGGGAGAAACACACATTAATCTCTGGGTGT 310
Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 311 ATGAAGATGAGAGGCTCTGATTTTCAATGCAAGGATTCACCGAAACCCAGCTACGAGG 370
Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 371 ACAATAGAATGTTGTGGGACCAATTTGTGCAACACCATGATTTGTGAGCCTACACTGCCCT 430
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QY 141 ValValIleGlyPropPheAspGlySerValArgTrpLeuAlaValIleuIleSerMet 160
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QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrIleHisTyrCys 180
Db 491 GCTGTCGTATAGTTGCTATGATCATCTTCTCCAGCTGCTTTTGTATAAGCATATTGCT 550
QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
Db 551 AAGAGTATCTCAAGCAGGGGTCGTATACAAACCGGTGATTTTGGAAACAGGATGAAGCATTTATT 610
QY 201 ProValGlyLysSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySer 220
Db 611 CCAGTAGGAGAAATCATTTGAAAGACCTTGATGGCCAGTCCCAAGCTCTGGAGTGGATCT 670
QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 671 GGATTGCCCTTTATGGTTCCAGCGAACTATTGCCAAACAGATTCCAGATGGTTCCGCCAGTT 730
QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
Db 731 GGTAAAGGCGCTATGGAGAGTATGGATGGGTAAATGGCTGGTCAAAAAGTGGCTGTC 790
QY 261 LysValPhePheThrThrGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db 791 AAAGTGTTTTTACCCTGAAAGAGCTAGCTGGTTAGAGAAACAGAAATCTACCAGAGC 850
QY 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db 851 GTGTTAATCGCTCATGAAATATACTTGGTTTATAGCTGCAGACATTAAGGCACTGGT 910
QY 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 911 TCCTGGACTCAGCTGATTGTTGTTACTGATTACCATGAAATGGATCTCTCATGACTTC 970
QY 321 LeuLysCysAlaThrIleuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 971 CTGAATGTGCCACACTAGACACAGAGCCCTACTCAAGTTAGCTTATTCTGCTGCTGT 1030
QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1031 GGTCGTGTCACCTCCACACAGAAATTTATGGTACCCAGGAGCCCTGCAATTGCTCAT 1090
QY 361 ArgAspLeuLysSerLysAsnIleLeuLysLysAsnGlySerCysCysIleAlaAsp 380
Db 1091 CGAGACCTGAAGAGCAAAACATCCTTATTAAGAAAAATGGAAGTTGCTGTATTGCTGAC 1150
QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1151 CTGGGCTTAGCTGTAAATTCACAGTGATACAAATGAAAGTTGACATACCTTGAATACC 1210
QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db 1211 AGGTGGGACCAAGCGGTACATGGCTCCAGAGTGTCTGGATGAAAGCCTGAAATAAAC 1270
QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
Db 1271 CATTTCCAGCCCTACATCATGCTGACATCTATAGCTTTGGTTTGTATCATCTTTGGGAAATG 1330
QY 441 AlaArgArgCysIleThrGlyGlyIleValGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1331 GCTCGCTGTGTATTACAGAGGAAATCGGGAGGAATATCAATATTACCATATTACAACTG 1390
QY 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1391 GTGCCAGTGACCCCTCATGAGACATCGCTGAGGTGTGTGTGTGAAACGCTTGGCG 1450
QY 481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1451 CCAATCGTCTCAACCGCTGGAACAGCGATGAATGTTCTCGAGCAGTTTTTGAAGCTAATG 1510
QY 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysIleThr 520

Db 1511 TCAGNATGTTGGCCCATTAATCCAGCTTCCAGACTCCAGCTTTGAGNATCAAGAGACA 1570
QY 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1571 CTTGCAAAATGGTTGAATCCAGGATGTAAAGATT 1606
RESULT 10
US-08-158-735A-3
; Sequence 3, Application US/08158735A
; Patent No. 6248554
; GENERAL INFORMATION:
; APPLICANT: COOK, JONATHAN S.
; APPLICANT: CORREA, PAUL E.
; APPLICANT: KOENIG, BETH B.
; APPLICANT: ROSENBAUM, JAN S.
; APPLICANT: TING, JERRY
; TITLE OF INVENTION: DNA SEQUENCE CODING FOR A BMP RECEPTOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE PROCTER & GAMBLE COMPANY
; STREET: 11810 EAST MIAMI RIVER ROAD
; CITY: ROSS
; STATE: OH
; COUNTRY: USA
; ZIP: 45061
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/158,735A
; FILING DATE: 24-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CORSTANJE, BRAHM J.
; REGISTRATION NUMBER: 34,804
; REFERENCE/DOCKET NUMBER: 5088
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 627-2858
; TELEFAX: (513) 627-0260
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2402 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(11..1606)
US-08-158-735A-3
Alignment Scores:
Pred. No.: 1,54e-315 Length: 2402
Score: 2823.00 Matches: 526
Percent Similarity: 99.81% Conservative: 5
Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 3 Gaps: 0
US-10-600-645-2 (1-532) x US-08-158-735A-3 (1-2402)
QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
Db 11 ATGACTCAGCTATACACTTACATCATGATTACTGGAGCCTGTCTGTTTCATCTCAT 70
QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db 71 GTTCAAGGGCGAATCTAGATAGTAGTATGCTCCACTGGCTGATGAAATCAGACTGGAC 130
QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60

Db 131 CAGAAGAGCCAGAAAATGGAGTGACTTTAGCCACGAGGATACCTTGGCTTTCTTAAAG 190
Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnThrCysIleThrAsnGly 80
Db 191 TGCTATTGCTCAGGACACTGCCAGATGATGCTATTAAACACATGCATTAATATGGC 250
Qy 81 HisCysPheAlaIleLeuGluAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 251 CATTTGCTTTGCCATTATAGAAGAAGATGATCAGGAGAAACCAACATTAACTCTGGGTGT 310
Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 311 ATGAAGTATGAAGCTCTGATTTTCAATGCAAGGATTCACCGAAAGCCAGCTACGACG 370
Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 371 ACAATAGATTGTCGACCAATTGTCGAAACAGTATTTGACGCTACACTGCCCTTCCCT 430
Qy 141 ValValIleGlyProPheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
Db 431 GTTGTATTAGTCCGTTCTTTGATGGCAGCATCCGATGGCTGGTGTGCTCAATTTCCATG 490
Qy 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
Db 491 GCTGTCTGTATAGTTGCTATGATCATCTCTCCAGCTGCTTTTGTGCTATAAGCAATTATTGT 550
Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
Db 551 AAGAGTATCTCAAGCAGGGGTGCTTTACACCGTGATTTGGAACAGGATGAAGCATTTATT 610
Qy 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
Db 611 CCAGTAGGAGAATCATTTGAAAGACCTGATTGACCAAGTCCCAAGCTCTGGAGTGATCT 670
Qy 221 GlyLeuProLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 671 GGATTCCCTTTATTTGTTGTCAGCAACTATTGCCCCAACAGATTGAGTGGTTCCGCAAGTT 730
Qy 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
Db 731 GGTAAGCGCGCTATGGAGAGTATGGATGGGTAATGGCGTGGTGAAGGAGTGGCTGTC 790
Qy 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db 791 AAAGTGTTTTTACCCTGAAGAAGCTAGCTGGTTTAGAGAAACAGAAATCTACACAGC 850
Qy 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db 851 GTGTTAATGCGTCATGAAAATATACTTGGTTTTATAGCTGCAGACATTAAGGCACTGCT 910
Qy 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 911 TCTGAGCTCAGCTGTATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTG 970
Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 971 CTGAATGTGCCACACTAGACACAGAGCCCTACTCAAGTTAGCTTATTCTGCTGCTTGT 1030
Qy 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1031 GGTCTGTGCCACCTCCACACAGAAATTTATGGTACCAAGGGAAGCTGCAATTTGCTCAT 1090
Qy 361 ArgAspLeuLysSerLysAsnIleLeuIleLysAsnGlySerCysIleAlaAsp 380
Db 1091 CGAGAGCTGAAGAGCAAAACATCTTTATTAAGAAAAATGGAAGTTGCTGATTGCTGAC 1150
Qy 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1151 CTGGGCTAGCTGTTAAATTTCAACAGTGATACAAATGAAGTTGACATCCCTTGAATACC 1210
Qy 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db 1211 AGGGTGGGCACCAAGCGGTACATGGTCTCCAGAAGTCTCGAAGTCTCGAAGTCTGAATAAAAC 1270

RESULT 11

US-08-334-179A-11
; Sequence 11, Application US/08334179A
; Patent No. 6306622
; GENERAL INFORMATION:
; APPLICANT: ROSENBAUM, JAN S.
; APPLICANT: NOHNO, TSUTOMU
; TITLE OF INVENTION: CDNA ENCODING A BMP TYPE II RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSES: THE PROCTER AND GAMBLE COMPANY
; STREET: 11810 EAST MIAMI RIVER ROAD
; CITY: ROSS
; STATE: OH
; COUNTRY: US
; ZIP: 45061
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.30, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 04-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CORSTANJE, BRAHM J.
; REGISTRATION NUMBER: 34,804
; REFERENCE/DOCKET NUMBER: 5473
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 513-627-2858
; TELEFAX: 513-627-0260
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2402 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(11..1606)
US-08-334-179A-11
Alignment Scores:
Pred. No.: 1.54e-315 Length: 2402
Score: 2823.00 Matches: 526
Percent Similarity: 99.81% Conservative: 5

Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 3 Gaps: 0

US-10-600-645-2 (1-532) x US-08-334-179A-11 (1-2402)

Qy 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
Db 11 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCCCTGCTGTTCATCATTTCTCAT 70

Qy 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db 71 GTTCAAGGGCAGAACTAGATAGTATGCTCCATGCGACTGGTATGAATCAGACTTGGAC 130

Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
Db 131 CAGAAAGAACCGAAATGGAGTACTTTAGCACCAGAGGATACCTTGCTTTCTTAAAG 190

Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
Db 191 TGTATTGCTCAGGACACTGCCACAGATGCTATTATAACACATGCATAACTAATGCG 250

Qy 81 HisCysPheAlaIleIleGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 251 CATTGCTTTGCCATTATAGAAGATGATCAGGGAGAAACACATTAACTTCTGGGTGT 310

Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 311 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCGAAAGCCAGCTACGCAGG 370

Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 371 ACAATAGATGTTTTCGACCAATTTTGCACACCATGATTTTGCAGCTACACTGCCCCCT 430

Qy 141 ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
Db 431 GTTGTATTAGGTCGGTCTTTCATGGCAGCATCCGATGGCTGGTGTGCTCATTTCCATG 490

Qy 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrIlyshisTyrCys 180
Db 491 GCTGTCTGTATAGTTGCTATGATCATCTTCTCAGCTGCTTTTGTGCTATAAGCATTTATGT 550

Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
Db 551 AAGAGTATCTCAAGCAGGGGTGCTTACAACCGTGATTTGGAACAGAGTGAACATTTATT 610

Qy 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySer 220
Db 611 CCAGTAGGAGAAATCATTGAAAGACCTGATTGACCAGTCCCAAGGCTCTGGAGTGGATCT 670

Qy 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 671 GGATTTGCCCTTTATTGGTTTTCAGCGAACTATTGCGCAACAGATTTCAGATGGTTTCGCGAGTT 730

Qy 241 GlyLysGlyArgTyrGlyValTrpMetGlyLysTrpArgGlyGlyLysValAlaVal 260
Db 731 GGTAAAGGCCGTATGGAGAAATGATGGATGGTAAATGGCGTAAAGTGGCTGTC 790

Qy 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db 791 AAAGTGTTTTACCACCTGAAGNAGCTAGCTGGTTTAGAGAAACAGAAATCTACCAGCG 850

Qy 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db 851 GTGTTAATCGTCATGAAATAATATCTTGGTTTTATAGCTGCAGACATTAAGGCACTGCT 910

Qy 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 911 TCTTGACTCAGCTGATTGTGATTACTGATTACCATGAAATGGATCTCTCTATGACTTC 970

Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaCys 340
Db 971 CTGAAATGTGCCACACTAGACACCAGAGCCCTACTCAAGTTAGCTTATTCTGCTGCTGT 1030

Qy 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1031 GGTCTGTGCCACCTCCACACAGAAATTTATGGTACCCAAAGGAAGCCTGCATTTGCTCAT 1090

Qy 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
Db 1091 CGAGACCTGAAGAGCAAAACATCTTATTAAAGAAAATGGAAGTTGCTGTATTGCTGAC 1150

Qy 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAlaAspIleProLeuAsnThr 400
Db 1151 CTGGCCCTAGCTGTAAATTCAACAGTACATAAAATGAAGTTGACATACCCCTTGAATACC 1210

Qy 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLysSerLysAsn 420
Db 1211 AGGTGGGCACCAACGCGGTACATGGCTCCAGAAAGTGTGGATGAAAGCCTGAATAAAAAC 1270

Qy 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleIleTrpGluMet 440
Db 1271 CATTTCCAGCCCTACATCATGCTGACATCTATAGCTTTGGTTTGATCATTTGGGAAATG 1330

Qy 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrTrpAsnMet 460
Db 1331 GCTCGTCTGTATTACAGGAGGAATCGTGAGGAATATCAATTACCATATTACAACATG 1390

Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1391 GTGCCAGTAGTACCCTCTATGAGGACATGCTGAGGTGTGTGTGTAACACGCTTGGCG 1450

Qy 481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1451 CCATTCGTGTCTAACCGCTGGAAACAGCATGAAATGTCTTCGAGCAGTTTTCGAGCTAATG 1510

Qy 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db 1511 TCAGAAATGTTGGGCCATAAATCCAGCTCCAGACTCCAGCTTTGAGAATCAAGAAGACA 1570

Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1571 CTTGCAAAATGGTTGAATCCAGGATGTAAAGATT 1606

RESULT 12
US-08-158-735A-1
; Sequence 1, Application US/08158735A
; Patent No. 6248554
; GENERAL INFORMATION:
; APPLICANT: COOK, JONATHAN S.
; APPLICANT: CORREA, PAUL E.
; APPLICANT: KOENIG, BETH B.
; APPLICANT: ROSENBAUM, JAN S.
; APPLICANT: TING, JERRY
; TITLE OF INVENTION: DNA SEQUENCE CODING FOR A BMP RECEPTOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE PROCTER & GAMBLE COMPANY
; STREET: 11810 EAST MIAMI RIVER ROAD
; CITY: ROSS
; STATE: OH
; COUNTRY: USA
; ZIP: 45061
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/158,735A
; FILING DATE: 24-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CORSTANJE, BRAHM J.
; REGISTRATION NUMBER: 34,804
; REFERENCE/DOCKET NUMBER: 5088

TELECOMMUNICATION INFORMATION:

TELEPHONE: (513) 627-2858
TELEFAX: (513) 627-0260
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2056 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(291...1790)
US-08-158-735A-1

Alignment Scores:

Pred. No.: 9.23e-313 Length: 2056
Score: 2798.00 Matches: 526
Percent Similarity: 94.48% Conservative: 5
Best Local Similarity: 93.59% Mismatches: 1
Query Match: 98.59% Indels: 30
DB: 3 Gaps: 1

US-10-600-645-2 (1-532) x US-08-158-735A-1 (1-2056)

QY 1 MetThrGlnLeuTyrThrTyrlleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
DB 291 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCCTGTCTGTTTCATCATTTCTCAT 350
QY 21 ValGlnGlyClnAsnLeuAspSerMetLeuHisGlyThrGlyMetIysSerAspValAsp 40
DB 351 GTTCAAGGGCAGAACTTAGATAGTATGCTCCATGGCACTGTGTATGAATCAGACTTTGGAC 410
QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
DB 411 CAGAGAGCCAGAAATGGAGTGACTTTAGCACCCAGAGGATACCTTGGCTTTCTTAAG 470
QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
DB 471 TGCTATTGCTCAGGACACTGCCCCAGATGATGCTATTATTAACACATGCTAATAATGTC 530
QY 81 HisCysPheAlaIleIleGluAspGlnGlyGluThrThrLeuThrSerGlyCys 100
DB 531 CATTTGCTTTGCCATTATAGAAGAAGATGATCAGGAGAAACCAACATTAATCTCTGGGTGT 590
QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
DB 591 ATGAAGTATGAAGCTCTGATTTTCAATGCAAGATTACCCGAAAGCCAGCTACCGCAGG 650
QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
DB 651 ACAATAGATTGTCGGACCAATTTGTGCAACCAAGTATTTGCGAGCTACACTGCCCCCT 710
QY 141 ValValIleGlyProPheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
DB 711 GTTGTATAGTCCGTTCTTTGATGGCAGCATCCGATGGCTGTGCTGCTCATTTCCATG 770
QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
DB 771 GCTGTCTGTATAGTATGATGATCATCTTCTCAGCTGCTTTGCTATGAAGCATTTATGT 830
QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
DB 831 AAGAGTATCTCAAGCAGGGGTCTTTACACCGTGATTTGGAACAGGATGAGCATTTAT 890
QY 201 ProValGlyClnSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
DB 891 CCAAGTAGGAGAAATCATTTGAAGACCTGATTGACCACTGCCAAAGCTCTGGGAGTGGATCT 950
QY 221 GlyLeuProLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
DB 951 GGATTGCCTTTATGGTTAGCCAACTATTGCCAAACAGATTCAGATGGTTCCGGCAGGTT 1010
QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260

DB 1011 GGTAAAGGCCGCTATGGAAGATGATGATGGGTAAATGGCGTGGTAAAAAGTGGCTGTC 1070
QY 261 LysValPhePheThrThrGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
DB 1071 AAAGTGTGTGTATACCACTGAAGAAGCTAGCTGTGTTTAGAGAAACAGAAATCTACCAAGACG 1130
QY 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
DB 1131 GTGTTAATGGTCATGAAATATATCTTGGTTTATAGCTGCAGACATTAAAGGCACCTGGT 1190
QY 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
DB 1191 TCCTGGACTCAGCTGTATTGTATTACTGATTACCATGAAATGCGATCTCTATGACTTTC 1250
QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaIleCys 340
DB 1251 CTGAAATGTGCCACACTAGACACCCAGAGCCCTACTCAAGTTAGCTTATTTCTGCTGTGT 1310
QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
DB 1311 GGTCTGTGCACCTCCACACAGAAATTTATGGTACCAGGAGGAGCTGCATTTGCTCAT 1370
QY 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
DB 1371 CGAGACCTGAAGAGCAAAACATCCTTATTAAAGAAAAATGGAAGTTGCTGTATTGCTGAC 1430
QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAanThr 400
DB 1431 CTGGGCCCTAGCTGTAAATTCACAGTGTATCAAAATGAAGTTGACATACCTTTGAATACC 1490
QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
DB 1491 AGGTTGGGACCACAGCGGTACATGCTCCAGAAAGTCTGGATGAAAGCCCTGATATAAAC 1550
QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
DB 1551 CATTTCCAGCCCTACATCATGCTGACATCTATAGCTTTGGTTTGATCATTTGGGAAATG 1610
QY 441 AlaArgArgCysIleThrGlyIleValGluGlyThrGlnLeuProTyrTyrAsnMet 460
DB 1611 GCTCGTGTGTATTACAGGAGGAATCGTGGAGGAATATCAATTTACCATATTACCAACATG 1670
QY 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
DB 1671 GTGCCAGTGCACCATCTCTATGAGACATGCTGAGGTGTGTGTGTGAAACGCTTCCGG 1730
QY 481 ProfileValSerAsnArgTrpAsnSerAspGlu----- 491
DB 1731 CCAATCGTGTCTAACCGCTGGAACAGCGATGAAGTGAAGTTGGAGCAAGTCCCTGTAAAG 1790
QY 491 ----- 491
DB 1791 TGATGAGTGAAGTCCGAGTTACTCTGTGCTCACACACTCTGTTGCAATTTATTTCTCTT 1850
QY 492 ---CysLeuArgAlaValLeuLysLeuMetSerGluCysTrpAlaHisAsnProAlaSer 510
DB 1851 TAGTGTCTCGAGCAGTTTGAAGCTAATGTGAGAAATGTTGGGCCCATTAATCAGCCTCC 1910
QY 511 ArgLeuThrAlaLeuArgIleLysLysThrLeuAlaLysMetValClnSerGlnAspVal 530
DB 1911 AGACTCAGACCTTTGAGAATCAAGAGACACTTGCAGAAATGTTGAATCCCGAGATGTA 1970
QY 531 LysIle 532
DB 1971 AAGATT 1976

RESULT 13

US-08-481-337A-5
; Sequence 5, Application US/08481337A
; Patent No. 5863738
; GENERAL INFORMATION:
; APPLICANT: TEN DIJKE, Peter

APPLICANT: HELDIN, Carl-Henrik
APPLICANT: MIYAZONO, Kohei
APPLICANT: SAMPATH, Kuber T.
TITLE OF INVENTION: Morphogenic Protein-Specific Cell
TITLE OF INVENTION: Surface Receptors and Uses Therefor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,337A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, Thomas C.
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: CRP-097CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2932 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 310..1905
OTHER INFORMATION: /product= "Human ALK3"

US-08-481-337A-5

Alignment Scores:

Pred. No.:	3,68e-309	Length:	2932
Score:	2769.00	Matches:	517
Percent Similarity:	98.50%	Conservative:	7
Best Local Similarity:	97.18%	Mismatches:	8
Query Match:	97.57%	Indels:	0
DB:	2	Gaps:	0

US-10-600-645-2 (1-532) x US-08-481-337A-5 (1-2932)

QY	1	MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis	20
DB	310	ATGACTCAGCTATACATTTACATCAGATTATTGGAGCCTATTGTTTCATCATTTCTCGT	369
QY	21	ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetCysSerValAsp	40
DB	370	GTTCAAGGACAGAATCTGGATAGTATGCTTCATGGCACTGGGATGAAATCAGACTCCGAC	429
QY	41	GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys	60
DB	430	CAGAAAAAGTCAGAAATGGATGATACCTTAGCACCAGAGGATACCTTGCTTTTAAAG	489
QY	61	CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly	80
DB	490	TCCTATTGCTCAGGCACCTGTCAGATGATGCTATTATAACACATGATCAATAATGGA	549
QY	81	HisCysPheAlaIleIleGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys	100
DB	550	CATTGCTTTGCCATCATAGAAGAAGATGACACCGGAGAGAACACATTAGCTTCAGGGTGT	609
QY	101	MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArg	120

Db	610	ATGAATATGAAGATCTGATTTTCAGTGCAGAAAGATTCTCCAAAAGCCAGCTACGCCGG	669
QY	121	ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro	140
DB	670	ACAATAGAATGTTGTCGGACCAATTTATGTAAACAGATATTTGCAACCCACACTGCCCT	729
QY	141	ValValIleGlyProPhePheAspGlySerValArgTyrLeuAlaValLeuIleSerMet	160
DB	730	GTTGTCTAGGTCCGTTTTTTGATGGCAGCATTCGATGGCTGGTTTGTCTCATTTCTATG	789
QY	161	AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys	180
DB	790	GCTGTCTGCATAATTTGCTATCATCTTCTCCAGCTGCTTTTGTTCACAAATATTATTC	849
QY	181	LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle	200
DB	850	AAGAGCATCTCAAGCAGACGCTCGTTACAACTCGTGATTTTGGAAACAGATGAGCAITATT	909
QY	201	ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer	220
DB	910	CCAGTTGGAGAAATCACTAAAAGACCTTATTGACCAGTCAAAAGTTCTGGTAGTGGTCT	969
QY	221	GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal	240
DB	970	GGACTACCTTTATTGGTTTCAGGAACTATTGCCAAACAGATTTCAGATGTCGCGCAATT	1029
QY	241	GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTyrPheArgGlyGlyLysValAlaVal	260
DB	1030	GGTAAAGGCCGATATGGAGAAAGTATGGATGGCAATGGCGTGGCGAAAAGTGGCGGTG	1089
QY	261	LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr	280
DB	1090	AAAGTATTCTTTTACCACCTGAAGAACCCAGCTGGTTTCGAGAAACAGAAATCTTACCAACT	1149
QY	281	ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly	300
DB	1150	GTGCTAATGGCCCATGAAACATATCTGTTTCATAGCGGCAGACATTAAGGTACAGT	1209
QY	301	SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe	320
DB	1210	TCCTGGACTCAGCTCTATTTCGATTTACCATGAAATGGATCTCTCTATGACTTC	1269
QY	321	LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys	340
DB	1270	CTGAATGTGTACACTGGACACAGACCCCTGCTTAAATTTGGCTTATTTCAGCTCCCTGT	1329
QY	341	GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis	360
DB	1330	GCTCTGTGCCACCTGACACAGAAATTTATGGACCCCAAGGAAGCCCGCAATTCCTCAT	1389
QY	361	ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysIleAlaAsp	380
DB	1390	CGAGACCTAAAGAGACAAACCATCTCATCAAGAAAAATGGAGTTGCTGCATTCCTGAC	1449
QY	381	LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr	400
DB	1450	CTGGGCCCTTGCTGTTAAATTTCAACAGTGACACAAATGAAGTTGATGTCCTTGAATACC	1509
QY	401	ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn	420
DB	1510	AGGTGGGCACCAACCGCTACATGCTCCCAAGTGTGGACGAAAGCCTGAACAAAAAC	1569
QY	421	HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet	440
DB	1570	CACITCCAGCCCTACATCATGCTGACATCTACAGCTTCGCGCTTAATCATTTGGGAGATG	1629
QY	441	AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet	460
DB	1630	GCTCGTGTGTTATCACAGAGGGATCGTGAAGAATAACCAATTTGCCATATTACAAATG	1689
QY	461	ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg	480

Db 1690 GTACCGAGTGCATCGTCATAGCAAGATATGCGTGAGGTTGTGTGTGTCACCAACGTTTCGGG 1749
Qy 481 ProileValSerAsnArgTtpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1750 CCAATGTGCTAATCGGTGGAACAGTGAATGCTCTACAGCAGCTTTTGAAGCTAATG 1809
Qy 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db 1810 TCAGATGCTGGGGCCCAATCCAGCCTCCAGACTCACAGCAATTGAGAAATTAAGAGACG 1869
Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1870 CTTGCCAAGATGGTTGAATCCCAAGATGTAAAAATC 1905

RESULT 14

US-09-382-256-5
Sequence 5, Application US/09382256A
Patent No. 6207814
GENERAL INFORMATION:
APPLICANT: MIYAZONO, Kohei
TEN DIJKE, Peter
FRANZEN, Petra
YAMASHITA, Hidetoshi
HELDIN, Carl-Henrik

TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS
HAVING SERINE THREONINE KINASE DOMAINS,
AND THEIR USE

NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/382,256A
FILING DATE: 24-Aug-1999
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: No. 6207814ember 17, 1993
APPLICATION NUMBER: GB 9224057.1
FILING DATE: No. 6207814ember 17, 1992
APPLICATION NUMBER: GB 9304677.9
FILING DATE: March 8, 1993
APPLICATION NUMBER: GB 9304680.3
FILING DATE: March 8, 1993
APPLICATION NUMBER: 9311047.6
FILING DATE: May 28, 1993
APPLICATION NUMBER: 9313763.6
FILING DATE: July 2, 1993
APPLICATION NUMBER: 9316099.2
FILING DATE: August 3, 1993
APPLICATION NUMBER: 321344.5
FILING DATE: October 15, 1993

ATTORNEY/AGENT INFORMATION:
NAME: No. 6207814man D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5298.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2932 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown

TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 310..1905
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-382-256-5
Alignment Scores:
Pred. No.: 3 68e-309 Length: 2932
Score: 2769.00 Matches: 517
Percent Similarity: 98.50% Conservative: 7
Best Local Similarity: 97.18% Mismatches: 8
Query Match: 97.57% Indels: 0
DB: 3 Caps: 0
US-10-600-645-2 (1-532) x US-09-382-256-5 (1-2932)
Qy 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleSerHis 20
Db 310 ATGACTCAGCTATACATTTTACATCAGATTATTGGGAGCCTATTATTGTTTCATCATTTCTCGT 369
Qy 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db 370 GTTCAAGAGCAGAACTCTGGATAGTATGCTTTCATGGCAGCTGGGATGAAATCAGATCCGAC 429
Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
Db 430 CAGAAAAGTCAGAAAATGGAGTAACTTAGCACCAGAGAGATACCTTGCCTTTTAAAG 489
Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
Db 490 TGCATTGCTCAGGGCAGCTGTCAGATGATGCTATTATAACACATGCATACTAATGGA 549
Qy 81 HisCysPheAlaIleIleGluGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 550 CATTGCTTTGCCATCATAGAAGAGATGACCAGGGAGAAACCACTTAGCTTCAGGGTGT 609
Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 610 ATGAATATGAAGATCTGATTTTCAGTGCAGAAAGATTCTCCAAAAGCCAGCTACGCCCG 669
Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 670 ACAATAGAAATGTTGTCGGACCAATTTATGTAACCAAGTATTGCAACCCACACTGCCCCCT 729
Qy 141 ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
Db 730 GTTGTATAGGTCGCTTTTTCATGGCAGCATTCGATGGCTGGTTTGTCTATTTCTATG 789
Qy 161 AlavalCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
Db 790 GCTGTCTGCATAATTGCTATGATCATCTTCTCAGCTGCTTTTGTTCACAAACATTATTGC 849
Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
Db 850 AAGAGCATCTCAAGCAGACGCTGTTTACAAATCGTATTGGAACAGCATGAAGCATTTATT 909
Qy 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
Db 910 CAGATTGGAGAAATCACTAAAGACCTTATTGACCAAGCTCAAAAGTTCTCGTAGTGGGTCT 969
Qy 221 GlyLeuProLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 970 GGACTACCTTTTATGTTCCAGCAACTATTGCCAAACAGATTTCAGATGTTCCGGCAAGTT 1029
Qy 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260

Db 1030 GGTAAAGGCGCATATGGAGAAGTATGGATGGGCAAAATGGTGGCGCAAAAAGTGGCGGTG 1089
Qy 261 LyeValPhePheThrThrGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db 1090 AAGATATCTTTACCACTGAAGAGCGCAGTGGTTTCGAGAAACAGAAATCTACCAACT 1149
Qy 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db 1150 GTGCTAATGGCCATGAAACATATCTGGTTTCATAGCGGCAGACATTAAGGTACAGGT 1209
Qy 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 1210 TCTGGACTCAGCTCTATTGTTACTGATTACCATGAAATGGATCTCTCTATGACTTC 1269
Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaIaCys 340
Db 1270 CTGAATGTGCTACACTGACACACAGAGCCCTGCTTAAATTTGGCTTATTTCAGCTGCTGT 1329
Qy 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1330 GGTCTGTGCCACTGCACACAGAAATTTATGGCAACCAAGAAAGCCCAATTTGCTCAT 1389
Qy 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysIleAlaAsp 380
Db 1390 CGAGACCTTAAGAGAGCAAAACATCTCTCATCAAGAAAAATGGGAGTTGCTGCATTTGCTGAC 1449
Qy 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1450 CTGGGCTTTGCTGTTAAATTCACAGTGCACACAAATGAAAGTTGATGTGCTGCTTGAATACC 1509
Qy 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db 1510 AGGTGGGACCAACACCTACATGCTCCCGAGTCTCGAGCAAGAAAGCCCTGACAAAAAC 1569
Qy 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
Db 1570 CACTTCAGCCCTTACATCATGCTGATCATCTACAGCTTCGGCTTAATCATTTTGGGAGATG 1629
Qy 441 AlaArgArgCysIleThrGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1630 GTCTGCTGTGTATCATCAGAGGGATCGTGGAGAAATACCAATTCGCATATTACAACTG 1689
Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1690 GTACCGAGTATCCGTCATACAGAGATATCGTGAGGTGTGTGTGTCAAACTTTGGCG 1749
Qy 481 ProlleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1750 CCAATTGTCTTAATCGGTGGAACAGTGTATGAATGTCTACGAGCAGTTTTTGAAGCTAATG 1809
Qy 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db 1810 TCAGATGTCTGGGCCACCAATCCAGCTCCAGACTCACAGCATTCAGAAATTAAGAAGAGC 1869
Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1870 CTTCGCAAGATGTTGAATCCCAAGATGTAATAATC 1905

RESULT 15

US-09-395-115-5
; Sequence 5, Application US/09395115
; Patent No. 6271365
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
; APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
; TITLE OF INVENTION: Activin Receptor-Like Kinase, proteins
; TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York

; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/395,115
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,265
; FILING DATE: 30-October-1995
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: 17-No. 6271365ember-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9224057.1
; FILING DATE: 17-No. 6271365ember-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304677.9
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304680.3
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9311047.6
; FILING DATE: 28-May-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9313763.6
; FILING DATE: 2-July-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9136099.2
; FILING DATE: 3-August-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9321344.5
; FILING DATE: 15-October-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohlei, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2932 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 310..1905
; US-09-395-115-5

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Score:	98.50%	Conservative:	7
Percent Similarity:	97.18%	Mismatches:	8
Best Local Similarity:	97.57%	Indels:	0
Query Match:	3	Gaps:	0
DB:			

US-10-600-645-2 (1-532) x US-09-395-115-5 (1-2932)

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Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
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Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnThrCysIleThrAsnGly 80
Db 490 TGCTATTGCTCAGGCGCATGTCAGAGATGATCTTAATAACATGATGAATAACTAATGGA 549
Qy 81 HisCysPheAlaIleIleGluGluAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 550 CATTTGCTTTGCCATCATAGAGAAGATGACCCAGGAGAAACCATTAGCTTCAGGSGTG 609
Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 610 ATGAATATATGAAGGATCTGATTTTCAGTGCAAGATTTCTCCAAAAGCCAGCTACGCCGG 669
Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrIleuGlnProThrLeuProPro 140
Db 670 ACAATAGATGTTGCGACCAATTTATGTAAACAGATTTTGCACCCACACATGCCCCCT 729
Qy 141 ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
Db 730 GTTGTCATAGTCCGTTTTTGTATGGCAGCATTCGATGGCTGGTTTTGCTCATTTCTATG 789
Qy 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
Db 790 GCTGCTGCATAATGCTATGATCATCTCTCCAGCTGCTTTTGTACAAACATATTATGC 849
Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluAspGluAlaPheIle 200
Db 850 AAGAGCATCTCAAGCAGACGTCGTACAAATCGTATTTGGAACAGGATGAAGCATTTATT 909
Qy 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
Db 910 CCAGTTGGAGNATCACTTAAAGACCTTATTGACCAGTCACAAAGTTCTGGTAGTGGGTCT 969
Qy 221 GlyLeuProLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
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Qy 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
Db 1030 GGTAAGCGCGCATATGGAGAAGTATGGATGGCAATGGCGTGGCGAAAAAGTGGCGGTG 1089
Qy 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db 1090 AAAGTATCTTTTACCCTGAAGAAGCCAGCTGGTTTCGAGAAACAGAAATCTTACCAACT 1149
Qy 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db 1150 GTGCTAATGCGCCATGAACAAACATACTTGGTTTCATAGCGGCAGACATTAAGGTACAGGT 1209
Qy 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 1210 TCCTGGACTCAGCTCTATTGTTGATTACTGATTACCATGAAATGGATCTCTCTATGACTTC 1269
Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 1270 CTGNAATGTGCTACACTGGACACAGAGCCCTGCTTAAATTTGGCTTATTGAGTGGCTGT 1329
Qy 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1330 GGTCTGTGCCACCTGCACACAGAAATTTATGGCACCCAGAAAGCCGCAATTGCTCAT 1389
Qy 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
Db 1390 CGAGACCTAAGAGCAAAAAACATCCTCATCAAGAAAAAATGGGAGTTGCTGCTATGCTGAC 1449
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Search completed: December 9, 2005, 22:26:59

Job Time: 1.249 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 9, 2005, 22:23:06 ; Search time 152 Seconds
(without alignments)

1308.491 Million cell updates/sec

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Perfect score: 2838
Sequence: 1 MTQLTYTIRLLGACLFISH.....TALRIKTKTLAKMVESQDVKI 532

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-Q=/cgn2_1/USPTO_spool/US10600645/runat_02122005_103607_23434/app_query.fasta_1.711
-DB=Published Applications_NA_New -QFMT=fastcap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -LOCAL=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA_New:

1: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
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5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
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8: /cgn2_6/ptodata/2/pubpna/US12_NEW_PUB.seq:
9: /cgn2_6/ptodata/2/pubpna/US13_NEW_PUB.seq:
10: /cgn2_6/ptodata/2/pubpna/US14_NEW_PUB.seq:

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	561.5	19.8	2090	6	US-10-420-192-7
2	280	9.9	3527	6	US-10-770-726-35
3	248	8.7	2505	7	US-11-186-283-3
4	248	8.7	3025	7	US-11-186-283-1
5	242	8.5	2505	7	US-11-186-283-9
6	242	8.5	3026	7	US-11-186-283-7
7	241.5	8.5	3105	7	US-11-021-441-3
8	230.5	8.1	1383	6	US-10-990-276-2

9	230	8.1	1542	6	US-10-990-276-4
10	226	8.0	6058	6	US-10-770-726-17
11	224	7.9	1437	7	US-11-021-441-19
12	222	7.8	1254	7	US-11-021-441-16
13	222	7.8	1254	7	US-11-021-441-17
14	222	7.8	1382	7	US-11-021-441-40
15	222	7.8	1716	7	US-11-021-441-25
16	222	7.8	1737	7	US-11-021-441-21
17	222	7.8	1737	7	US-11-021-441-23
18	222	7.8	2778	7	US-11-021-441-39
19	212.5	7.5	2981	6	US-10-949-720-399
20	212.5	7.5	3955	6	US-10-821-234-349
21	212.5	7.5	4235	6	US-10-949-720-392
22	211	7.4	3805	6	US-10-510-524-2
23	211	7.4	3805	6	US-10-955-054A-144
24	211	7.4	4234	6	US-10-955-054A-133
25	209.5	7.4	951	7	US-11-137-315A-3
26	209.5	7.4	2042	6	US-10-770-726-12
27	206.5	7.3	2197	6	US-10-750-185-35470
28	203.5	7.2	3890	6	US-10-821-234-269
29	202.5	7.1	1082144	7	US-11-117-187-211
30	199	7.0	1866	6	US-10-955-054A-5
31	195.5	6.9	2328	6	US-10-770-726-7
32	195.5	6.9	4034	7	US-11-115-086-5
33	195	6.9	1611	7	US-11-186-284-114
34	195	6.9	2820	7	US-11-112-908-2
35	194	6.8	4989	7	US-11-090-351-3
36	193.5	6.8	3711	7	US-11-115-086-3
37	193.5	6.8	4975	6	US-10-770-726-19
38	193	6.8	717	7	US-11-115-086-1
39	193	6.8	1224	6	US-10-523-477-2
40	193	6.8	1224	6	US-10-770-726-40
41	193	6.8	1224	7	US-11-136-815A-4
42	191.5	6.7	5484	6	US-10-955-054A-86
43	188.5	6.6	3052	6	US-10-770-726-34
44	186	6.6	1888	6	US-10-770-726-25
45	186	6.6	2838	6	US-10-770-726-27

ALIGNMENTS

RESULT 1

US-10-420-192-7
; Sequence 7, Application US/10420192
; Publication No. US20050260579A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Herbert Y.
; APPLICANT: Wang, Xiao-Fan
; APPLICANT: Weinberg, Robert A.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded Products and Uses
; FILE OF INVENTION: Therefore
; FILE REFERENCE: 0399.1086-022
; CURRENT APPLICATION NUMBER: US/10/420,192
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US 09/584,929
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 08/446,936
; PRIOR FILING DATE: 1995-05-23
; PRIOR APPLICATION NUMBER: US 08/311,703
; PRIOR FILING DATE: 1994-09-23
; PRIOR APPLICATION NUMBER: US 07/786,063
; PRIOR FILING DATE: 1991-10-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2090
; TYPE: DNA
; ORGANISM: genomic
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (136) ... (2038)

US-10-420-192-7

Alignment Scores:
Pred. No.: 3,52e-55 Length: 2090
Score: 561.50 Matches: 144
Percent Similarity: 50.20% Conservative: 104
Best Local Similarity: 29.15% Mismatches: 195
Query Match: 19.79% Indels: 51
DB: 6 Gaps: 13

US-10-600-645-2 (1-532) x US-10-420-192-7 (1-2090)

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Db 534 TGCATGAGCATGCG-----AGCATCACTCCATCTGTGAGAGCCACAGGAAGTC 584

QY 82 CysPheAlaIleIleGluAspGlnGlyGluThrThrLeuThrSerGlyCys--- 100
Db 585 TGTGTGGCTGTATGGAGAAAGAAATGACGAG--AACATAACACTAGAGACAGTTGGCAT 641

QY 101 ---MetLysTyrGluCysSerAspPheGlnCysLysAsp-----SerProLysAlaGln 117
Db 642 GACCCCAAGCTCCCTACCATGACTTATTTCTGGAAGATGCTGCTTCTCCAAAGTGCATT 701

QY 118 LeuArgArgThrIleGlu-----CysCysArgThrAsnLeu 129
Db 702 ATGAAGGAAAAAAGCCTGGTGAGACTTTCCTCATGTGTTCTGTAGCTCTGATGAG 761

QY 130 CysAsnGlnTyrLeu-----GlnProThrLeuProPro 140
Db 762 TGCATGACAAACATCATCTTCTCAGAAGAATATAACACAGCAATCTCTGACTTGTGCTA 821

QY 141 ValValIleGlyProPheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
Db 822 GTCATATTT-----CAAGTCAGCAGGCATCAGCCCTCTGCCACCACTG 863

QY 161 AlaValCysIleValAlaMetIleValPheSerCysPheCysTyrLysHisTyrCys 180
Db 864 GGAGTTGCCATATCTGTCAATCATCTTC-----TACTGC 899

QY 181 LysSerIleSerArgGlyArgTyrAsnArgAspLeuGlu-----GlnAspGluAla 198
Db 900 TACCGGCTTTAAACCGGACAGAGAGTGAGTTCAACCTGGGAAACCGGCAAGACGCGAAG 959

QY 199 PheIleProValGlyLysSerLeuLysAspLeuIleAspGlnSerGlnSerGlySer 218
Db 960 CTCTAGGAGTTACGAGCAGCTGTGCCATCATCTCTGGGAAGATGACCGCTCTGACATCAGC 1019

QY 219 GlySerGlyLeuProLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArg 238
Db 1020 TCCACGTGTGCCAACAAACATCAACACACAGAGCTGCTGCCCATTTGAGCTGGACACC 1079

QY 239 GlnValGlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpA-gGly----- 255
Db 1080 CTGTGGGGAAGGTCGCTTTCTGAGGTCTATAAGGCCAAGCTGAAGCAGAACACTTCA 1139

QY 256 -----GluLysValAlaValLysValPhePheThrThrGluGluAlaSerTrpPhe 272
Db 1140 GAGCAGTTTGAGACAGTGCATCAAGATCTTTCCCTATGAGGAGATGCTCTTGTGAAG 1199

QY 273 ArgGluThrGluIleTyrGlnThrValLeuMetArgHisGluAsnIleLeuGlyPheIle 292
Db 1200 ACAGAGAAGGACATCTTCTCAGACATCAATCTGAAGCATGAGACATACTCCAGTTCCTG 1259

QY 293 AlaAlaAspIleLysGlyThrGlySerTrpThrGlnLeuTyrLeuIleThrAspTyrHis 312
Db 1260 ACGGCTTGAGAGCGGAAGCGAGTGTGGGAAACAAATACTAGCTGATCAGCGCTCCAC 1319

QY 313 GluAsnGlySerLeuTyrAspPheLeuLysCysAlaThrLeuAspThrArgAlaLeu 332
Db 1320 GCCAAGGGCAACTCAGAGGTACTCTGACGGCGCATGTCTACAGCTGGGAGGACCTCGC 1379

QY 333 LysLeuAlaTyrSerAlaAlaCysGlyLeuCysHisLeuHisThrGluIleTyrGlyThr 352
Db 1186 CGGCACACTAC-----AAGATCTGGCGCGCTGCCGGGGCCGGCTGCACCTGAAACGAGCGC 1239


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Qy 197 GluAlaPheIleProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSer 216
Db 1240 GTGTCCTTCTC-----AGCTGCCGAGCTTGTGAATACACAGGCGCCAG 1287
Qy 217 GlySerGlySerGlyLeuProLeuLeuValGln----- 227
Db 1288 AGCCTGTCCACGCGCTGCGCTGCGCGCCCTGCGGAAGCAGCAGCCTGAGCCCTG 1347
Qy 228 -----ArgThrIleAlaLysGlnIleGlnMetValArgGlnValGly 241
Db 1348 CCCATTGGGATGACTGGGAGAGCCGAGGAGGAGTTCAGCTCTCCAGAGAGCTGGG 1407
Qy 242 LysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGlu-----LysValAlaVal 260
Db 1408 TCCGGCTACTTGGGAGGCTTCGAGGCGCTCTGGAAGACACCGGGTCCAGGTGGCCATT 1467
Qy 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db 1468 AAGGTGATT-----TCTCGAGACAACTCTCCGACCCAGCAG 1503
Qy 281 ValLeu-----MetArgHisGluAsnIleLeuGlyPhe 291
Db 1504 ATGCTGAGTCGGAGATCCAGGCATGAAGAGCTGCGGCACAAACACATCTTGGCGCTG 1563
Qy 292 IleAlaAlaAspIleLysGlyThrGlySerTrpThrGlnLeuTyrLeuIleThrAspTyr 311
Db 1564 TACGCCGTGTGTCGTTGGG-----GACCCCGTGTATCATCATCAGGAGCTC 1611
Qy 312 HisGluAsnGlySerLeuTyrAspPheLeuLysCysAla-----ThrLeuAspThr 328
Db 1612 ATGCCCAAGGCGACCTGCTGGAGCTGCTCCGGCACTCTGATGAGAAAGTCTCGCCGTT 1671
Qy 329 ArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCysGlyLeuCysHisLeuHisThrGlu 348
Db 1672 TCGAGCTGTGACATCGCTGCGAGTGGCTGAGGGCATGTGTACCTGGAGTGGCAG 1731
Qy 349 IleTyrGlyThrGlnGlyLysProAlaIleAlaHisArgAspLeuLysSerLysAsnIle 368
Db 1732 AATTAC-----ATCCACGCGGACCTGCGCGCCAGGACATC 1767
Qy 369 LeuIleLysLysAsnGlySerCysIleAlaAspLeuGlyLeuAlaValLysPheAsn 388
Db 1768 CTGCTCGGGGAACACCTCTCAAAGTTGGGGACTTCGGGTAGCCAGGCTTATCAAG 1827
Qy 389 SerAsp-----ThrAsnGluValAspIleProLeuAsnThrArgValGlyThrArg 405
Db 1828 GAGGAGCTTACTCTCCCATGACCAATATCCCTAC----- 1866
Qy 406 ArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsnHisPheGlnProTyr 425
Db 1867 AAGTGGAGCGCCCT-----GAAGCGCTCTCCGAGGCCATTACTCC----- 1908
Qy 426 IleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMetAlaArgCysIle 445
Db 1909 ACCAAATCCGACGCTGCTGCTTGGGATTTCTCTGCATGAGATGTTTCAGCAGG----- 1962
Qy 446 ThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMetValProSerAspPro 465
Db 1963 -----GTCAGGTGCCCTAC-----CCAGGCATGTCC 1989
Qy 466 SerTyrGluAspMetArgGluValValCysValLysArgLeuArg-----ProIleValSer 484
Db 1990 AACCATGAGCCTTCTGAGGTGGACCGCGGTACCGCATGCGCTGCGCTCTG----- 2043
Qy 485 AsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMetSerGluCysTrp 504
Db 2044 -----GAGTCCCGCCCGCGGTGCACAAAGCTGATGCTGATGATGCTG 2085
Qy 505 AlaHisAsnProAlaSerArg-----LeuThrAlaLeuArg 516
Db 2086 TGCAGGAGACCCCGAGCAGACCCCTGCTTCAAGGCCCTCGCG 2127
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RESULT 3

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US-11-186-283-3
; Sequence 3, Application US/11186283
; Publication No. US20050255520A1
; GENERAL INFORMATION:
; APPLICANT: Raju, Jeyaseelan
; TITLE OF INVENTION: NOVEL CARP PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MNI-068CP2
; CURRENT APPLICATION NUMBER: US/11/186,283
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/626,173
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: US/09/947,199A
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/111,938
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 09/291,839
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/458,457
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2505)
US-11-186-283-3
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Best Local Similarity:	25.95%	Mismatches:	132
Query Match:	8.74%	Indels:	74
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US-10-600-645-2 (1-532) x US-11-186-283-3 (1-2505)

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Qy 189 TyrAsnArgAspLeuGlnAspGluAlaPheIleProValGlyGluSerLeuLysAsp 208
Db 1261 -----GGAGATGGCTCTCTATGTGTCTGTTCATCACCCCTTGGGGAAG 1302
Qy 209 LeuIleAspGlnSerGlnSerSerGlySer-----GlySerGlyLeuProLeu 224
Db 1303 ATTAAGAGCATGACAAAGAGAGAGGAGGAGATATTCCTCTTAAGAGCTGGATTGCCTTCA 1362
Qy 225 LeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnValGlyLysGlyArg 244
Db 1363 CATTTCCATCTTCAGCTCTCA---GAAATTGAGTTCCATGAGATATTATTCGCTCAGCTTCT 1419
Qy 245 TyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaValLys----- 261
Db 1420 TTTGGGAAGATATATAAAGGACGATGCAGAAATAAATAGTGGCTATAAAACGTTATCGA 1479
Qy 262 -----ValPhePheThrThrGluGluAlaSerTrpPhe---ArgGluThrGluIleTyr 278
Db 1480 GCCAATACCTACTGCTCCCAAGTCAGATGGATATGTTTGGCAGAGGTGCCATT--- 1536
Qy 279 GlnThrValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGly 298
Db 1537 ---CTCTGCCAGCTCAATCATCTCCCTCGGTAATTTCAGTTTGTGGTCTTGTGTTGAATGAT 1593
Qy 299 ThrGlySerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyr 318
Db 1594 CCC-----AGCAGGTTTGGCCATTGTCTCAATACATATCAGGGGGTCTCTGTGTTTC 1644
```

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QY 319 AspPheLeu-----LysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyr 336
Db 1645 TCCCTCTTCATGACGAGAGAGGATCTTGATTTGCACTTAATAATTATTCAGTA 1704
QY 337 SerAlaAlaCysGlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysPro 356
Db 1705 GATGTGTCGCAAGGACATGAGTACCTTCACAACCTG-----ACACAG----- 1746
QY 357 AlaIleAlaHisArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCys 376
Db 1747 CCAATTATATCATCGTGACTTGACAGTACCAATATTTCTCTATGAGGATGGCATGCT 1806
QY 377 CysIleAlaAspLeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIle 396
Db 1807 GTGGTGGCAGATTTGGAGATCA---AGATTTCTACAGTCTCTGATGAAGACAAC--- 1860
QY 397 ProLeuAsnThrArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSer 416
Db 1861 ---ATGACAAAACAACCTGGAAACCTCCGTGGATGGCTCTGAGGTGTTACGCAGTGC 1917
QY 417 LeuSerLysAsnHisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIle 436
Db 1918 ACTCGGTACACC-----ATCAAGCAGATGTTCTCAGCTATGCTCTGTGT 1962
QY 437 IleTrpGluMetAlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuPro 456
Db 1963 CTGTGGGAAATT-----CTCACTGGC-----GAAATTCCA 1992
QY 457 TyrTyrAsnMetValPro-----SerAspProSerTyrGluAspMetArgGlu 472
Db 1993 TTGCTCATCTCAAGCCAGCGGTGGCGCAGCAGCATGGCTTACCACCACATCAGACT 2052
QY 473 ValValCysValLysArgLeuArgProIleValSer-----AsnArgTrpAsnSer 489
Db 2053 CCATTGGCTATTCCATTCCCAAGCCCATATCATCTCTGCTGATACGAGGGTGGAAACGCA 2112
QY 490 -----AspGluCysLeuArgAlaValLeuLysLeuMetSerGluCysTrp 504
Db 2113 TGTCCTGAAGGAGAGCCCAATTTCTGAAGTTGTATCAAGTTA---GAAGAGTGTCTC 2169
QY 505 AlaHis-----AsnProAlaSer 510
Db 2170 TGAACATTGAGCTGATGCTCTCTGCATCA 2199
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RESULT 4

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US-11-186-283-1
; Sequence 1, Application US/11186283
; Publication No. US20050255520A1
; GENERAL INFORMATION:
; APPLICANT: Raju, Jayaseelan
; TITLE OF INVENTION: NOVEL CARP PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MNI-068CP2
; CURRENT APPLICATION NUMBER: US/11/186,283
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/626,173
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: US/09/947,199A
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/111,938
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 09/291,839
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/458,457
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3025
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: (48)..(2552)
US-11-186-283-1
Alignment Scores:
Pred. No.: 6,2e-18 Length: 3025
Score: 248.00 Matches: 96
Percent Similarity: 44.32% Conservative: 68
Best Local Similarity: 25.95% Mismatches: 132
Query Match: 8.74% Indels: 74
Db: 21
US-10-600-645-2 (1-532) x US-11-186-283-1 (1-3025)
QY 177 LysHisTyr-----CysLysSerIleSerSerArgGlyArg 188
Db 1251 AAGCATATAAGACAGACACAGATGAATGGCCCTGAATGAATATTCACGCTCGA--- 1307
QY 189 TyrAsnArgAspLeuGlnAspGluAlaPheIleProValGlyGluSerLeuLysAsp 208
Db 1308 -----GGAGATGGCTCCTATGTGTCTGTTCATCACCTTGGGGAAG 1349
QY 209 LeuIleAspGlnSerGlnSerSerGlySer-----GlySerGlyLeuProLeu 224
Db 1350 ATTAAGACATGACAAAAGAGAGACAGATATTCCTCTCTTAAGAGCTGGATTGCCTTCA 1409
QY 225 LeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnValGlyLysGlyArg 244
Db 1410 CATTTCATCTTCAGCTCTCA---GAAATTGAGTTCCATGAGATTATTGGCTCAGGTTCT 1466
QY 245 TyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaValLys----- 261
Db 1467 TTTGGGAAGTATATAAAGGACGATGCAGAAATAAATAGTGGCTATAAAGCTTATCGA 1526
QY 262 -----ValPhePheThrGluGluAlaSerTrpPhe---ArgGluThrGluIleTyr 278
Db 1527 GCCAATACCTACTGCTCCCAAGTCAGATGTGATATGTTTTCGCGAGAGGTGCCATT--- 1583
QY 279 GlnThrValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGly 298
Db 1584 ---CTCTCCAGCTCAATATCCCTGCGTAATTCAGTTTGTGGTGTCTTGAATGAT 1640
QY 299 ThrGlySerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyr 318
Db 1641 CCC-----AGCCAGTTTGCCATGCTCACTCAATACATATCAGGGGTTCTCTGTTC 1691
QY 319 AspPheLeu-----LysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyr 336
Db 1692 TCCCTCTCTCATGACGAGAGAGGATCTTGATTTGCAGTCTAAATTAATTATTCAGTA 1751
QY 337 SerAlaAlaCysGlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysPhe 356
Db 1752 GATGTGTCGCAAGGACATGGATGACTTCCAAACCTG-----ACACAG----- 1793
QY 357 AlaIleAlaHisArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCys 376
Db 1794 CCAATTATATCATGCTGACTTGAACAGTCACAAATATTTCTCTCTATGAGATGGGATGCT 1853
QY 377 CysIleAlaAspLeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIle 396
Db 1854 GTGGTGGCAGATTTGGAGAAATCA---AGATTTCTACAGTCTCTCGATGAAGACAAC--- 1907
QY 397 ProLeuAsnThrArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSer 416
Db 1908 ---ATGACAAAACAACCTGGGAAACCTCGTTGGATGGCTCTCTGAGGTGTTACAGCATGC 1964
QY 417 LeuSerLysAsnHisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIle 436
Db 1965 ACTCGGTACACC-----ATCAAGCAGATGTTCTCAGCTATGCTCTGTGT 2009
QY 437 IleTrpGluMetAlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuPro 456
Db 2010 CTGTGGGAAATT-----CTCACTGGC-----GAAATTCCA 2039
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QY 457 TyrTyrAsnMetValPro-----SerAspProSerTyrGluAspMetArgGlu 472
Db 2040 TTGCCTCATCTCAAGCCAGCGGTGCGGACAGACATGGCTTACCACACATCAGACCT 2099
QY 473 ValValCysVallysArgLeuArgProIleValSer-----AsnArgTrpAsnSer 489
Db 2100 CCATTGGCTATTCTCCATTCCCAAGCCCATATCATCTCTGTGATACGAGGTGGAACGCA 2159
QY 490 -----AspGluCysLeuArgAlaValLeuLysLeuMetSerGluCysTrp 504
Db 2160 TGTCTGAAGGAAGACCCGAAATTTCTGAAGTTGTCTGAAGTTA---GAAGAGTGTCTC 2216
QY 505 AlaHis-----AsnProAlaSer 510
Db 2217 TGCAACATTGAGCTGATGCTCTCTGCATCA 2246

RESULT 5

US-11-186-283-9
; Sequence 9, Application US/11186283
; Publication No. US2005025520A1
; GENERAL INFORMATION:
; APPLICANT: Raju, Jeyaseelan
; TITLE OF INVENTION: NOVEL CARP PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: THEREFOR
; CURRENT APPLICATION NUMBER: US/11/186,283
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/626,173
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: US/09/947,199A
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/111,938
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 09/291,839
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/458,457
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2505
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2505)
US-11-186-283-9

Alignment Scores:
Pred. No.: 2 34e-17 Length: 2505
Score: 242.00 Matches: 144
Percent Similarity: 40.44% Conservative: 95
Best Local Similarity: 24.37% Mismatches: 177
Query Match: 8.53% Indels: 178
DB: 7 Gaps: 34

US-10-600-645-2 (1-532) x US-11-186-283-9 (1-2505)

QY 25 AsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAspGlnLysLysPro 44
Db 640 AACATTGTGAACACTCCTGGTAGAAGAGGAGGCAAGCAGATGTGAACGCTCAG----- 693
QY 45 GluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLysCysTyrCysSer 64
Db 694 GACAAT-----GAAGACCAGTCCCTCTGCACCTCTGTTCTCGATTT 735
QY 65 GlyHis----- 66
Db 736 GGACACCAATATAGTAGCTACCTGCTCCAGAGTGACTTAGAGGTCCAGCCTCAGTTC 795
QY 67 -----CysProAspAspAlaIleAsnAsnThrCysIleThrAsnGlyHisCysPhe 83
Db 796 ATTAACATCTATGGTGACACTCTCTTGGCACCTGGCATGCTAC---AATGGAAT---TTT 849

QY 84 AlaIleIleGluGluAspAspGln-----GlyGluThrThrLeuThrSerGlyCysMet 101
Db 850 GAAGTTGCCAGGAATTTGTCAGGTACAGGAATGAAAGTCTGACTAA-GGAAACAT 908
QY 102 LysTyrGluGlySerAspPheGlnCys-----LysAspSerProLysAlaGln 117
Db 909 CTTACGCGAGACAGCTTTTTCACAGTCTTGTTACCTATATGCAAGAACATTGACCTGCTCAA 968
QY 118 LeuArgArgThrIleGluCysCys-----Arg 126
Db 969 ATTTCTTCTTGATCAGAAATGCTGTGAACATTAACCAACGAGGAGATGGGCACACAGG 1028
QY 127 ThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProValIleGlyProPhe 146
Db 1029 ATTGCACCTCTGC-----TTGCTACCA-----CGGCCATAT 1058
QY 147 PheAspGlySerValArgTrpLeuAlaValLeuIleSerMetAlaValCysIleValAla 166
Db 1059 CGCCCTGGTTTCAGTTCC-TAC-----TTGATAATGGTGCAGATATGAATCTTTGTCG 1108
QY 167 MetIleValPheSer-----SerCysPheCysTyr--- 176
Db 1109 CTTGTGATCCC-AGCAGGTTCTAGTGGTGAAAGATGAGCAGACATGTTTGATGTGGGCT 1167
QY 177 -----LysHisTyrCysLysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGlu 194
Db 1168 TAGGAGAAGGACATGATGCCATTGTTACATCTCTGAAGCATTACAGAGACCCAGGAG 1227
QY 195 GlnAspGluAlaPheIleProValGlyGluSerLeuLysAspLeuIleAspGlnSerGln 214
Db 1228 GAG-----CTGCCATGTAACGAA-----TATTCCCAG 1254
QY 215 SerSerGlySerGlySerGlyLeu-----ProLeuLeuValGlnArgThrIle 230
Db 1255 CCTGGAGGAGATGGCTCTCTATGTCTGTCTTCCCTTGGCAAGATTAAAGCATG 1314
QY 231 AlaLys----- 232
Db 1315 ACAAAAGAGAGGACGATGTTCTCTCTGAGGGGTGAACCTACCTCCCGCTTCCATCTC 1374
QY 233 -----GlnIleGlnMetValArgGlnValGlyLysGlyArgTyrGlyGluValTrp 249
Db 1375 CAACCTCTCGAATTCGAGTTCCACGAGATTATCGGCTCGGGTTCCTTTGGGAAGTCTAT 1434
QY 250 MetGlyLysTrpArgGlyGluLysValAlaValLys-----ValPhePhe 264
Db 1435 AAAGGGCGATGCAGAAATAAATAAGTGGCGATCAACGATACCGAGCCACCACTACTGC 1494
QY 265 ThrThrGluGluAlaSerTrpPhe---ArgGluThrGluIleTyrGlnThrValLeuMet 283
Db 1495 TCCAAAGTCAGACGTGGATATGTTTTCGCGAGAGAGGTGTCCATT-----CTCTGCCAGCTC 1548
QY 284 ArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGlySerTrpThr 303
Db 1549 AACCAACCCCTCGCTGCTTCTGCTGGTGGCTGCTGCTGGATGACCCC-----ACT 1599
QY 304 GlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPheLeu----- 321
Db 1600 CAGTTTGGCATTTGCTCACTCAGTACATTTTCAGGAGGCTCCCTGTTCTCTCCCTTTCATGAA 1659
QY 322 LysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCysGly 341
Db 1660 CAGAAGAAATTTCTTGACTTGCAGTCTAAATTAATCATTTGCCGTAGACCTTCCCAAGGC 1719
QY 342 LeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHisArg 361
Db 1720 ATGGAGTACCTGCACAGCTTG-----ACCCAG-----CCAATCATACACCCG 1761
QY 362 AspLeuLysSerLysAsnIleLeuLysLysAsnGlySerCysCysIleAlaAspLeu 381
Db 1762 GACCTGAACAGCACAATATTCTGCTATGAGGATGGCCATGCTGCTGTGTGGCAGATTTT 1821


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QY 394 ValAspIleProLeuAsnThrArgValGlyThrArgArgTyrMetAlaProGluValLeu 413
Db 2506 GCAGATGATCCCATC-----CGCTGACCGCCCGAGGCCATT 2544
QY 414 AspGluSerLeuSerLysAsnHisPheGlnProTyrIleMetAla--AspIleTyrSer 432
Db 2545 TCC-----TACCGGAAGTTACACTCTGCCAGCGAGTGTGGAGC 2583
QY 433 PheGlyLeuIleIleTyrPheGluMetAlaArgCysIleThrGlyGlyValGlu 452
Db 2584 TTTCGCAATGTCATCTGGAGGTG-----ATGACCTATGGC----- 2619
QY 453 TyrGlnLeuProTyrTyrAsnMetValProSerAspProSerTyrGluAspMetArgGlu 472
Db 2620 ---GAGCGGCCCTACTGGAGTTG-----TCCAAACACGAGGTGATGAAGCC 2664
QY 473 ValValCysValLysArgLeu--ArgProIleValSerAsnArgTyrAsnSerArgGlu 491
Db 2665 ATCAATGATGGCTTCCGGCTCCCCACACCCATG-----GAC 2700
QY 492 CysLeuArgAlaValLeuLysLeuMetSerGluCysTyrPheAlaHisAsnProAlaSerArg 511
Db 2701 TGCCCTCGCCCATCTACAGCTCATGTCAGTCTGCAGCAGGAGCGTCCCGCCGC 2760
QY 512 LeuThrAlaLeuArgIleLysLysThrLeuAlaLysMetValGluSerGlnAsp 529
Db 2761 CCCAAGTTCGCTGACATCGTCAGCATCTCTGGACAAGCTCAATTCGTGCCCTGAC 2814
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RESULT 8

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US-10-990-276-2
; Sequence 2, Application US/10990276
; Publication No. US2005025549A1
; GENERAL INFORMATION:
; APPLICANT: Wesche, Holger
; APPLICANT: Li, Shyun
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
; FILE REFERENCE: 018781-003910US
; CURRENT APPLICATION NUMBER: US/10/990,276
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US/09/759,595
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 60/176,395
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1383
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human IL-1 receptor-associated kinase 4 (IRAK-4)
; OTHER INFORMATION: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1383)
; OTHER INFORMATION: human IRAK-4
US-10-990-276-2
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Alignment Scores:

Pred. No.:	2,07e-16	Length:	1383
Score:	230.50	Matches:	87
Percent Similarity:	44.12%	Conservative:	48
Best Local Similarity:	28.43%	Mismatches:	118
Query Match:	8.12%	Indels:	53
DB:	6	Gaps:	12

US-10-600-645-2 (1-532) x US-10-990-276-2 (1-1383)

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QY 239 GlnValGlyLysGlyArgTyrGlyGluValTyrPheMetGlyLysTyrArgGlyGluLysVal 258
Db 571 AAAATGGGAGGAGGAGGATTTGGAGTTGTATATAAAGGCTACGTAATAACACAACTGTG 630
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QY 259 AlaValLys-----ValPhePheThrThrGluGluAlaSerTrpPheArg 273
Db 631 GCAGTGAAGAAGCTTGCAGCAATGGTTGACATTACTACTGAAGAACCTGAAACAGCAGTTT 690
QY 274 GluThrGluIleTyrGlnThrValLeuMetArgHisGluAsn-----IleLeuGly 290
Db 691 GATCAAGAAATAAAGTAATGGCAAGTGTCAACATGAAACTTAGTAGAACTACTCTGGT 750
QY 291 PheIleAlaAlaAspIleLysGlyThrGlySerTrpThrGlnLeuTyrLeuIleThrAsp 310
Db 751 TTC-----TCAAGTCATGGAGATGACCTCTGCTTAGTATATGTT 789
QY 311 TyrHisGluAsnGlySerLeuTyrAspPheLeuLysCys-----AlaThrLeu 326
Db 790 TACATGCTAATGGTTTCATTCCTAGACAGACACTCTCTCTTGGATGGTACTCCACCACTT 849
QY 327 AspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCysGlyLeuCysHisLeuHis 346
Db 850 TCTTGGCACATGAGATGCAAGATTGCTCAGGGTCAGCTAATGGCATCAATTTTCTACAT 909
QY 347 ThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHisArgAspLeuLysSerLys 366
Db 910 GAAATCATCAT-----ATTCATAGAGATATTAAAGTGCA 945
QY 367 AsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAspLeuGlyLeuAlaValLys 386
Db 946 AATATCTTACTGGATGAAGCTTTTACTGCTAAAATATCTGACTTTGGCTTGGCAGGGCT 1005
QY 387 PheAsnSerAspThrAsnGluValAspIleProLeuAsnThrArgValGlyThrArgArg 406
Db 1006 -----TCTGAGAAAGTTTGGCCAGACAGTCATGATGACAGAAATGTGGGAACAAACAGCT 1059
QY 407 TyrMetAlaProGluValLeuAspGluSerLeuSerLysAsnHisPheGlnProTyrIle 426
Db 1060 TATATGGCACAGAGCTTTTGGTGGAGAAATAACACCCAAA----- 1101
QY 427 MetAlaAspIleTyrSerPheGlyLeuIleIleTyrPheGluMetAlaArgCysIleThr 446
Db 1102 ---TCTGATATTTACAGCTTTGGTGTGTTTTTACTAGAAATA-----ATAACT 1146
QY 447 Gly---GlyIleValGluGluTyrGlnLeuProTyrTyrAsnMetValProSerAspPro 465
Db 1147 GGACTTCCAGCTGTGGATGAACACCGTGAACCTCAGTTATTGGCTA----- 1191
QY 466 SerTyrGluAspMetArgGluValVal-----CysValLysArgLeuArgProIleVal 483
Db 1192 -----GATATTAAAGAAAGAAATTCAGATGAAGAAAGACAAATTGAAGATTATATT 1242
QY 484 SerAsnArgTrpAsnSerAspGlu-----CysLeuArgAlaValLeuLysLeuMetSer 501
Db 1243 GATAAAAGATGAATGATGCTGATTCCACTTTCAGTTGAAGCTATCTACTCTGTTGCTAGT 1302
QY 502 GluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThrHis 527
Db 1303 CAATGCTGTCATGAAAAAGAAAAATAAGAGACCAGACATTAAAGAGGTTCAACAGCTGCTG 1362
QY 522 AlaLysMetValGluSer 527
Db 1363 CAAGAGATGACAGCTTCT 1380
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RESULT 9

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US-10-990-276-4
; Sequence 4, Application US/10990276
; Publication No. US2005025549A1
; GENERAL INFORMATION:
; APPLICANT: Wesche, Holger
; APPLICANT: Li, Shyun
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
; FILE REFERENCE: 018781-003910US
; CURRENT APPLICATION NUMBER: US/10/990,276
; CURRENT FILING DATE: 2004-11-15
```

;; PRIOR APPLICATION NUMBER: US/09/759,595
;; PRIOR FILING DATE: 2001-01-13
;; PRIOR APPLICATION NUMBER: US 60/176,395
;; PRIOR FILING DATE: 2000-01-13
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: Patent in ver. 2.1
;; SEQ ID NO 4
;; LENGTH: 1542
;; TYPE: DNA
;; ORGANISM: Mus sp.
;; FEATURE:
;; OTHER INFORMATION: murine IL-1 receptor-associated kinase 4 (IRAK-4)
;; OTHER INFORMATION: CDNA
;; NAME/KEY: CDS
;; LOCATION: (163)..(1542)
;; OTHER INFORMATION: murine IRAK-4
US-10-990-276-4

Alignment Scores:
Pred. No.: 2,82e-16 Length: 1542
Score: 230.00 Matches: 86
Percent Similarity: 43.00% Conservative: 43
Best Local Similarity: 28.67% Mismatches: 103
Query Match: 8.10% Indels: 68
DB: 6 Gaps: 13

US-10-600-645-2 (1-532) x US-10-990-276-4 (1-1542)

QY 177 LysHisTyrCysLysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluInAsp 196
Db 586 GAACACAGCTGCGAGCCGCGACTCTCAAGCCAGACCAACAGAGTGTAGAGTCCAGC 645
QY 197 Glu-----AlaPheIleProValGlyGluSerLeuLysAspLeuLe 210
Db 646 GACACTCGGTCCACAGCTTCTCGTTCCATGAACCTG---AAGAGCATCAACAACTTC 702
QY 211 AspGlnSerGlnSerGlySerGlySerGlyLeuProLeuValGlnArgThrIle 230
Db 703 GACGAGCAACCCGCGTCTCGCGGTGGCAAC----- 732
QY 231 AlaLysGlnIleGlnMetValArgGlnValGlyLysGlyArgTyrGlyGluValTrpMet 250
Db 733 -----CGGATGGGAGAGGGGATTTCGAGTGGGTGTACAG 768
QY 251 GlyLysTrpArgGlyGluLysValAlaValLys-----ValPhePheThr 265
Db 769 GGCTGTGTGAACAAACACCATCGTGGCGGTGAAGAAGCTCGAGCGATGGTTGAAATCAGT 828
QY 266 ThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThrValLeuMetArgHis 285
Db 829 ACTGAAGNACTAAGCAACAGTTTGAICAGAATAAAGTAATGGCAACGGTGTACGAC 888
QY 286 GluAsn-----IleLeuGlyPheIleAlaAlaAspIleLysGlyThrGlySerTrp 302
Db 889 GAGAACCTGGTGAGCTGCTCGGCTTC-----TCCAGCGACAGC 927
QY 303 ThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPheLeuLys 322
Db 928 GACAACCTGTGTAGTGTATGTCTTACATGCCCAACGGGTCTTGTGTGGACAGACTGTCC 987
QY 323 Cys-----AlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAla 338
Db 988 TGCTGTAGGTGATACACCGCTTCTTCTGGCACACAAAGGTGCAAGGTGTCTACGGGGACA 1047
QY 339 AlaCysGlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIle 358
Db 1048 GCAATGGCATCAGGTTCTGCATGAAATCATCAC----- 1083
QY 359 AlaHisArgAspLeuLysSerLysAsnIleLeuIleLysAsnGlySerCysLysIle 378
Db 1084 ATTCATAGAGATATTAAGTGAATAATCTTACTAGACAAAGACTTTTACTGCCAAATA 1143

QY 379 AlaAspLeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeu 398
Db 1144 TCTGACTTTGGGCTTGCA-----CGGCTTCGCAAGGCTAGCGACGGTCAATG 1194
QY 399 AsnThrArg---ValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeu 417
Db 1195 ACCAGCGAATCGTGGGCACACAGCGCTTACATGGCACCCAGAGCTTTGGCGGAGAAATA 1254
QY 418 SerLysAsnHisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIle 437
Db 1255 ACACCCAAA-----TCTGACATCTACAGCTTCGCGGTGGTCTG 1293
QY 438 TrpGluMetAlaArgArgCysIleThrGly---GlyIleValGluGluTyrGlnLeuPro 456
Db 1294 TTGAGACTG-----ATAACCGGCTCGCGGCTGTGGATGAAACCGTGAACCT 1341
RESULT 10
US-10-770-726-17
;; Sequence 17, Application US/10770726
;; Publication No. US20050266409A1
;; GENERAL INFORMATION:
;; APPLICANT: Wyeth
;; APPLICANT: Brown, Eugene
;; APPLICANT: Liu, Wei
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
;; TITLE OF INVENTION: CANCERS
;; FILE REFERENCE: AM101079 (031896-010000)
;; CURRENT APPLICATION NUMBER: US/10/770,726
;; CURRENT FILING DATE: 2004-02-04
;; NUMBER OF SEQ ID NOS: 48640
;; SOFTWARE: Patent in version 3.2
;; SEQ ID NO 17
;; LENGTH: 6058
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-770-726-17

Alignment Scores:
Pred. No.: 7,37e-15 Length: 6058
Score: 226.00 Matches: 99
Percent Similarity: 40.80% Conservative: 74
Best Local Similarity: 23.35% Mismatches: 137
Query Match: 7.96% Indels: 114
DB: 6 Gaps: 21

US-10-600-645-2 (1-532) x US-10-770-726-17 (1-6058)

QY 140 ProValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSer 159
Db 1642 CCACCTCATCGGCTCTCGCGCGCTGGCTTCTCTCATCTGCTGGTGTGCATC 1701
QY 160 MetAlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyr 179
Db 1702 GCCATCGTGTGT----- 1713
QY 180 CysLysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPhe 199
Db 1714 -----AACAGAACCGGGGTTTGAGCGTGTGCTGATC 1746
QY 200 IleProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGly 219
Db 1747 -----GAGTACACGGACAACTGCAACACTACACCATGGTGGC 1782
QY 220 -----SerGlyLeuProLeuValGln----- 227
Db 1783 CACATGACCCAGGATGAAGATCTACATGATCTTTTCCCTTACGAGGACCCCAACGAG 1842
QY 228 -----ArgThrIleAlaLysGlnIleGlnMet-----ValArgGlnVal 240
Db 1843 GCAGTGGCGGAGTTTGCCCAAGAAATTGACATCTCTCTGTGTCAAAATTCAGCAGGTGATC 1902
QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGly-----LysTrpArgGlyGluLys 257

```
Dbb 1903 GGAGCAGGGGAGTTTGGCGAGGTCTGCAGTGGCCACCTGAAGCTGCCAGGCAAGAGAG 1962
Qy 258 -----ValAlaValLysValPhe-----PheThrThrGluGluAlaSerTrpPhe 272
Db 1963 ATCTTTGTGGCCATCAAGACGCTCAAGTGGGCTACACGGAGACAG-----2010
Qy 273 ArgGluThrGluIleTyGlnThrValLeuMet-----ArgHisGluAsnIleLeu 289
Db 2011 CCGCGGGAGCTTCTGAGCAAGCCTCATCATGGGCCAGTTCGACATCCCAACGTATC 2070
Qy 290 GlyPheIleAlaAlaAspIleLysGlyThrGlySerTrpThrGlnLeuTyRleIleThr 309
Db 2071 CACCTGGAGGTGCTGCACACAGAGC-----ACACCTGTGATGATCATCACC 2118
Qy 310 AspTyRHisGluAsnGlySerLeuTyRAspPheLeuLys-----CysAlaThrLeuAsp 327
Db 2119 GAGTTTCATGGAATGGCTCCCTGGACTCTTCTCGGCAAAACGATGGCGAGTTTACA 2178
Qy 328 ThrArgAlaLeuLeuLysLeuAlaTyRSerAlaAlaCysGlyLeuCysHisLeuHisThr 347
Db 2179 GTCATCCAGCTGGTGGGCATGCTTCGGGGCATCGCAGCTGGCATGAAGTACCTGGCAGAC 2238
Qy 348 GluIleTyRThrGlnGlyLysProAlaIleAlaHisArgAspLeuLysSerLysAsn 367
Db 2239 ATGAACTAT-----GTTTCCCGTGACTGGCTGCCCGCAAC 2274
Qy 368 IleLeuIleLysLysAsnGlySerCysCysIleAlaAspLeuGlyLeuAlaValLysPhe 387
Db 2275 ATCTCGTCAACAGCAACCTGTCTGCAAGGTGTCGAGCTTGGGCTCTCACGCTTTCTA 2334
Qy 388 AsnSerAspThrAsnGluValAspIleProLeuAsnThrArgValGlyThrArg-----405
Db 2335 GAGGACGATACCTCA-----GACCCCACTACACAGTGCCTCGGGGGAAGATCCCC 2388
Qy 406 ---ArgTyRMetAlaProGluValLeuAspGluSerLeuSerLysAsnHisPheGlnPro 424
Db 2389 ATCCGCTGGACAGCCCGGAAGCCATC-----CAGTACCGGAAG 2427
Qy 425 TyrIleMetAla---AspIleTyRSerPheGlyLeuIleIleTrpGluMetAlaArgArg 443
Db 2428 TTCACTCGCGCAGTGATGTGGAGCTACGGCATTGTTCATGGGAG-----2475
Qy 444 CysIleThrGlyGlyIleValGluGluTyRLeuLeuProTyRThrAsnMetValProSer 463
Db 2476 -----GTGATGTCCTATGGGGAGCGGCCCTACTGGACATACCAACACAG 2520
Qy 464 AspProSerTyRLeuAspMetArgGluValValCysValLysArgLeuArgProfileVal 483
Db 464 ATCTATATCTATATCTATATCTATATCTATATCTATATCTATATCTATATCTATAT 2568
Qy 484 SerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMetSerGluCys 503
Db 2569 -----GACTGCCGAGCGCCCTGCACCACTCATGTGGACTGT 2607
Qy 504 TrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThrLeuAlaLys 523
Db 2608 TGGCAGAGGACCGCAACACCGCCCAAGTTTCGGCCAAATTTGTCAACACGCTAGACAAG 2667
Qy 524 MetValGluSer 527
Db 2668 ATGATCCGCNAAT 2679
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RESULT 11

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US-11-021-441-19
; Sequence 19, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; AND METHODS OF USE
```

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; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 282172003900
; CURRENT APPLICATION NUMBER: US/11/021,441
; FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/616,750
; FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/615,287
; FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/599,377
; FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: PCT/US2004/23881
; FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 10/883,599
; FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/556,744
; FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 1437
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein coding sequence
US-11-021-441-19
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Alignment Scores:
Pred. No.: 1,29e-15 Length: 1437
Score: 224.00 Matches: 91
Percent Similarity: 41.33% Conservative: 64
Best Local Similarity: 24.27% Mismatches: 150
Query Match: 7.89% Indels: 70
DB: 7 Gaps: 18
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US-10-600-645-2 (1-532) x US-11-021-441-19 (1-1437)

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Qy 177 LysHisTyRcysLysSerIleSerSerArgGlyArgTyRAsnArgAspLeuGluGln--- 195
Db 166 AAACAC-----GCGGATCTCGACACCGCAGGAGGAAGAACCCAGCTGCCAGTCC 219
Qy 196 ---AspGluAlaPheIleProValGlyGluSerLeuLysAspLeu-----IleAsp 211
Db 220 CCGAGGAGCTTACTTCTCAAGTCAGAAACAACCTGAAGCCCTGAAGACATACGTGGAC 279
Qy 212 GlnSerGlnSerSerGlySerGlySerGlyLeuProLeuLeuValGlnArgThrIleAla 231
Db 280 CCCACACATATGAGGACCCCAACAGGCTGTGTGAAGTTCACTACCGAGATCCATCCA 339
Qy 232 LysGlnIleGlnMetValArgGlnValGlyLysGlyArgTyRgLyGluValTrpMetGly 251
Db 340 TCCTGTGTCACTCGGCAGAGGTGATCGGACGAGAGATTGGGGAGGTGTACAAGGCG 399
Qy 252 -----LysTrpArgGlyGluLysValAlaValLysValPhePheThrThrGluGluAla 269
Db 400 ATGCTGAAGACATCTCTGGGGAAGAAGAGGTGCGGTGGCCATCAACACGCTGAAGGCC 459
Qy 270 SerTrpPheArgGluThrGluIleTyRglnThrValLeuMetArgHisGluAsnIleLeu 289
Db 460 GGCTAC-----ACAGAGAAGCAGCGAGTGGACTTCTCTCGGCGAGCGGCATCATG 510
Qy 290 GlyPheIleAla-----AlaAspIleLysGlyThr---GlySerTrpThrGln 304
Db 511 GGCCAGTTTCAGCCACCACCAACATCATCCGCTAGAGGCGCTCATCTCCAAATACAAGGCC 570
Qy 305 LeuTyRleIleThrAspTyRHisGluAsnGlySerLeuTyRAspPheLeu-----Lys 322
Db 571 ATGATGATCATCACTAGTATAGATGAGATGGGCCCTGGACAAGTTCTCTCGGAGAGAAG 630
Qy 323 CysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyRSerAlaAlaCysGlyLeu 342
Db 631 GATGCGAGTTTCAGCGTCTCGAGCTGGTGGGCATGCTCGCGGGCATCGCAGCTGGCATG 690
Qy 343 CysHisLeuHisThrGluIleTyRglnGlnGlyLysProAlaIleAlaHisArgAsp 362
```



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Db 691 AAGTACCTGCCCAACATGAATAT-|||||
Qy 363 LeuLysSerLysAsnIleLeuLysAsnGlySerCysCysIleAlaAspLeuGly 382
Db 727 CTGGTCCCGCAACATCTCTGCAAGAGTGTCTGACTTTGGC 786
Qy 383 LeuAlaValLysPheAsnSerAsp-|||||
Db 787 CTGTCCCGCTGTGGAGGACGACCCGAGGCGCACCTACACCACTGTGGCGCAAGATC 846
Qy 397 ProLeuAsnThrArgValGlyThrArgArgTyMetAlaProGluValLeuAspGluSer 416
Db 847 CCCATC-|||||
Qy 417 LeuSerLysAsnHisPheGlnProTyIleMetAla-AspIleTySerPheGlyLeu 435
Db 880 -|||||
Qy 436 IleIleTrpGluMetAlaArgCysIleThrGlyGlyIleValGluGluTyGlnLeu 455
Db 925 GTCATGTGGAGGTG-|||||
Qy 456 ProTyTrpAsnMetValProSerAspProSerTyGluAspMetArgGluValValCys 475
Db 958 CCCTACTCTGGAGTTG-|||||
Qy 476 ValLysArgLeu-ArgProIleValSerAsnArgTrpAsnSerAspGluCysLeuArg 494
Db 1006 GGCTTCGGCTCCCCACACCATG-|||||
Qy 495 AlaValLeuLysLeuMetSerGluCysTrpAlaHisAsnProAlaSerArgLeuThraLa 514
Db 1042 GCATCTACAGCTCATGTCAGTCTGGCAGCAGGCGGTGCCCGCCCAAGTTC 1101
Qy 515 LeuArgIleLysLysThrLeuAlaLysMetValGluSerGlnAsp 529
Db 1102 GGTGACATCGTCAGCATCTCTGGACAAGCTCATTCGTGGCCCTGCAC 1146
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RESULT 12

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US-11-021-441-16
; Sequence 16, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 282172003900
; CURRENT APPLICATION NUMBER: US/11/021,441
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/616,750
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/615,287
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/599,377
; PRIOR FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: PCT/US2004/23881
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 10/883,599
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/556,744
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1254
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-021-441-16
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Alignment Scores:
Pred. No.: 1,79e-15 Length: 1254
Score: 222.00 Matches: 89
Percent Similarity: 41.53% Conservative: 63
Best Local Similarity: 24.32% Mismatches: 146
Query Match: 7.82% Indels: 68
DB: 7 Gaps: 17
US-10-600-645-2 (1-532) x US-11-021-441-16 (1-1254)
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Qy 186 ArgGlyArgTyAsnArgAspLeuGluGln-----AspGluAlaPheIleProValGly 203
Db 4 CGCAGGAGGAAGAACCGAGCTGCCCGCCAGTCCCGGAGGACGCTTTACTTCTCCAAGTCA 63
Qy 204 GluSerLeuLysAspLeu-----IleAspGlnSerGlnSerSerGlySerGlySer 220
Db 64 GAACAACCTGAAGCCCTGAAGACATACGTGGAGCCCGCCACACATATAGGAGCCCAACCCAG 123
Qy 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 124 GCTGTGTTGAAGTTCACTACCGAGATCCATCTCTGTCTACTCGGAGAAAGGTGATC 183
Qy 241 GlyLysGlyArgTyArgGlyValTrpMetGly-----LysTrpArgGlyGluLysVal 258
Db 184 CGAGCAGGAGAGTGTGGGAGGTGTACAAGGGCATCTCTGAAGACATCTCTCGGGGAAGAAG 243
Qy 259 AlaValLysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTy 278
Db 244 GAGGTGCGGTGGCCCATCAAGACGCTGAAAGCGGGCTAC-----ACAGAGAAGCAG 294
Qy 279 GlnThrValLeuMetArgHisGluAsnIleLeuGlyPheIleAla-----Ala 294
Db 295 CGAGTGGACTTCTCGCGCGCGCCGATCATGGCCAGTTCAGCCACCAACATCATC 354
Qy 295 AspIleLysGlyThr---GlySerTrpThrGlnLeuTyLeuIleThrAspTyHisGlu 313
Db 355 CGCTAGAGGGCGTCAATCCAAATACAGCCCATGATCATCATCATCATCTGAGTACATGGAG 414
Qy 314 AsnGlySerLeuTyAspPheLeu-----LysCysAlaThrLeuAspThrArgAlaLeu 331
Db 415 AATGGGCGCTCGACAAGTTCTCTCGGAGAAAGGATGGCGAGTTTCAGCGTGTGTCAGCTG 474
Qy 332 LeuLysLeuAlaTySerAlaAlaCysGlyLeuCysHisLeuHisThrGluIleTyGly 351
Db 475 GTGGCGATGCTCGGGGCGATCCAGCTGCAAGTACCTGGCAAGTACCTGGCCAAACATGAAT 531
Qy 352 ThrGlnGlyLysProAlaIleAlaHisArgAspLeuLysSerLysAsnIleLeuLys 371
Db 532 -----GTGCACCGCTGACCTGGCTGGCTGCCCGCCGCAACATCTCTCGTCAAC 570
Qy 372 LysAsnGlySerCysCysIleAlaAspLeuGlyLeuAlaValLysPheAsnSerAsp 390
Db 571 AGCAACCTGTCTGCAAGGTGTCTGACTTTGGCTGTCTCCGCTGTCTGGAGGAGCAGCCCC 630
Qy 391 -----ThrAsnGluValAspIleProLeuAsnThrArgValGlyThrArg 405
Db 631 GAGGCCACTACACCAGCGGCGCAAGATCCCATC-----TACCGGAAGTTTC 669
Qy 406 ArgTyMetAlaProGluValLeuAspGluSerLeuSerLysAsnHisPheGlnProTy 425
Db 670 CGCTGGACCGCCCGGAGGCCATTTCC-----TACCGGAAGTTTC 708
Qy 426 IleMetAla---AspIleTySerPheGlyLeuIleTrpGluMetAlaArgCys 444
Db 709 ACCTCTGCCAGCGAGTGTGGAGCTTTGGCATTGTGTCATGTGGAGGTG----- 756
Qy 445 IleThrGlyGlyIleValGluGluTyGlnLeuProTyTrpAsnMetValProSerAsp 464
Db 757 ATGACCTATGGC-----GAGCGGCCCTACTGGGAGTTG----- 789
Qy 465 ProSerTyGluAspMetArgGluValValCysValLysArgLeu---ArgProIleVal 483
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 9, 2005, 19:17:20 ; Search time 4008 Seconds
(without alignments)

6210.261 Million cell updates/sec

Title: US-10-600-645-2

Perfect score: 2838

Sequence: 1 MTQLTYIRLLGACLFISH.....TALRIKKTAKWVESODVKI 532

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame_plus_p2n.model -DRV=xlh

-Q=/cgn2_1/USPTO.spool/US1060645/runat_02122005_103605_23292/app_query.fasta_1.711

-DB=EST -QFMT=fastap -SUFFIX=rest -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0

-UNITG=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45

-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL

-OUTFMT=pco -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000

-USER=US1060645_@CEN_1_1_4015@runat_02122005_103605_23292 -NCPU=6 -ICPU=3

-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG

-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hic:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gss1:*

10: gb_gss2:*

11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2648.5	93.3	1521	10 AY411158	AY411158 Mus muscu
2	2640	93.0	1532	10 AY411156	AY411156 Homo sapi
3	1992	70.2	1532	10 AY411157	AY411157 Pan trogl
4	1942	68.4	1911	4 AK086130	AK086130 Mus muscu
5	1941	68.4	1509	10 AY418113	AY418113 Homo sapi
6	1933.5	68.1	1509	10 AY418115	AY418115 Mus muscu
7	1795	63.2	1509	10 AY418114	AY418114 Pan trogl

8	1626.5	57.3	1121	3	BM473726	BM473726 AGENCOURT
9	1501	52.9	874	1	AU124197	AU124197 HES2C.59
10	1432	50.5	826	8	DR156725	DR156725 HES2C.59
11	1384.5	48.8	842	8	CX204646	CX204646 MNS075.40
12	1353	47.7	779	7	CK638737	CK638737 UI-M-H2O-
13	1342	47.3	783	6	CF744610	CF744610 UI-M-GVO-
14	1342	47.3	807	1	AU124052	AU124052 UI-M-H2O-
15	1332	46.6	763	7	CV557698	CV557698 UI-M-H2O-
16	1299	45.8	849	6	CD244444	CD244444 AGENCOURT
17	1295	45.6	978	3	BI767168	BI767168 603060542
18	1285.5	45.3	1073	7	CN643937	CN643937 ILLUMIGEN
19	1277	45.0	820	8	DR877125	DR877125 JGI_CAB19
20	1272.5	44.8	772	7	CN460181	CN460181 UI-M-H30-
21	1268	44.7	769	6	CD351417	CD351417 UI-M-GIO-
22	1267	44.6	775	6	CD352514	CD352514 UI-M-GIO-
23	1260	44.4	915	7	CV558493	CV558493 UI-M-H2O-
24	1257.5	44.3	955	5	BUI225490	BUI225490 603946507
25	1255	44.2	773	1	AU123612	AU123612 UI-M-H2O-
26	1252	44.1	717	7	CO045435	CO045435 UI-M-H2O-
27	1240	43.7	722	6	CF534538	CF534538 UI-M-GIO-
28	1235	43.5	800	7	CN457338	CN457338 UI-M-HNO-
29	1234	43.5	708	7	CN457827	CN457827 UI-M-HNO-
30	1226	43.2	752	3	BP698098	BP698098 BP698098
31	1224	43.1	736	6	CA749455	CA749455 UI-M-FY0-
32	1220	43.0	689	7	CN535314	CN535314 UI-M-H30-
33	1204.5	42.4	3091	4	BC036748	BC036748 Homo sapi
34	1203	42.4	708	8	DR004359	DR004359 TC120927
35	1199	42.2	1713	4	AK015337	AK015337 Mus muscu
36	1191.5	42.0	1533	10	AY406401	AY406401 Homo sapi
37	1189	41.9	1409	11	DQ031141	DQ031141 Homo sapi
38	1186	41.8	1497	10	AY406403	AY406403 Mus muscu
39	1185	41.8	677	7	CV558110	CV558110 UI-M-H2O-
40	1184	41.7	1427	10	AY417399	AY417399 Homo sapi
41	1182	41.6	1427	10	AY417400	AY417400 Pan trogl
42	1179.5	41.6	3295	4	AK053428	AK053428 Mus muscu
43	1179	41.5	1427	10	AY417401	AY417401 Mus muscu
44	1164	41.0	817	6	CD352073	CD352073 UI-M-GIO-
45	1152	40.6	679	7	CK965863	CK965863 4080965 B

ALIGNMENTS

RESULT 1	AY411158	1521 bp	DNA	linear	GSS 16-DEC-2003
LOCUS	Mus musculus BMPRIA gene, VIRTUAL TRANSCRIPT, partial sequence,				
DEFINITION	Genomic survey sequence.				
ACCESSION	AY411158				
VERSION	AY411158.1	GI:39767126			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	1 (bases 1 to 1521)				
AUTHORS	Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1521)				
AUTHORS	Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering				

them based on alignment.
 FEATURES Location/Qualifiers
 source 1. .1521
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 gene <1..>1521
 /gene="BMPRIA"
 /locus_tag="HCM4130"
 ORIGIN
 Alignment Scores: 5,75e-289 Length: 1521
 Pred. No.: 2648.50 Matches: 499
 Score: 2648.50
 Percent Similarity: 99.02% Conservative: 5
 Best Local Similarity: 98.04% Mismatches: 2
 Query Match: 93.32% Indels: 4
 DB: 10 Gaps: 1
 US-10-600-645-2 (1-532) x AY411156 (1-1521)
 QY 24 GlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAspGlnLysLys 43
 |||||
 Db 3 CAGAATCTAGATAGTAGTCTCCATGGCACTGGTATGAAATCAGACTTGGACCAAGAAG 62
 QY 44 ProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLysCysTyrCys 63
 |||||
 Db 63 CAGAAAATGGAGTGACTTTAGCACAGAGGATACCTTGGCTTTCTTAAAGTGCTATTGC 122
 QY 64 SerGlyHisCysProAspAspAlaIleAsnAsnThrCysAlaThrAsnGlyHisCysPhe 83
 |||||
 Db 123 TCAGACACTGCCAGATGATGCTATTATAACACATGCATGAATTAATGGCCATTGCTTT 182
 QY 84 AlaIleIleGluAspAspGlnGlyThrThrLeuThrSerGlyCysMetLysTyr 103
 |||||
 Db 183 GCCATTATAGAAGAAGATGATCAGGAGAGAACCAATTAACTTCTGGGTATGAAGTAT 242
 QY 104 GluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgThrIleGlu 123
 |||||
 Db 243 GAAGGCTCTGATTTTCAATGCAAGGATTCACCGAAAGCCAGCTACGACGAGCAATAGAA 302
 QY 124 CysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProValValIle 143
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 Db 303 TGTTGCGGACCAATTTGTGCAACCAAGTATTTGACAGCTTACACTGCCCTGTTGTTATA 362
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 1 (bases 1 to 1532)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
 Todd,W.A., Tanenbaum,D.M., Clivello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 TITLE
 JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302
REFERENCE 2 (bases 1 to 1532)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sminsky, J.J., Adams, M.D., and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
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DB 843 CAGCTCTATTGATTACTGATTACCATGAAATGGATCTCTCTATGACTTCTCTGAAATGT 902
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DB 1023 AAGACCAAAACATCTCTCATCAAGAAATGGAGTTGCTGCAATTCGACCTGGGCCCTT 1082
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RESULT 3

AY411157
LOCUS Pan troglodytes BMPRIA gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY411157
VERSION AY411157.1 GI:39767125
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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1 (bases 1 to 1532)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 1532)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
Location/Qualifiers
1..1532
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Query Match: 70.19% Indels: 0
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QY 24 GlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValaAspGlnLysLys 43
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Db 1503 ATGGTTGAATCCCAAGATGTAATAATC 1529
RESULT 4

AK086130

LOCUS

DEFINITION

AK086130 1911 bp mRNA linear HTC 03-APR-2004
Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched
library, clone:D930007102 product:bone morphogenetic protein
receptor, type 1B, full insert sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AK086130.1 GI:26351960
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

REFERENCE

AUTHORS

1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159

REFERENCE

AUTHORS

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861

TITLE

JOURNAL

PUBLISHED

REFERENCE

AUTHORS

4 The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

REFERENCE

AUTHORS

5 The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

REFERENCE

AUTHORS

6 (bases 1 to 1911)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
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Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuura, T., Miyazaki, A., Murata, M.,
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Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

TITLE

JOURNAL

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to

COMMENT

prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/

FEATURES

source

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CDS

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DB: 4 Gaps: 4
US-10-600-645-2 (1-532) x AK086130 (1-1911)

ORIGIN

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46 AsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLysCysTyrCysSerGly 65
203 GATGGAGAGAGTACAGCCCCACCCCTCGGCCCAAGATCTCTGTTGTAATGCCACCAC 262
66 HisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGlyHisCysPheAlaIle 85
263 CACTGTCCGGAAGACTCAGTCAACAATATCTGCAGCACAGATGGGTACTGCTTCACGATG 322
86 IleGluGluAspAspGlnGlyGluThrLeuThrSerGlyCysMetLysTyrGluGly 105
323 ATAGAAGAAGAGTACTCTCGAATCGCTGTGTTCACCTCTGGATGCTCTAGGACAGAGGG 382
106 SerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArgThrIleGluCysCys 125
383 TCAGATTTTCAATGCTGTGACACTCCCATTCCTCATCAAGAAGATCAATTTGAATGCTGC 442
126 ---ArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProProValIleGly 144
443 ACAGAAAGGAATGAGTGTATAAAGACCTCCACCCACCTCTGCTCTCTCAAGGACAGA 502
145 PropPheAspGlySerValArgTrpLeuAlaValIleSerMetAlaValCysIle 164
503 GATTTTGTGGGGCCCATACACCAAGGCCCTTCTTCTCTCTGCTGCTCTAGT 562
165 ValAlaMetIleValPheSerSerCysPheCysTyr-LysHisTyrCysLysSerIleSer 194

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Db      563  TTA---CTTGTGCTCTCATTATTTATTTCTGTTACTTCCAGGTAT---AAAAGACAGAA 616
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Db      617  GCCCGACCTCGGTACAGCATTTGGCTGGAGCAGGACGACATACATTCCTCTGGAGAG 676
QY      205  SerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySerGlyLeuProLeu 224
Db      677  TCCTCAGAGACTGTGATCAGCAGCTCTCAGAGCTCGGAAGTGGATCAGCGCTCCCTCTG 736
QY      225  LeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnValGlyLysGlyAsp 244
Db      737  CTGTGTCNAAAGNCATAGCTAAGCAAAATTCAGATGTTGAGCAGAGATTCGAAAGCCGC 796
QY      245  TyrGlyGluValTrpMetGlyLysTrpArgGlyGlyGluLysValAlaValLysValPhe 264
Db      797  TATGGCAGGTGTGGATGGAAAGTGGCTGGAGAAAGTGGCTGTGAAAGTGTTCCTTC 856
QY      265  ThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThrValLeuMetArg 284
Db      857  ACCACGGAGAACCCAGCTGGTTCGAGAGACTGAGATATATCAGACGGTCTGTGTCGG 916
QY      285  HisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGlySerTrpThrGln 304
Db      917  CATGAGAATATTCGGGGTTCATTCGTGCAGATATCAAGGACCTGGGTCCTGGACTCAG 976
QY      305  LeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPheLeuLysCysAla 324
Db      977  TTGTACCTCATCACAGACTATCATGAAACGGCTCCCTTTATGACTATCTGAAATCCACC 1036
QY      325  ThrLeuAspThrArgAlaLeuLysLeuAlaTyrSerAlaAlaCysGlyLeuCysHis 344
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QY      345  LeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHisArgAspLeuLys 364
Db      1097  TTACACACCGAAATCTTTAGCACTCAAGCAGCCAGCAATCGCCCATCGAGACTTGAA 1156
QY      365  SerLysAsnIleLeuIleLysLysAsnGlySerCysIleAlaAspLeuGlyLeuAla 384
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QY      385  ValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThrArgValGlyThr 404
Db      1217  GTCAAGTTTATTAGTACACAAATAGAGTTGACATCCCAACCAACCCGGGTTGGCACC 1276
QY      405  ArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsnHisPheGlnPro 424
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QY      425  TyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMetAlaArgCys 444
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QY      465  ProSerTyrGluAspMetArgGluValValCysValLysValArgLeuArgProIleValSer 484
Db      1457  CCTTCTTATGAGACATGAGAAATTTGTGCATGAAGAAGTTACGGCTTCATTCCTCCC 1516
QY      485  AsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMetSerGluCysTrp 504
Db      1517  AATCGATGAGCAGTGTAGTGTCTCAGGCGAGATGGGGAAGCTTATGACAGAGTGTGG 1576
QY      505  AlaHisAsnProAlaSerArgIleThrAlaLeuArgIleLysLysThrLeuAlaLysMet 524
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QY      525  ValGluSerGlnAspValLysIle 532
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Db      1637  TCAGAGTCCCGAGACATTAAACTC 1660
RESULT 5
LOCUS   AY418113
DEFINITION Homo sapiens BMP1B gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY418113
VERSION   AY418113.1
KEYWORDS  GSS.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1509)
AUTHORS  Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarimal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL   Science 302 (5652), 1960-1963 (2003)
PUBMED    14671302
REFERENCE 2 (bases 1 to 1509)
AUTHORS  Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarimal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE     Direct Submission
JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Score:          1941.00      Matches:      365
Percent Similarity: 83.96%      Conservative: 59
Best Local Similarity: 72.28%      Mismatches:  77
Query Match:    68.39%      Indels:       4
DB:             10           Gaps:         4
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QY      49  ThrLeuAlaProGluAspThrLeuProPheLeuLysCysTyrCysSerGlyHisCysPro 68
Db      58  AGTACAGCCCCACCCCCCGTCCAAAGGCTTTCGTTGTAATATGCACCAACCATTTGTCCA 117
QY      69  AspAspAlaIleAsnAsnThrCysIleThrAsnGlyHisCysPheAlaIleIleGluGlu 88
Db      118  GAAGACTCAGTCAACAATATTTTGCAGACACAGCGGATATTTTCCACGATGATAGAAGAG 177
QY      89  AspAspGlnGlyGluThrThrLeuThrSerGlyCysMetLysTyrGluGlySerAspPhe 108
Db      178  GATGACTCTGGTTCCTCTGTCCTCTCTGTCCTCTGTCCTCTGTCCTCTGTCCTCTGTCCT 237
QY      109  GlnCysLysAspSerProLysAlaGlnLeuArgArgThrIleGluCysCys---ArgThr 127
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QY 128 AsnLeuCysAsnGlnTyrLeuGlnProThrLeuProProValValIleGlyProPhePhe 147
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QY 168 IleValPheSerSerCysPheCysTyrLysHisTyrCysLysSerIleSerSerArgGly 187
Db 415 TTGGTCTCTTATCATATTATTGTTACTTCCGGTAT---AAAAACACAAGAAACACAGACCT 471
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QY 208 AspLeuIleAspGlnSerGlnSerGlySerGlySerGlyLeuProLeuLeuValGln 227
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QY 228 ArgThrIleAlaLysGlnIleGlnMetValArgGlnValGlyLysGlyArgTyrGlyGlu 247
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QY 268 GluAlaSerTrpPheArgGluThrGluIleTyrGlnThrValLeuMetArgHisGluAsn 287
Db 712 GAAGCCAGCTGGTTTCAGAGACAGAAATATATCAGACAGCTGTTGATGAGGCATGAAAC 771
QY 288 IleLeuGlyPheIleAlaAlaAspIleLysGlyThrGlySerTrpThrGlnLeuTyrLeu 307
Db 772 ATTTTGGTTTTCATTGCTGCAGATATCAAAAGGACAGGGTCTCGACCCAGTTGTACCTA 831
QY 308 IleThrAspTyrHisGluAsnGlySerLeuTyrAspPheLeuLysCysAlaThrLeuAsp 327
Db 832 ATCAGACATCATGAAATGGTTCCCTTTATGATTATCTGAAGTCCACCCCTAGAC 891
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QY 348 GluIleTyrGlyThrGlnGlyLysProAlaIleAlaHisArgAspLeuLysSerLysAsn 367
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QY 408 MetAlaProGluValLeuAspGluSerLeuSerLysAsnHisPheGlnProTyrIleMet 427
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QY 428 AlaAspIleTyrSerPheGlyLeuIleIleTrpGluMetAlaArgArgCysIleThrGly 447
Db 1192 GCTGACATGATATAGTTTGGCCCTCATCTTTGGAGAGTCTGCTAGGAGATGTGATCAGGA 1251
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Db 1252 GGTATAGTGAAGAAATACACAGTCTCTTATCATGACCTAGTGGCCAGTACCCCTCTTAT 1311
QY 468 GluAspMetArgGluValValCysValLysArgLeuArgProIleValSerAsnArgTrp 487
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508 ProAlaSerArgLeuThrAlaLeuArgIleLysLysThrLeuAlaLysMetValGluSer 527
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 genomic survey sequence.
 AY418115
 AY418115.1 GI:39774075
 GSS.
 Mus musculus (house mouse)
 Mus musculus
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 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 REFERENCE
 1 (bases 1 to 1509)
 Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
 Adams, M.D. and Cargill, M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL
 Science 302 (5652), 1960-1963 (2003)
 PUBMED
 14671302
 REFERENCE
 2 (bases 1 to 1509)
 Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
 Adams, M.D. and Cargill, M.
 Direct Submission
 JOURNAL
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
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 Location/Qualifiers
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 Pred. No.: 8.8e-208 Length: 1509
 Score: 1933.50 Matches: 364
 Percent Similarity: 83.96% Conservative: 60
 Best Local Similarity: 72.08% Mismatches: 76
 Query Match: 68.13% Indels: 5
 DB: 10 Gaps: 5
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 Db 4 CTCTTACGAAGCTCTGGA---AAATTAATGTTGGCACCACCAAGAAG---GAGGATGGAG 57
 QY 49 ThrLeuAlaProGluAspThrLeuProPheLeuLysCysTyrCysSerGlyHisCysPro 68
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QY      89 AspAspGlnGlyThrThrLeuThrSerGlyCysMetLysThrGluGlySerAspPhe 108
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      ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY      168 IleValPheSerSerCysPheCysTyrLysHisTyrCysLysSerIleSerSerArgGly 187
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      ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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      ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY      428 AlaAspIleTyrSerPheGlyLeuIleIleTyrGluMetAlaArgCysIleThrGly 447
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QY      448 GlyIleValGluGluTyrGlnLeuProTyrTyrAsnMetValProSerSerAspProSerTyr 467
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QY      468 GluAspMetArgGluValValCysValLysArgLeuArgProIleValSerAsnArgTrp 487
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      ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1372 AGCACTGATGAGTGTCTCAGGAGATGGGAAGCTTATGACAGAGTGTGGGGCAGAT 1431
      ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      508 ProAlaSerArgLeuThrAlaLeuArgIleLysLysThrLeuAlaLysMetValGluSer 527
      ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1432 CTTGCTCCAGGCTCAGCGCCTGAGAGTTAAGAAAACCTTTGCCAAAATGTGCAGAGTCC 1491
      ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      528 GlnAspValLysIle 532
      ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1492 CAGGACATTAAATC 1506
      ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 7
LOCUS   AY418114                      1509 bp      DNA      linear      GSS 17-DEC-2003
DEFINITION Pan troglodytes BMP1B gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION AY418114
VERSION   AY418114.1  GI:39774074
KEYWORDS GSS.
SOURCE   Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1 (bases 1 to 1509)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
            Adams,M.D. and Cargill,M.
            Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
JOURNAL   Science 302 (5652), 1960-1963 (2003)
PUBMED   14671302
REFERENCE 2 (bases 1 to 1509)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
            Adams,M.D. and Cargill,M.
            Direct Submission
TITLE     Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES   Location/Qualifiers
            source          1..1509
                        /organism="Pan troglodytes"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9598"
            gene            1..1509
                        /gene="BMP1B"
            ORIGIN          /locus_tag="HCM6449"
Alignment Scores:
Pred. No.:      4,69e-192      Length:      1509
Score:          1795.00      Matches:      346
Percent Similarity: 79.01%      Conservative: 53
Best local Similarity: 68.51%      Mismatches: 102
Query Match:    63.25%      Indels:      4
DB:              10      Gaps:      4
US-10-600-645-2 (1-532) x AY418114 (1-1509)

```

```
QY 29 MetLeuHisGlyThrGlyMetLysSerAspValAspGlnLysLysProGluAenGlyVal 48
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 ATGCTTTTGGCAAGTCAGCAAAATTAATGTGGGCACCAAGAAA---GAGGATGTGAG 57

QY 49 ThrLeuAlaProGluAspThrLeuProPheLeuLysCysTyrCysSerGlyHisCysPro 68
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 58 AGTACAGCCCCACCCCGCTCAAAAGGTCTTACGTTGTAATGCCACCAACCATGTTNN 117

QY 69 AspAspAlaIleAenAsnThrCysIleThrAsnGlyHisCysPheAlaIleGluGlu 88
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 118 NNNNCTCAGTCAACAATATTTCCAGCACAGCGGATATTTGTTCCAGATGATAGAAG 177

QY 89 AspAspGlnGlyGluThrThrLeuThrSerGlyCysMetLysTyrGluGlySerAspPhe 108
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 178 GATGACTCTGGTGTCTGGTCACTTCTGGATGCTAGGACTAGAGGCTCAGATTTT 237

QY 109 GlnCysLys---AspSerProLysAlaGlnLeuArgThrIleGluCysCysArgThr 127
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 238 CAGTGTCCGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 297

QY 128 AsnLeuCysAsnGlnTyrLeuGlnProThrLeuProValIleGlyProPhePhe 147
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 298 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNATTTTGT 357

QY 148 AspGlySerValArgTyrLeuAlaValLeuIleSerMetAlaValCysIleAlaMet 167
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 358 GATGGACCTATACACCAAGCTTACTTATCTGTGACTCTGTGTGTTG---CTC 414

QY 168 IleValPheSerSerCysPheCysTyrLysHisTyrCysLysSerIleSerArgGly 187
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 415 TTGGTCTCTATCATATTTTGTACTTCCGGTAT---AAAAGACAAAGAACACGACCT 471

QY 188 ArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIleProValGlyGluSerLeuLys 207
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 472 CGATACAGATTTGGGTAGAACAGATGAACATTTACATTCCTCGGAGAATCCCTGAGA 531

QY 208 AspLeuIleAspGlnSerGlnSerSerGlySerGlyLeuProLeuLeuValGln 227
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 532 GACTTAATTCAGACAGTCTCAGAGCTCAGGAGTGGATCAGGCCCTCCTCTGCTGGTCCA 591

QY 228 ArgThrIleAlaLysGlnIleGlnMetValArgGlnValGlyLysGlyArgTyrGlyGlu 247
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 592 AGGACTATAGCTAAGCAGATTCAGATGGTGAACAGATTGGAAGGTCGCTATGGGAA 651

QY 248 ValTrpMetGlyLysTrpArgGlyGluLysValAlaValLysValPheThrThrGlu 267
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 652 GTTTGGATGGAAAGTGGCGTGGCGAAAGGTAGCTGTGAAGTGTCTTCCACCAGAG 711

QY 268 GluAlaSerTrpPheArgGluThrGluIleTyrGlnThrValLeuMetArgHisGluAsn 287
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 712 GAAGCCAGCTGGTTCCAGAGACAGCAAGAAATATATACACAGTGTGTGATGGCATGAAAC 771

QY 288 IleLeuGlyPheIleAlaAlaAspIleLysGlyThrGlySerTrpThrGlnLeuTyrLeu 307
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 772 ATTTTGGTTTCTATGCTGCAGATATCAAGGGACAGGGTCTCGGACCCAGTTGTACCTA 831

QY 308 IleThrAspTyrHisGluAsnGlySerLeuTyrAspPheLeuLysCysAlaThrLeuAsp 327
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 832 ATCACAGACTATCATGAAATGTGTTCCCTTTATGATTATCTGAAGTCCACCCCTAGAC 891

QY 328 ThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCysGlyLeuCysHisLeuHisThr 347
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 892 ACTTAATCAATGCTGAAGTTAGCTTACTTCTGTCAGTGGCTATGTCATTATACACA 951

QY 348 GluIleTyrGlyThrGlnGlyLysProAlaIleAlaHisArgAspLeuLysSerLysAsn 367
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 952 GAAATCTTTAGTACTCAAGGCAAAACAGCAATTTGCCATCGAGATCTGAAAAGTAAAC 1011

QY 368 IleLeuIleLysLysAsnGlySerCysCysIleAlaAspLeuGlyLeuAlaValLysPhe 387
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1012 ATTTCTGGTGAAGAAAAATGGAACCTTGTCTGTTGCTGACCTGGCGCTGTTAAATTT 1071
```

388 AsnSerAspThrAsnGluValAspIleProLeuAsnThrArgValGlyThrArgArgTyr 407
| | | | | :
| | | | | :
| | | | | :
Db 1072 ATTAGTGATACAAATGAAGTTGACATACACCTAACACCTCGAGTTGGCACCACGCTAT 1131

408 MetAlaProGluValLeuAspGluSerLeuSerLysAsnHisPheGlnProTyrIleMet 427
| | | | | :
| | | | | :
| | | | | :
Db 1132 ATGCTCTCCAGAAAGTGTGGACGAGAGCTTGAACAGAAATCCTTCCAGCTTACATCATG 1191

428 AlaAspIleTyrSerPheGlyLeuIleIleTyrGluMetAlaArgCysIleThrGly 447
| | | | | :
| | | | | :
| | | | | :
Db 1192 GCTGACATGATATAGTTTGGCCCTCATCCTTGGAGGTGCTAGGAGATGTGATCAGGA 1251

448 GlyIleValGluGluTyrGlnLeuProTyrTyrAsnMetValProSerAspProSerTyr 467
| | | | | :
| | | | | :
| | | | | :
Db 1252 GGTATAGTGAAGATACACAGCTTCTTATCATGACCTAGTGCACGAGTACCCCTCTTAT 1311

468 GluAspMetArgGluValValCysValLysArgLeuArgProIleValSerAsnArgTyr 487
| | | | | :
| | | | | :
| | | | | :
Db 1312 GAGGACATCAGGAGATTTGTGTCATCAAGAAAGTTACGCCCTCATTTCCCAAAACCGGTGG 1371

488 AsnSerAspGluCysLeuArgAlaValLeuLysLeuMetSerGluCysTyrAlaHisAsn 507
| | | | | :
| | | | | :
| | | | | :
Db 1372 AGCAGTGTAGTGTCTTAAGGCANNTGGGAAACTCATGACANNATGCTGGGCTCACAAT 1431

508 ProAlaSerArgLeuThrAlaLeuArgIleLysLysLeuAlaLysMetValGluSer 527
| | | | | :
| | | | | :
| | | | | :
Db 1432 CCTGCATCAAGCTGACAGCCCTCGGGGTAAAGAAACACTTGCCTCAAAATGTCCAGAGTCC 1491

528 GlnAspValLysIle 532
| | | | | :
| | | | | :
| | | | | :
Db 1492 CAGGACATTAAACTC 1506

RESULT 8
BM473726 1121 bp mRNA linear EST 05-FEB-2002
LOCUS AGENCOURT_6466656 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5562094
DEFINITION 5', mRNA sequence.
ACCESSION BM473726
VERSION BM473726.1 GI:18522768
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1121)
NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LLM12290 row: 0 column: 23
High quality sequence stop: 679.
Location/Qualifiers
1. .1121
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5562094"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 88"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site 1: Noti; Site 2: Sail; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life

Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 3,976-173 Length: 1121
Score: 1626.50 Matches: 316
Percent Similarity: 92.02% Conservative: 7
Best Local Similarity: 90.03% Mismatches: 23
Query Match: 57.31% Indels: 5
DB: 3 Gaps: 1

US-10-600-645-2 (1-532) x BM473726 (1-1121)

```
QY 37 SerAspValAspGlnLysProGluAsnGlyValThrLeuAlaProGluAspThrLeu 56
DB 2 TCAGACTCCGACGACAGAAAAGTCAGAAAATGGAGTAACCTTAGCACCGAGAGATACCTTG 61

QY 57 ProPheLeuLysCysTyrCysSerGlyHisCysProAspAspAlaIleAsnThrCys 76
DB 62 CTTTTTNAAGTGTATTGCTCAGGGCACTGTCAGATGATGCTATTATTAACACATGC 121

QY 77 IleThrAsnGlyHisCysPheAlaIleIleGluGluAspAspGlnGlyGluThrLeu 96
DB 122 ATAACCTAATGGACATTTGCTTCCCATCATAGAAGAAGATGACCGAGAGAAACACATTA 181

QY 97 ThrSerGlyCysMetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAla 116
DB 182 GCTTCAGGGTGTATGAATATATGAAGATCTGATTTTCAGTGCAGAAAGATTCCTCAAAAGCC 241

QY 117 GlnLeuArgThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnPro 136
DB 242 CAGCTACGGCGGACATAGAAATGTTGTCGACCAATTTATGTAAACAGTATTTCGAACCC 301

QY 137 ThrLeuProProValIleGlyProPheAspGlySerValArgTrpLeuAlaVal 156
DB 302 ACACATGCCCCCTGTTGCATAGTCCGTTTTTTTGTATGGCAGCATTCGATGGCTGTTTG 361

QY 157 LeuIleSerMetAlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyr 176
DB 362 CTCATTTCCTATGGCTGTCGCAATAATGCTATGATCATCTCTCCAGCTGCTTTTGTATAC 421

QY 177 LysHisTyrCysLysSerIleSerArgGlyArgTyrAsnArgAspLeuGlnAsp 196
DB 422 AAACATATTGCAAGAGCATCTCAGCAGACGCTGTTACATCGTATTTGGAAACAGGAT 481

QY 197 GluAlaPheIleProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSer 216
DB 482 GAAGCATTTATTCAGTTGGAGAATCACTAAAAGACCTTTATTGACCAAGTCACAAAAGTTCT 541

QY 217 GlySerGlySerGlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMet 236
DB 542 GGTAGTGGGTCCTGGACTACCTTTATTGGTTCAGCGAACTATTTCGCCAAAACAGATTCAGATG 601

QY 237 ValArgGlnValGlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGlu 256
DB 602 GTCCGCGAAGTTGGTAAAGCCGATATGGAGAAGTATGGATGGCCAAATGGCGTGGCGAA 661

QY 257 LysValAlaValLysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGlu 276
DB 662 AAAGTGGCGGTGAAAGTATCTTTTACCACCTGAAGAAGCCAGCTGGTTCGAGAAAACAGAA 721

QY 277 IleTyrGlnThrValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIle 296
DB 722 ATCTACCAAACTGTGCTAATGCGCCATGAAACATACACTTGGTTTTCATAGCGGCAGACATT 781

QY 297 LysGlyThrGlySerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySer 316
DB 782 AAAGTACAGGTTCTCTGGACTCACCCTCTATTGTTGATTGATTACATTCAGAAAATGGAATCT 841

QY 317 LeuTyrAsp-PheLeuLysCysAlaThrIleuAspThrArgAlaLeuLeuLysLeuAlaTyr 336
DB 842 CTCCTATGAACCTCTCTGAAATGTGTACACTGGACACCGAGCCCTGCTTAAATGGCTTA 901
```

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QY 336 rSerAla-AlaCysGlyLeuCysHisIleuHisThrGluIleTyrGlyThrGlnGlyLys- 355
DB 902 TCCAGCTGGCTGGGNGCTGGCCACCTGCCCCCAGAAATTTATGGGCCCCCAAGAAAG 961

QY 356 --ProAlaIleAlaHisArgAspLeuLysSerLysAsnIleLeuIle-LysLysAsn-GI 374
DB 962 CCCCAGCAATGGCTCTCCGAAACCTTAAGGAGCAAAACATCTCTTCCAAAAAATGGG 1021

QY 374 ySerCysCysIleAlaAspLeuGly 382
DB 1022 AGATTGCTGCTATTCGCTGAACCGG 1046

RESULT 9
AUI24197
LOCUS AUI24197 NT2RM2 Homo sapiens cDNA clone NT2RM2001814 5', mRNA
DEFINITION sequence.
ACCESSION AUI24197
VERSION AUI24197.1 GI:10948913
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 874)
AUTHORS Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J.,
Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
Isogai,T.
TITLE HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S.,
Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T.,
Suzuki,Y., Sugano,S., Isogai,T.)
JOURNAL Unpublished (2000)
COMMENT Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
Location/Qualifiers
source
1..874
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RM2001814"
/cell_type="teratocarcinoma"
/cell_lines="NT2"
/clone_lib="NT2RM2"
/notes="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal
precursor cells"

ORIGIN
Alignment Scores:
Pred. No.: 4,75e-159 Length: 874
Score: 1501.00 Matches: 279
Percent Similarity: 98.62% Conservative: 6
Best Local Similarity: 96.54% Mismatches: 4
Query Match: 52.89% Indels: 0
DB: 1 Gaps: 0

US-10-600-645-2 (1-532) x AUI24197 (1-874)

QY 98 SerGlyCysMetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGln 117
DB 3 TCAGGGTGTATGAAATATGAAGGATCTGATTTTCAGTCAAAAGATTCTCCAAAGCCAG 62

QY 118 LeuArgArgThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThr 137
```

```
Db 63 CTAGCCGGACAAATAGAAATGTTGCGACCAATTTATGTAACCAAGTATTGGCAACCCACA 122
Qy 138 LeuProValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeu 157
Db 123 CTGCCCCCTGTTGTCATAGTCCGTTTTTGTATGGCAGCATTCATGCGCTGGTTTGCTC 182
Qy 158 IleSerMetAlaValCysIleValAlaMetIleValPheSerCysPheCysTyrLys 177
Db 183 ATTTCTATGGCTGTCTGCATAATGCTATGATCATCTCTCCAGCTGCTTTTGTACAAA 242
Qy 178 HisTyrCysLysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGlu 197
Db 243 CATTTATGCAAGACATCTCAAGCAGACGTCGTTACATCGTATTTGGAACAGGATGAA 302
Qy 198 AlaPheIleProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGly 217
Db 303 GCATTTATTCAGTTGGAGATCTCTAAAGACCTTATTGACCAAGTTCACAAAGTTCTGGT 362
Qy 218 SerGlySerGlyLeuProLeuValGlnArgThrIleAlaLysGlnIleGlnMetVal 237
Db 363 AGTGGGTCTGGACTACCTTTATTGGTTTCAGCAACTATTGCCAACAGATTTCAGATGGTC 422
Qy 238 ArgGlnValGlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLys 257
Db 423 CGGCAAGTTGGTAAAGCCGATATGGAGAAAGTATGGATGGCAAAATGGCGTGGCAAAA 482
Qy 258 ValAlaValLysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIle 277
Db 483 GTGGCGGTGAAGTATTTCTTACACTGAAGATGCCAGCTGGTTTCGAGAAACAGAAATC 542
Qy 278 TyrGlnThrValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLys 297
Db 543 TACCAAACTGTGCTAATGCCCATGAAACATACTTGTGTTTCATGCGGCAGACATTAA 602
Qy 298 GlyThrGlySerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeu 317
Db 603 GGTACAGGTTCTCGGACTCAGCTCTATTTGATTACTGATTACCATGAAATGGATCTCTC 662
Qy 318 TyrAspPheLeuLysCysAlaThrLeuAspThrArgAlaLeuLysLeuAlaTyrSer 337
Db 663 TATGACTTCTGAAATGTGCTACACTGGACACAGAGCCCTGCTTAAATTTGGCTTATTC 722
Qy 338 AlaAlaCysGlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAla 357
Db 723 GCTGCTGTGTGCTGTGCTGCTGCACAGAAATTTATGCAACCCAGCAAGCCGCA 782
Qy 358 IleAlaHisArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCys 377
Db 783 ATTTGCTCATCGAGACCTTAAGAGCAAAACATNCTCATCAAGAAATAATGGAAATGCTGC 842
Qy 378 IleAlaAspLeuGlyLeuAlaValLys 386
Db 843 ATTTGCTGACCTGGGCTTGTGTTAA 869

RESULT 10
DR156725
LOCUS
DEFINITION
HESC2_69_D09.g1_A035_NIH_MGC_258 Homo sapiens cDNA clone
IMAGE:7965451.5", mRNA sequence.
DR156725
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 826)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
```

```
FEATURES
source
1..826
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7965451"
/sex="male"
/tissue_type="human embryonic stem cells differentiated to
an early endodermal cell type"
/cell_type="human embryonic stem cells"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="NIH MGC 258"
/notes="Vector: pExpress-1; Site 1: NotI; Site 2: EcoRV;
RNA obtained from human embryonic stem cells isolated from
the inner cell mass of blastocyst stage embryos and
differentiated to an early endodermal cell type. Cell line
id and NIH Registry designation is BG01. Positive for
GATA4, MixL1, Mex1, HNF4alpha expression; negative for AFP
expression. Passage number 40. cDNA primed using oligo-dT
primer: 5'-pGACTAGTCTAGATCGGAGCGGCCCT(T)25-3' and
cloned into the EcoRV/NotI sites of pExpress-1. This
primary library is non-normalized (normalized primary
library is NIH MGC 259). It was constructed by Express
Genomics (Frederick, MD). Sequence ends have been trimmed
to exclude vector and regions below Phred quality 16.
Three-prime sequences are presented as their reverse
complement and have been trimmed to exclude polyA. Note:
this is a Mammalian Gene Collection library."

ORIGIN
Alignment Scores:
Pred. No.: 2,97e-151 Length: 826
Score: 1432.00 Matches: 268
Percent Similarity: 98.91% Conservative: 4
Best Local Similarity: 97.45% Mismatches: 3
Query Match: 50.46% Indels: 0
DB: Gaps: 0

US-10-600-645-2 (1-532) x DR156725 (1-826)
Qy 118 LeuArgArgThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThr 137
Db 1 CTACGCCGACAAATAGAAATGTTGTCGACCAATTTATGTAACCAAGTATTGGCAACCCACA 60
Qy 138 LeuProValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeu 157
Db 61 CTGCCCCCTGTTGTCATAGTCCGTTTTTGTATGGCAGCATTCGATGGCTGGTTTGCTC 120
Qy 158 IleSerMetAlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLys 177
Db 121 ATTTCTATGGCTGTCTGCATAATGCTATGATCATCTCTCCAGCTGCTTTTGTACAAA 180
Qy 178 HisTyrCysLysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGlu 197
Db 181 CATTTATGCAAGACATCTCAAGCAGACGTCGTTACAAATCGTATTCGATTTGGAACAGGATGAA 240
Qy 198 AlaPheIleProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGly 217
```

National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Bresagen, Inc.
cDNA Library Preparation: Express Genomics, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Laboratory for Genomics and Bioinformatics,
University of Georgia
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM 17072 row: g column: 17
Seq primer: JENREV (CAGGAACAGCTATGACC)
High quality sequence stop: 826.

Db 241 GCATTATTCCAGTTGGAGAACTCACTAAAGACCTATTATGACCGTCACAAAGTTCTGGT 300
Qy 218 SerGlySerGlyLeuProLeuLeuValGlnArgThrIleAlaIysGlnIleGlnMetVal 237
Db 301 AGTGGGCTCTGGACTACCTTTATTGGTTTCAGCGAACTATTGCGCAAAACAGATTCCAGATGGTCTC 360
Qy 238 ArgGlnValGlyIysGlyArgTyrGlyGluValTrpMetGlyIysTrpArgGlyGluIys 257
Db 361 CGCGAAGTTGGTAAAGCCGATATGGAGAAGTATGGATGGGCAAAATGGCGTGGCGAAAAA 420
Qy 258 ValAlaValIysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIle 277
Db 421 GTGGCGGTGAAGATATCTTTACCACTGAAGAGCCAGCTGGTTTCGAGAAACAGAAATC 480
Qy 278 TyrGlnThrValLeuMetArgHisGluAenIleLeuGlyPheIleAlaAlaAspIleIys 297
Db 481 TACCAAACTGTCTAATGCGCCATGAAACATACACTTGGTTTTCATAGCGCGACACATTAAA 540
Qy 298 GlyThrGlySerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAenGlySerLeu 317
Db 541 GGTACAGGTTCTCGGACTCAGCTCTATTATTTGATTACTGATTACCATGAAAAATGGATCTCTC 600
Qy 318 TyrAspPheLeuIysCysAlaThrLeuAspThrArgAlaLeuLeuIysLeuAlaTyrSer 337
Db 601 TATGACTTCTGAAATGTCTACACTGGACACCCAGAGCCCTGCTTAAATTTGCTTATTTCA 660
Qy 338 AlaAlaCysGlyLeuCysHisIleuHisThrGluIleTyrGlyThrGlnGlyIysProAla 357
Db 661 GCTGCTGTGGTCTGTGCCACCTGCACACAGAAATTTATGGCACCCGAAAGCCCGCA 720
Qy 358 IleAlaHisArgAspLeuIysSerIysAenIleLeuIleLeuIysAenGlySerCysCys 377
Db 721 ATTGCTCATCGAGACCTAAGAGCAAAACATCCTCATCAAGAAAAATGGGAGTTGCTGC 780
Qy 378 IleAlaAspLeuGlyLeuAlaValIysPheAenSerAspThrAsn 392
Db 781 ATTGCTGACCTGNGCCTTCTGTTAAATTTCAACAGTCGACACAAAT 825

RESULT 11
CX204646
LOCUS
DEFINITION MNS07540 Mouse Neurosphere Normalized cDNA library Mus musculus
ACCESSION cDNA 5', mRNA sequence.
VERSION CX204646
KEYWORDS CX204646.1 GI:56859818
SOURCE EST.
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE Williams,C., Wirta,V., Lundberg,J. and Friese,J.
AUTHORS 1 (bases 1 to 842)
TITLE Expressed sequence tags of cDNA clones from murine neurospheres
JOURNAL Unpublished (2005)
COMMENT Contact: Williams, C.
Molecular Biotechnology
Institution of Biotechnology
Albion University Center, KTH-Royal Institute of Technology, 106
91 Stockholm, Sweden
Tel: +46855378332.
Fax: +46855378481.
Email: cecilia.williams@biotech.kth.se
Seq primer: M3REW.

FEATURES
Location/Qualifiers
1..842
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/sex="MALE"
/tissue_type="Lateral wall of lateral ventricle"
/cell_type="Early passage neurosphere"

/dev_stage="Adult"
/clone_lib="Mouse Neurosphere Normalized cDNA library"
/note="Organ: Adult brain; Vector: pCMVSPORT6.0; A cDNA library was constructed in pCMVSPORT6.0 from RNA isolated from neurospheres of adult male and female mice. Custom normalized cDNA library by Invitrogen/ResGen"

ORIGIN
Alignment Scores:
Pred. No.: 7,59e-146 Length: 842
Score: 1384.50 Matches: 268
Percent Similarity: 98.19% Conservative: 4
Best Local Similarity: 96.75% Mismatches: 5
Query Match: 48.78% Indels: 3
DB: 8 Gaps: 0
US-10-600-645-2 (1-532) x CX204646 (1-842)

Qy 91 GlnGlyGluThrThrLeuThrSerGlyCysMetIysTyrGluGlySerAspPheGlnCys 110
Db 3 CAGGAGAAACCCACATTAACTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATGC 62
Qy 111 LysAspSerProIysAlaGlnLeuArgArgThrIleGluCysCysArgThrAsnLeuCys 130
Db 63 AAGGATTCACCGAAGCCCGAGCTACGACAGGACAATAGAAATGTTGTCGGACCAATTTTGTGC 122
Qy 131 AsnGlnTyrLeuGlnProThrLeuProProValValIleGlyProPhePheAspGlySer 150
Db 123 AACCAAGTATTTGACGCTTACACTGCCCCCTGTGTTATAGGTCCCTCTTCTTGATGGCAGC 182
Qy 151 ValArgTrpLeuAlaValLeuIleSerMetAlaValCysIleValAlaMetIleValPhe 170
Db 183 ATCCGATGGCTGGTGTGCTCATTTCCATGGCTGTCTGTATAGTTGCTATGATCATCTTC 242
Qy 171 SerSerCysPheCysTyrLysHisTyrCysLysSerIleSerSerArgGlyArgTyrAsn 190
Db 243 TCCAGCTGCTTTTGCATATAGCAATTTATTTGAAGAGTATCTCAAGCAGGGTCTGTTTACAAC 302
Qy 191 ArgAspLeuGluGlnAspGluAlaPheIleProValGlyGluSerLeuIysAspLeuIle 210
Db 303 CGTGATTTGGAAACAGGATGAAGCAATTTATTCAGTAGGAGAATCATTTGAAGACCTGATT 362
Qy 211 AspGlnSerGlnSerSerGlySerGlyLeuProLeuValGlnArgThrIle 230
Db 363 GACCAGTCCCAAGCTCTGGGAGTGGATCTGGATTTGCCCTTTATTGTTTCAGCGCAACTATT 422
Qy 231 AlalysGlnIleGlnMetValArgGlnValGlyIysGlyArgTyrGlyValTrpMet 250
Db 423 GCCAAACAGATTTCAGATGTTTCGGCAGCTTGGTAAAGCCCGCTATGGAGAGTATGGATG 482
Qy 251 GlyIysTrpArgGlyGluIysValAlaValIysValPhePheThrThrGluGluAlaSer 270
Db 483 GGTAATGGCGTGGTGAAGAAAGTGGCTGTCTCAAAAGTGTTTTTTACCACCTGAAGAAGCTAGC 542
Qy 271 TrpPheArgGluThrGluIleTyrGlnThrValLeuMetArgHisGluAenIleLeuGly 290
Db 543 TGGTTTAGAGAAACAGAAATCTTACCAGACGGGTGTTAATGCGTCATGAAATATATCTTGT 602
Qy 291 PheIleAlaAlaAspIleLysGlyThrGlySerTrpThrGlnLeuLeuIleThrAsp 310
Db 603 TTTATAGCTGCAGACATTTAAAGGCACCTGGTTCTCTGACTCACCTGTATTGATTACTGAT 662
Qy 311 TyrHisGluAenGlySerLeuTyrAspPheLeuIysCysAlaThrLeuAspThrArgAla 330
Db 663 TACCATGAAATGGATCTCTCTATGACTTCTCGAAATGTGCACACTAGACACCGAGCC 722
Qy 331 LeuLeuIysLeuAlaTyrSerAlaAlaCysGlyLeuCysHisLeuHisThrGluIleTyr 350
Db 723 CTACTCAAGTTAGCTTATTTCTGCTGCTGTGGTCTGTGCTGCCACTCCC-ACAGAAATTTAT 781
Qy 351 GlyThrGlnGlyIysProAlaIleAlaHisArgAspLeuIysSerLysAsn 367
Db 782 GGTACCCA-GGGAAGCCTGC-ATTGCTCATCGAGACCTGAAAGCAACAT 830


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RESULT 12
CK638737
LOCUS
DEFINITION
  779 bp mRNA linear EST 28-JAN-2004
  UI-M-HO0-cnw-o-09-0-UI.r1 NIH_BMAP_HO0 Mus musculus cDNA clone
  IMAGE:30644216 5', mRNA sequence.
CK638737
ACCESSION
VERSION
KEYWORDS
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
  1 (bases 1 to 779)
  NIH-MGC http://mgi.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgabbs-remail.nih.gov
  Tissue Procurement: Dr. James Lin University of Iowa
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Distribution information can be found at
  http://genome.uiowa.edu/distribution/mousefl.html
  This clone was contributed by the Brain Molecular Anatomy Project
  (BMAP)
  Seq primer: pyX-5.
  Location/Qualifiers
  1. 779
    /organism="Mus musculus"
    /mol_type="mRNA"
    /strain="C57BL/6"
    /db_xref="taxon:10090"
    /clone="IMAGE:30644216"
    /tissue_type="Upper Head"
    /dev_stage="9.5-10.5 dpc"
    /lab_host="DH10B (TI phage resistant)"
    /clone_lib="NIH_BMAP_HO0"
    /notes="Organ: Head; Vector: pyX-Asc; Site 1: EcoR I;
    Site 2: Not I; The library was constructed according
    Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
    1996. Denatured RNA was size fractionated on a 1% agarose
    gel. First strand cDNA synthesis was primed with oligo-dT
    primer containing a Not I site. Double strand cDNA was
    size selected according to mRNA size fraction, ligated
    with EcoR I adaptor, digested with NotI and then cloned
    directionally into pyX-Asc vector. The library tag
    sequence located between the Not I site and the polyA tail
    is CGAAGTGAAT. This library was created for the University
    Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
    Developing Mouse Nervous System', supported by National
    Institute of Mental Health (NIMH)."
```

ORIGIN

```

Alignment Scores:
Pred. No.: 2,53e-142 Length: 779
Score: 1353.00 Matches: 253
Percent Similarity: 99.22% Conservative: 2
Best Local Similarity: 98.44% Mismatches: 2
Query Match: 47.67% Indels: 0
DB: 7 Gaps: 0
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US-10-600-645-2 (1-532) x CK638737 (1-779)

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QY 88 GluAspAspGlnGlyGluThrThrLeuThrSerGlyCysMetLysTyrGluGlySerAsp 107
|||||
Db 1 GAGATGATCAGGAGGAGAACCATTAATCTTCGGGTGATGAAGTATGAAGCTCTGAT 60
|||||
QY 108 PheGlnCysLysAspSerProLysAlaGlnLeuArgThrIleGluCysCysArgThr 127
|||||
Db 61 TTTCAATGCAAGGATTCCCGAAAGCCAGCTACGAGGACCAATAGAAATGTTGTCGACC 120
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```

QY 128 AsnLeuCysAsnGlnTyrLeuGlnProThrLeuProProValValIleGlyProPhePhe 147
|||||
Db 121 AATTTGTGCACACAGTATTTTGAGCCCTACTGCCCCCTGTTGTTATAGTTCGTTCTTT 180
|||||
QY 148 AspGlySerValArgTrpLeuAlaValLeuIleSerMetAlaValCysIleValAlaMet 167
|||||
Db 181 GATGGCAGCATCCGATGGCTGGTTGTCTCATTTCCATGGCTGCTCTGTATAGTTGCTATG 240
|||||
QY 168 IleValPheSerSerCysPheCysTyrLysHisTyrCysLysSerIleSerSerArgGly 187
|||||
Db 241 ATCATCTTCTCCAGCTGCTTTTCTGCTATAAGCATTTATTGTAAGAGTATCTCAAGCAGGGT 300
|||||
QY 188 AtgTyrAsnArgAspLeuGluGlnAspGluAlaPheIleProValGlyGluSerLeuLys 207
|||||
Db 301 CGTTACACCGTGATTTGGAACAGGATGAAGCAATTTATCCAGTAGAGAGTAATCATTGAAA 360
|||||
QY 208 AspLeuIleAspGlnSerGlnSerSerGlySerGlyLeuProLeuLeuValGln 227
|||||
Db 361 GACCTGATTGACCACTCCCAAGCTCTGGAGTGGATCTGGATTGCTTTTATTGTTTCAG 420
|||||
QY 228 ArgThrIleAlaLysGlnIleGlnMetValArgGlnValGlyLysGlyArgTyrGlyGlu 247
|||||
Db 421 CGAACTATTGCCAAACAGATTCAGATGGTTCCGACAGTTGGTAAAGGCCCTATGGAGAA 480
|||||
QY 248 ValTrpMetGlyLysTrpArgGlyGluLysValAlaValLysValPhePheThrThrGlu 267
|||||
Db 481 GTATGGATGGTAAATGGCGTGGTGAAGAGTGGCTGTCAAAGTGTGTTTACACACTGAA 540
|||||
QY 268 GluAlaSerTrpPheArgGluThrGluIleTyrGlnThrValLeuMetArgHisGluAsn 287
|||||
Db 541 GAAGCTAGCTGGTTTAGAGAAACAGAAATCTACCACAGGTGTTATGCGTCATGAAT 600
|||||
QY 288 IleLeuGlyPheIleAlaAlaAspIleLysGlyThrGlySerTrpThrGlnLeuTyrLeu 307
|||||
Db 601 ATACTTGGTTTATAGCTGCAGACATTAAGGACACTGGTTCTCTGGACTCAGCTGATTTG 660
|||||
QY 308 IleThrAspTyrHisGluGlnGlySerLeuTyrAspPheLeuLysCysAlaThrLeuAsp 327
|||||
Db 661 ATTACTGATTACCATGAAGTGGATCTCTCTATGACTTCTGAAATGTGCCACTAGAC 720
|||||
QY 328 ThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCysGlyLeuCysHis 344
|||||
Db 721 ACCAGAGCCCTACTCAAGTTAGCTTAATCTGCTGCTGTTGGTCTGTGCCAC 771
|||||
CF744610 783 bp mRNA linear EST 10-OCT-2003
UI-M-GV0-clt-q-20-0-UI.r1 NIH_BMAP_GV0 Mus musculus cDNA clone
IMAGE:30617467 5', mRNA sequence.
CF744610
ACCESSION
VERSION
KEYWORDS
SOURCE
  Mus musculus (house mouse)
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
  1 (bases 1 to 783)
  NIH-MGC http://mgi.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgabbs-remail.nih.gov
  Tissue Procurement: Dr. James Lin, University of Iowa
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Distribution information can be found at
  http://genome.uiowa.edu/distribution/mousefl.html
  This clone was contributed by the Brain Molecular Anatomy Project
  (BMAP)
  Seq primer: pyX-5.
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FEATURES

source

Location/Qualifiers

1..783
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:30617467"
 /tissue_type="whole brain"
 /dev_stage="1,5, and 15 days newborn"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIM_BMAP_GVO"
 /note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I. The library was constructed according to Bonafide, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAAGTGAAT. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:

Pred. No.: 4,53e-141 Length: 783
 Score: 1342.00 Matches: 253
 Percent Similarity: 98.46% Conservatives: 2
 Best Local Similarity: 97.68% Mismatches: 3
 Query Match: 47.29% Indels: 1
 DB: 6 Gaps: 0

US-10-600-645-2 (1-532) x CF744610 (1-783)

QY 87 GluGluAspAspGln-GlyGluThrThrLeuThrSerGlyCysMetLysTyrGluGlySe 106
 Db 2 GAAGAAGATGATCAAGGGAGAAACCAATTAATCTCTGGGTGTATGAAGTATGAAGGCTC 61
 QY 106 rAspPheGlnCysLysAspSerProlyeAlaGlnLeuArgArgThrIleGluCysCysAr 126
 Db 62 TGATTTTCAATGAAGGATTCACCGAAGCCAGCTACCGACGACAAAGATAATGTGTG 121
 QY 126 gThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProValValIleGlyProPh 146
 Db 122 GACCAATTTGTCAACACAGTAITTCGAGCCTACACTGCCCCCTGTTGTATAGGTCGGTT 181
 QY 146 ePheAspGlySerValArgTrpLeuAlaValIleSerMetAlaValCysIleValAl 166
 Db 182 CTTTGATGCGAGCATCCGATGGTGGTTGTGCTCATTTCCATGGCTGTCTGTATAGTTGC 241
 QY 166 aMetIleValPheSerSerCysPheCysTyrLysHisTyrCysLysSerIleSerSerAr 186
 Db 242 TATGATCATCTCTCTCAGCTGCTTTTGTCTAAGCATTTATTGAAGAGTATCTCAAGCAG 301
 QY 186 gGlyArgTyrAsnArgAspLeuGlnAspGluAlaPheIleProValGlyGlySerLe 206
 Db 302 GGGTCGTACACCGTGATTTGGACAGAGTGAAGCATTTATTCAGTAGGAGATCATTT 361
 QY 206 uLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySerGlyLeuProLeuLeuVa 226
 Db 362 GAAAGACCTGATTAACAGCTCCCAAGCTCTGGAGTGGATCTGGATTCCTTTATTTGGT 421
 QY 226 lGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnValGlyLysGlyArgTyrGl 246
 Db 422 TAGCGCAACTATTTGCCAAACACAGATTCAGATGGTTGGCAGGTTGGTAAGGCCGCTATGG 481
 QY 246 yGluValTrpMetGlyLysTrpArgGlyGluLysValAlaValLysValPhePheThrPh 266
 Db 482 AGAAGTATGATGGGTAAATGGCGTGTGTAAGAGTGGCTGTCAAGAGTGTCTTTTACCAC 541

QY 266 rGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThrValLeuMetArgHisGl 286
 Db 542 TGAAGAAGCTAGCTGGTTTAGAGAAACAGAATCTTACCAGACGGTGTAAATCGCGTCATGA 601
 QY 286 uAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGlySerTyrThrGlnLeuTy 306
 Db 602 AAATATACTTGGTTTATAGCTGCAGACATTAAGGCACCTGGTCTCTGGACCTGACCTGTA 661
 QY 306 rLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPheLeuLysCysAlaThrIle 326
 Db 662 TTTGATTAATGATTAACATGAATAATGGATCTCTCTATGACTTCTCTGATGATGTGCCACT 721
 QY 326 uAspThrArgAlaIleLeuLysLeuAlaTyrSerAlaAlaCysGlyLeuCysHis 344
 Db 722 AGACACCAGAGCCCTACTCAAGTTAGCTTANTCTGCTGCTTGTGCTGTGTGCCAC 776

RESULT 14
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 LOCUS AUI24052 NT2RM2 Homo sapiens cDNA clone NT2RM2001576 5', mRNA
 DEFINITION sequence.
 ACCESSION AUI24052
 VERSION AUI24052 GI:56201134
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 807)
 AUTHORS Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J.,
 Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
 Isogai,T.
 TITLE HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S.,
 Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T.,
 Suzuki,Y., Sugano,S., Isogai,T.)
 JOURNAL Unpublished (2000)
 COMMENT On Oct 23, 2000 this sequence version replaced gi:55779243.
 Contact: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
 Research Institute; cDNA library construction: Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.
 The reason of remaining 5'-end 'N': This sequence was generated
 from 5'-end region of cDNA insert including about 20 base of the
 sequence before 'N'. This cDNA was obtained from oligo-capped cDNA
 library by which method 5'-end of mRNA was efficiently cloned.
 Therefore remaining 5'-end 'N' is important for a detection of
 transcription start site of this mRNA.
 FEATURES
 Location/Qualifiers
 1..807
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="NT2RM2001576"
 /cell_type="teratocarcinoma"
 /cell_line="NT2"
 /clone_lib="NT2RM2"
 /note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal
 precursor cells"

ORIGIN
 Alignment Scores:
 Pred. No.: 4,75e-141 Length: 807
 Score: 1342.00 Matches: 261
 Percent Similarity: 98.14% Conservatives: 3


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QY 434 GlyLeuIleIleTrpGluMetAlaArgArgCysIleThrGlyGlyIleValGluGluTyr 453
Db 483 GGTTTGATCATTTTGGGAAATGGCTCGTCTGTATTACAGGAGGAATCGTGGAGGAATAT 542

QY 454 GlnLeuProTyrTyrAsnMetValProSerAspProSerTyrGluAspMetArgGluVal 473
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QY 494 ArgAlaValLeuLysLeuMetSerGluCysTrpAlaHisAsnProAlaSerArgLeuThr 513
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QY 514 AlaLeuArgIleLysLysThrLeuAlaLysMetValGlu 526
Db 723 GCTTTGAGAATCAAGAAGACACTTTTGC AAAATGGTTGAA 761

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Search completed: December 9, 2005, 22:23:00
Job time : 4028 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: December 9, 2005, 21:16:39 ; Search time 805 Seconds
(without alignments)
5464.980 Million cell updates/sec

Title: US-10-600-645-2
Perfect score: 2838
Sequence: 1 MTQLTYIRLLGACLFIIH.....TALRIKTKLAKMVESQDVKI 532

Scoring table: BLOSUM62
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Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Published Applications NA.Main.*
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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	ID	Description	
1	2838	100.0	1813	3	US-09-874-628-1	Sequence 1, Appli
2	2838	100.0	1813	7	US-10-600-645-1	Sequence 1, Appli
3	2838	100.0	3003	6	US-10-463-190-121	Sequence 121, App
4	2838	100.0	3003	9	US-10-868-497-90	Sequence 90, Appl
5	2838	100.0	3167	6	US-10-463-190-119	Sequence 119, App
6	2838	100.0	3167	6	US-10-463-190-120	Sequence 120, App
7	2838	100.0	3167	9	US-10-868-497-88	Sequence 88, Appl
8	2838	100.0	3167	9	US-10-868-497-89	Sequence 89, Appl

9	2823	99.5	2070	3	US-09-903-068-13	Sequence 13, Appl
10	2823	99.5	2070	9	US-10-739-413-13	Sequence 13, Appl
11	2823	99.5	2402	3	US-09-742-153-11	Sequence 11, Appl
12	2798	98.6	2056	7	US-10-641-319-3	Sequence 3, Appli
13	2769	97.6	1599	9	US-10-745-237-307	Sequence 307, App
14	2769	97.6	2623	5	US-10-153-217-1	Sequence 1, Appli
15	2769	97.6	2932	3	US-09-903-068-5	Sequence 5, Appli
16	2769	97.6	2932	3	US-09-982-543A-5	Sequence 5, Appli
17	2769	97.6	2932	6	US-10-286-152A-37	Sequence 37, Appl
18	2769	97.6	2932	6	US-10-463-190-116	Sequence 116, App
19	2769	97.6	2932	9	US-10-739-413-5	Sequence 5, Appli
20	2769	97.6	2932	9	US-10-868-497-85	Sequence 85, Appl
21	2769	97.6	2932	9	US-10-492-380-37	Sequence 37, Appl
22	2769	97.6	2932	9	US-10-450-763-22861	Sequence 22861, A
23	2769	97.6	2932	10	US-11-098-889-5	Sequence 5, Appli
24	2635.5	92.9	1743	8	US-10-128-558-48	Sequence 48, Appl
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26	2601	91.6	2730	9	US-10-450-763-22868	Sequence 22868, A
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28	2011	70.9	1185	6	US-10-029-386-20369	Sequence 20369, A
29	1972	69.5	1612	6	US-10-169-051-1	Sequence 1, Appli
30	1968	69.3	1612	6	US-10-169-051-3	Sequence 3, Appli
31	1952	68.8	1575	6	US-10-463-190-117	Sequence 117, App
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33	1952	68.8	2032	5	US-10-044-716-13	GENERAL INFORMATI
34	1952	68.8	2032	6	US-10-286-152A-39	Sequence 39, Appl
35	1952	68.8	2032	6	US-10-139-814-13	Sequence 13, Appl
36	1952	68.8	2032	6	US-10-172-118-570	Sequence 570, App
37	1952	68.8	2032	6	US-10-295-027-67	Sequence 67, Appl
38	1952	68.8	2032	6	US-10-295-027-788	Sequence 788, App
39	1952	68.8	2032	6	US-10-295-027-836	Sequence 836, App
40	1952	68.8	2032	6	US-10-295-027-880	Sequence 880, App
41	1952	68.8	2032	6	US-10-173-999-63	Sequence 63, Appl
42	1952	68.8	2032	6	US-10-463-190-118	Sequence 118, App
43	1952	68.8	2032	7	US-10-058-270A-5	Sequence 5, Appli
44	1952	68.8	2032	7	US-10-342-887-570	Sequence 570, App
45	1952	68.8	2032	7	US-10-692-824-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-874-628-1
; Sequence 1, Application US/09874628
; Patent No. US20020137133A1
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; CELESTE, Anthony J.
; THIES, R. Scott
; YAMAJI, No. US20020137133A1oru
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute Inc.- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/874,628
; FILING DATE: 05-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,934
; FILING DATE: 17-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, Steven R

```

; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 876 1170
; TELEFAX: 617 876 5951
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: CEK1-23a
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 61..1656
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-874-628-1

Alignment Scores:
Pred. No.: 0 Length: 1813
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Dbs: 3 Gaps: 0

US-10-600-645-2 (1-532) x US-09-874-628-1 (1-1813)

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Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
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Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
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Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
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Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
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Db 1261 AGGGTGGGCACACGCGGTACATGGCTCCAGAAGTGTCTGGACGAGGCTTGAGTAAAC 1320

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RESULT 2

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US-10-600-645-1
; Sequence 1, Application US/10600645
; Publication No. US20040142417A1
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; CELESTE, Anthony J.
; THIES, R. Scott
;

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YAMAJI, Noboru
TITLE OF INVENTION: RECEPTOR PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute Inc.- Legal Affairs
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/600,645
FILING DATE: 23-Jun-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/123,934A
FILING DATE: 17-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5203
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 876 1170
TELEFAX: 617 876 5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1813 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: CPK1-23a
FEATURE:
NAME/KEY: CDS
LOCATION: 61..1656
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-600-645-1

Alignment Scores:
Pred. No.: 0 Length: 1813
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-10-600-645-2 (1-532) x US-10-600-645-1 (1-1813)

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QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
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QY 301 SerTrpThrGlnLeuTyrIleuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
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QY 321 LeuLysCysAlaThrIleuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
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DB 1081 GGTCTGTGCCACCTCCACAGAAATTTATGGCAGCAAGGCAAGCTGCAATTTGCTCAT 1140
QY 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
DB 1141 CGAGACCTGAAGAGCAAAACATCTCTATTAGAAAAATGGTAGTTGCTGTATTGCTGAC 1200
QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
DB 1201 CTGGGCCCTAGCTGTTAAATTTCAACAGTGCACAAAATGAAGTTGACATACCTCTGAACACC 1260
QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
DB 1261 AGGTTGGGCCACCCAGCGGTACATGGCTCCAGAAAGTGTGGCAGAGGCTGTAGTAAAAAC 1320
QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
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DB 1381 GCCCGCTCGCTGATTACAGGAGGAATCGTGGAGGAATCAATTAACCATATTACAACATG 1440

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QY 481 ProfileValSerAsnArgTyrAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1501 CCAATCGTCTTAACCGCTGGACAGTGATGATGCTCTCGAGCGGTTTGAAGCTGATG 1560
QY 501 SerGluCysTyrAlaHisAsnProLaserArgLeuThrAlaLeuArgileLysLysThr 520
Db 1561 TCAGAATGCTGGGCCCATTAATCCAGCATCCAGACTCACAGCTTTGAGAATCAAGAAGACG 1620
QY 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1621 CTCGCAAGATGGTTGAATCCAGGATGTAAGATT 1656

RESULT 3
US-10-463-190-121
; Sequence 121, Application US/10463190
; Publication No. US2004000935A1
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary E.
; APPLICANT: Galas, David J.
; APPLICANT: Kovacevich, Brian
; APPLICANT: Mulligan, John T.
; APPLICANT: Paepel, Bryan W.
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Winkler, David G.
; TITLE OF INVENTION: COMPOSITIONS AND MEHTODS FOR
; TITLE OF INVENTION: INCREASING BONE MINERALIZATION
; FILE REFERENCE: 240083.508C2
; CURRENT APPLICATION NUMBER: US/10/463,190
; CURRENT FILING DATE: 2003-06-16
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 121
; LENGTH: 3003
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-463-190-121

Alignment Scores:
Pred. No.: 0 Length: 3003
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-600-645-2 (1-532) x US-10-463-190-121 (1-3003)
QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
Db 83 ATGACTCAGCTATACATTCATCAGATTACTTGGAGCGCTGCTGTTTCATCATTTCTCAT 142
QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db 143 GTTCAAGGGCAGAATCTAGATAGTATGCTCCATGTTGCTGTTATGAAATCAGACGTTGAC 202
QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
Db 203 CAGAGAAGCCGGAATAATGGATGACGTTAGCAGAGGACACCTTACCTTTCTTAAAA 262
QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
Db 263 TGCTATTGCTCAGGACACTGCCAGATGACGCTATTATAACACATGATCACTAATATGCG 322
QY 81 HisCysPheAlaIleGluGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 323 CATTCGCTTGGCATTTATAGAAGAAGATGATCAGGAGGAACACACGTTTAACTTCTGGGTG 382
QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
```

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Db 383 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCAAAAGCCCGCTACGCAGG 442
QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 443 ACAATAGAAATGTTGCGGACCAATTTGTGCAACCAATATTTGCGAGCTTACACTGCCCCCT 502
QY 141 ValValIleGlyProPhePheAspGlySerValArgTyrLeuAlaValLeuIleSerMet 160
Db 503 GTCGTTATAGGCCCATTTCTTTGATGGCAGCGTCGATGGCTGGCTGCTCATCTCTATG 562
QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
Db 563 GCTGCTGTATTTGTCGCCATGATCGTCTTCTCCAGCTGCTCTCTGTTACAAACATTTACTGT 622
QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
Db 623 AAGAGTATCTCAAGCAGAGGTCGTTTACAACCGTGACTTGGAAACAGGATGAAGCAITTTATT 682
QY 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
Db 683 CCAGTAGAGAAATCACTGAAAGACCTGATTGACCAAGTCAAAAGCTCTGGTAGTGGATCT 742
QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 743 GGATTACCTTTTATGGTTCAGCGAACTATTGCCAAACAGATTTCAGATGGTTCGGCAGGTT 802
QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTyrPArgGlyGluLysValAlaVal 260
Db 803 GGTAAGGCCGCTATGGAGAAAGTAGTGGTAAATGGCGTGTGTAAGAAAGTGGCTGTC 862
QY 261 LysValPheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db 863 AAAGTATTTTTCACACTGAAGAGCTAGCTGGTTTAGAGAAACAGAAATCTTACCAGACG 922
QY 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db 923 GTGTTAATGCGTCATGAAATAATATCTTGTTTTTATAGCTGCAGACATTTAAAGGCCCGGT 982
QY 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 983 TCCTGGACTCAGCTGATTTTGATTACTGATTACCATGAGATGGGTCTCTCTATGACTTC 1042
QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 1043 CTGAAATGTGCCACCTCGACACCCAGACCCCTACTCAAGTTAGCTTATTTCTGCTGCCGTG 1102
QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1103 GGTCTGTGCCACCTCCACACAGAAATTTATGGCAGCAGGCAAGCCTGCAATTCCTCAT 1162
QY 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
Db 1163 CGAGACCTGGAAGAGCAAAACATCCTTATTAGAAAAATGGTAGTTGCTGTTATGCTGAC 1222
QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1223 CTGGCCCTTAGCTGTATAATTCACAGTGACAAATGAAGTTGACATACCTTGAACACC 1282
QY 401 ArgValGlyThrArgTyrMetAlaProGluValLeuAspGluSerLysLysAsn 420
Db 1283 AGGTGGGCACAGCGGTATATGGCTCCAGAGTGTCTGGACGAGAGCTGATGTAANAAC 1342
QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
Db 1343 CATTTCCAGCCCTCATCATCGCTGACATCTACAGCTTTGGTTTGTATCATTTGGGAGATG 1402
QY 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1403 GCGCGTCGCTGTATTTACAGGAGGAATCGTGAGGAATATCAATTTACCATATTTACAACTG 1462
QY 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1463 GTGCTAGTAGCCCATCTTATGAAGACATGCGTGAGGTGCTGTTGTTGTAAGCGCTTGGCG 1522
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Qy 481 ProfileValSerAsnArgTTPAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1523 CCAATCGTCCTAACCGCTGAACAGATGATGCTTCGAGCCGTTTGAAGCTGATG 1582
Qy 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgLleLysLysThr 520
Db 1583 TCAGAAATGCTGGGCCCAATATCCAGCATCCAGACTCACAGCTTTGAGAAATCAAGAGACG 1642
Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1643 CTCGCAAAAGATGGTTGAATCCAGGATGTAAGATT 1678

RESULT 4

US-10-868-497-90
; Sequence 90, Application US/10868497
; Publication No. US20050106683A1
; GENERAL INFORMATION:
; APPLICANT: Winkler, David G.
; APPLICANT: Shi, Jiye
; APPLICANT: Latham, John
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR SCLEROSTIN AND
; TITLE OF INVENTION: METHODS FOR INCREASING BONE MINERALIZATION
; FILE REFERENCE: 60117-128
; CURRENT APPLICATION NUMBER: US/10/868,497
; CURRENT FILING DATE: 2004-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 3003
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-868-497-90

Alignment Scores:

Pred. No.: 0 Length: 3003
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-600-645-2 (1-532) x US-10-868-497-90 (1-3003)

Qy 1 MetThrGlnLeuThrTrpLleArgLeuLeuGlyAlaCysLeupheLleSerHis 20
Db 83 ATGACTCAGTATACACTTACATCAGATTACTGGAGCCTGTCTGTTCATCTTCTCAT 142
Qy 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db 143 GTTCAAGGCGAGAACTCTAGATAGTATGCTCCATGGTACTGTTATGAAATCAGACGTGGAC 202
Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
Db 203 CAGAAGAAGCGGAAATGAGTGACGTTAGCACCAGAGACACCTTACCTTTCTTAAAA 262
Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysLleThrAsnGly 80
Db 263 TGCTATTGCTCAGGACATGCCAGATGACGCTATTAAATACACATGCATAATATGCG 322
Qy 81 HisCysPheAlaIleLeuGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 323 CATTTGCTTGGCAATTATAGAAAGAGATGATCAGGGAGAAACCACTTCTCTGGGTGT 382
Qy 101 MetLysThrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 383 ATGAAGTATGAAGCTCTGATTTTCAATGCAAGGATTCACCAAAAGCCAGCTACGCAGG 442
Qy 121 ThrIleGluCysCysArgThrAnLeuLeuAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 443 ACAATGAATGTTGTGGACCAATTTGTGCAACCAATATTGTGAGCCTACACTGCCCCCT 502
Qy 141 ValValIleGlyProPheAspGlySerValArgTripleuAlaValLeuIleSerMet 160

Db 503 GTCTTTATAGGCCCATCTTTTGATGCGAGCGTCCGATGGCTGGCTGCTCATCTCTATG 562
Qy 161 AlaValCysLleValAlaMetLleValPheSerSerCysPheCysTyrLysHisTyrCys 180
Db 563 GCTGTCTGTATTGTCGCCATGATCGTCTTCTCCAGCTGCTTCTGTTCACAAACATTTACTGT 622
Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGlnAspGluAlaPheIle 200
Db 623 AAGAGTATCTCAAGCAGAGGTCGTTACACCGTACTTTGGAAACAGGATGAAGCATTTATT 682
Qy 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
Db 683 CCAGTAGGAGAAATCACTGAAAGACCTGATTGACCAAGTCACAAAGCTCTGCTAGTGGATCT 742
Qy 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 743 GGATTACCTTTATTGGTTTTCAGCGAATATTGCGCAAAACAGATTTCAGATGGTTCGCGAGTT 802
Qy 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
Db 803 GGTAAAGCGCGTATGAGAGATGATGGTGGTAAATGGCTGGTGAAGAAGTGGCTGTC 862
Qy 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db 863 AAAGTATTTTACCCTGAAAGAGCTAGCTGGTTTAGAGAAACAGAAATCTACCAGACG 922
Qy 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspLleLysGlyThrGly 300
Db 923 GTGTTAATGCTCATGAAATATACTTGGTTTTATAGCTGCAGACATTAAGGCACCGGT 982
Qy 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 983 TCTTGACTCAGCTGATTGTTGATTACTGATTTACCATGAGAAATGGGTCTCTCTATGACTTC 1042
Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaCys 340
Db 1043 CTGAAATGTGCCACCTCGACACCCAGAGCCCTACTCAAGTAGCTTATTCTGCTGCTGT 1102
Qy 341 GlyLeuCysHisLeuHisThrGluLleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1103 GGTCTGTGCCACCTCCACACAGAAATTTATGGCAGCAAGGCAAGCTGCAATTTGCTCAT 1162
Qy 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysLleAlaAsp 380
Db 1163 CGAGACCTGAAGAGCAAAACATCTTATTAAGAAAAATGGTAGTTGCTGTATTGCTGAC 1222
Qy 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1223 CTGGGCTTAGCTGTTAAATTTCAACAGTGACACAAATGAAGTTGCACATACCTTGAACACC 1282
Qy 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db 1283 AGGGTGGGCACCCAGCGGTACATGGCTCCAGAAGTGTCTGGAGAGACCTGAGTAAAAAC 1342
Qy 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
Db 1343 CATTTCCAGCCCTTACATCATGCTGACATCTACAGCTTTGGTTTGAATCATTTGGGAGATG 1402
Qy 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1403 GCGCGCTGCTGTATTACAGGAGGAATCTGGGAGGAATATCAATTACCATATTACACATG 1462
Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1463 GTGCTTAGTGACCCATCTTATGAAGACATGCGTGAGGTCTGTGTGTAACCGCTTCCCG 1522
Qy 481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1523 CCAATCGTCTCTAACCGCTTGAACAGTGTATGAATGTCTTCGAGCCGTTTTGAAGCTGATG 1582
Qy 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520

Db 1583 TCAGATGCTGGGCCCAATAATCCAGCATCCAGACTCCAGCTTTTGAGAATCAAGAAGACG 1642

Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532

Db 1643 CTCGCAAGATGGTTGAATCCCGAGATGTAAGATT 1678

RESULT 5

US-10-463-190-119

Sequence 119, Application US/10463190

Publication No. US20040009535A1

GENERAL INFORMATION:

APPLICANT: Brunkow, Mary E.

APPLICANT: Galas, David J.

APPLICANT: Kovacevich, Brian

APPLICANT: Mulligan, John T.

APPLICANT: Paepker, Bryan W.

APPLICANT: Van Ness, Jeffrey

APPLICANT: Winkler, David G.

TITLE OF INVENTION: COMPOSITIONS AND MEHTODS FOR

TITLE OF INVENTION: INCREASING BONE MINERALIZATION

FILE REFERENCE: 240083.508C2

CURRENT APPLICATION NUMBER: US/10/463,190

CURRENT FILING DATE: 2003-06-16

NUMBER OF SEQ ID NOS: 143

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 119

LENGTH: 3167

TYPE: DNA

ORGANISM: Rattus sp.

US-10-463-190-119

Alignment Scores:

Pred. No.: 0 Length: 3167

Score: 2838.00 Matches: 532

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-600-645-2 (1-532) x US-10-463-190-119 (1-3167)

Qy 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20

Db 226 ATGACTCAGCTATACCTTACATCATGATTACTGGGAGCCTGCTGTTTCATCATTTCTCAT 285

Qy 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40

Db 286 GTTCAAGGCGACAATCTAGATAGTAGTCTCCATGGTACTGGTATGAAATCAGACGTGGAC 345

Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60

Db 346 CAGAAAGACCGGAAATGGAGTGACGTTAGCACCAGAGGACACCTTACCTTTCTTAAAA 405

Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80

Db 406 TGCTATGTCTCAGGACACTGCCCATGACGCTATTATTAACATGATCACTAACTAATGCC 465

Qy 81 HisCysPheAlaIleIleGluAspAspGlnGlyThrThrLeuThrSerGlyCys 100

Db 466 CATTGCTTTGCCATTATAGAAGAAGATGATCAGGAGAAACCACTTAATCTCTGGGTGT 525

Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120

Db 526 ATGAAGATGTAAGGCTCTGATTTTCAATGCAAGGATTACCAAAAAAGCCAGCTACGCAGG 585

Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140

Db 586 ACAATAGAAATGTGTGGACCAATTTGTGCAACCAATATTTTCAGCCCTACACTGCCCCCT 645

Qy 141 ValValIleGlyProPheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160

Db 646 GTCTGTTATAGGCCCATCTCTTTGATGGCAGCGTCCGATGGCTGGCTGCTCATCTCATG 705

Qy 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180

Db 706 GCTGTCTGTATTGTGCGCATGATCGTCTTCCAGCTGCTTCTGTTCACAAACATTACTGT 765

Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200

Db 766 AAGAGTATCTCAAGCAGAGGTCGTTACAAACCGTGACTTGGAACAGGATGAAGCAITTTATT 825

Qy 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220

Db 826 CCAGTAGGAGAATCACTGAAAGACCTGATTGACCAGTCACAAAGCTCTGTGATGTGATCT 885

Qy 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240

Db 886 GGATTACCTTTATTGGTTCAGCGAACTATTGCCAAACAGATTGATGTTTCGGCAGGTT 945

Qy 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260

Db 946 GGTAAGGCCCGGTATGGAGAAAGTATGGATGGTAAATGGCGTGGTGAAGAAAGTGGCTGTC 1005

Qy 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280

Db 1006 AAAGTATTTTATACCACTGAAAGAGCTAGCTGGTTTAGAGAAACAGAAATCTTACCAGACG 1065

Qy 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300

Db 1066 GTGTTAATGCGTCATGAAATAATATCTTGGTTTATAGCTGCAGACATTAAAGGCCACCGGT 1125

Qy 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320

Db 1126 TCCTGGACTCAGCTGATTTCGATTACTGATTACCATGAGATGGGTCTCTCTATGACTTC 1185

Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340

Db 1186 CTGAAATGTGCGACCTCGACACCAGAGCCCTACTCAAGTTAGCTTATTTCTGCTGCCCTGT 1245

Qy 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360

Db 1246 GGTCTGTGCCACCTCCACACAGAAATTTATGGCAGCGAAGCAAGCCCTGCAATTCCTCAT 1305

Qy 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380

Db 1306 CGAGACCTGAAGACGAAAAACATCTTATTAAAGAAAAATGGTAGTTGCTGATTCTCTGAC 1365

Qy 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400

Db 1366 CTGGGCTAGCTGTTAAATTCACAGTGACACAAATGAAGTTGACATACCTTGAACACC 1425

Qy 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420

Db 1426 AGGTTGGGCACCGCGGTACATGGCTCCAGAAAGTGTGGACGAGAGCTCAGTAAAAAC 1485

Qy 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440

Db 1486 CATTTCCAGCCCTACATCATCGCTGACATCTACAGCTTTGGTTGATCATTTGGAGATG 1545

Qy 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460

Db 1546 GCCCGTCTGCTATTACAGGAGGAATCGTGAGGAATATCAATTAACCATATTTTACAAACATG 1605

Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480

Db 1606 GTGCTTAGTGACCATCTTATGAAGACATGCGTGAGGTGCTGTGTGTAAGACGCTTGGCG 1665

Qy 481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500

Db 1666 CCAATCGTCTCTAACCGCTGGAAACAGTGATGAATGCTTCGAGCGCTTTTGAAGCTGATG 1725

Qy 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysThr 520

Db 1726 TCAGAAATGCTGGGCCCAATAATCCAGATCCAGACTCCAGACTTTTGAGAATCAAGAAGACG 1785

Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532

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Db 1786 CTCGCAAGATGGTTGAATCCAGGATGTAAAGATT 1821
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RESULT 6
US-10-463-190-120
; Sequence 120, Application US/10463190
; Publication No. US20040009535A1
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary E.
; APPLICANT: Galas, David J.
; APPLICANT: Kovacevich, Brian
; APPLICANT: Mulligan, John T.
; APPLICANT: Paepker, Bryan W.
; APPLICANT: Paepker, Bryan W.
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Winkler, David G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; INCREASING BONE MINERALIZATION
; FILE REFERENCE: 240083.508C2
; CURRENT APPLICATION NUMBER: US/10/463,190
; CURRENT FILING DATE: 2003-06-16
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 120
; LENGTH: 3167
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-463-190-120

Alignment Scores:
Pred. No.: 0 Length: 3167
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-600-645-2 (1-532) x US-10-463-190-120 (1-3167)

QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyValaCysLeuPheIleIleSerHis 20
|||||
Db 226 ATGACTCAGCTATACCTTACATCAGATTACTCGGAGCCTGCTGTTTCATCTTCAT 285
|||||
QY 21 ValGlnGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
|||||
Db 286 GTTCAAGGGCAGAACTTAGATAGTATGCTCCATGGTACTGGTATGAAATCAGACGTGGAC 345
|||||
QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
|||||
Db 346 CAGAAGAAGCCGGAAATGGAGTGACGTTAGCACACGAGGACACCTTACCTTTCTTAAAA 405
|||||
QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
|||||
Db 406 TGCATTGCTCAGACACCTGCCAGATGACGCTATTAAATACACATGCAATAATGGC 465
|||||
QY 81 HisCysPheAlaIleIleGluGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
|||||
Db 466 CATTGCTTTGCCATTATAGAAGATGATCAGGAGAAACACACGTTAACTTCTGGGTGT 525
|||||
QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
|||||
Db 526 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCAAAAGCCAGCTACGCAGG 585
|||||
QY 121 ThrIleGluCysCysArgThrAsnLeuLeuAsnGlnTyrLeuGlnProThrLeuProPro 140
|||||
Db 586 ACAATAGATGTTGTGGACCAATTTGTGCAACCAATATTGCGAGCCTACACTGCCCCCT 645
|||||
QY 141 ValValIleGlyProPheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
|||||
Db 646 GTCGTTATAGGCCCATCTTTGATGGCAGCGTCCGATGGCTGGCTGCTCATCTCTATG 705
|||||
QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
|||||
Db 706 GCTGTCTGTATTGTCGCCCATGATCGTCTTCTCCAGCTGCTTCTGTTTACAAACATTACTGT 765
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RESULT 7
US-10-868-497-88
; Sequence 88: Application US/10868497
; Publication No. US20050106683A1
; GENERAL INFORMATION:
; APPLICANT: Winkler, David G.
; APPLICANT: Shi, Jiye
; APPLICANT: Latham, John
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR SCLEROSTIN AND
; FILE REFERENCE: 60117-128
; CURRENT APPLICATION NUMBER: US/10/868,497
; CURRENT FILING DATE: 2004-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 3167
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-868-497-88

Alignment Scores:
Pred. No.: 0 Length: 3167
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-600-645-2 (1-532) x US-10-868-497-88 (1-3167)

QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
DB 226 ATGACTCAGCTATACACTTACATCAGATTACTGGGAGCCTGCTGTTCATCTCTCAT 285

QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
DB 286 GTTCAAGGCGAGATCTAGATAGTATGCTCCATGGTACTGGTATGAAATCAGACGTGGAC 345

QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
DB 346 CAGAGAAGCCGGAATGGAGTGAGCTTTAGCACAGAGGACACCTTTACTTTCTTAAAA 405

QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
DB 406 TGCATTGTCTCAGGACACTGCCAGATGACGCTATTAAATACACATGCAATACTAATGGC 465

QY 81 HisCysPheAlaIleIleGluAspAspGlnGlyThrThrLeuThrSerGlyCys 100
DB 466 CATTTGCTTTGCCATTATAGAGAGATGATCAGGGAGAAACACCGTTAACTTCTGGGTGT 525

QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
DB 526 ATGAAGTATGAAGCTCTGATTTTCAATCAAGAGATTACACAAAGCCAGCTACGCAGG 585

QY 121 ThrIleGluCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
DB 586 ACAATAGAAATGTTGTCGACCAATTTGTGCAACCAATATTTCAGCCTCACTGCCCCCT 645

QY 141 ValValIleGlyProPheAspGlySerValArgTyrLeuAlaValLeuIleSerMet 160
DB 646 GTGCTGTATTGTGCGCCATGATCGTCTTCTCAGCTGCTTCTGTGTACAAACATTACTGT 705

QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
DB 706 GCTGTCTGTATTGTGCGCCATGATCGTCTTCTCAGCTGCTTCTGTGTACAAACATTACTGT 765

QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGlnAlaPheIle 200
DB 766 AAGAGTATCTCAAGCAGAGGTCGTTACAAACCGTGACTTGGAAACAGGATGAAGCATTTAT 825

QY 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
DB 945 GATTTACCTTTATTGGTTTTCAGCGAACTATTGCAAAACAGATTTCAGATGGTTTCGGCAGGTT 945

DB 826 CCAGTAGGAGAACTCACTGAAAGACCTGATTGACCAGTCAACAAGCTCTGGTAGTGGATCT 885
QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
DB 886 GGATTTACCTTTATTGGTTTTCAGCGAACTATTGCAAAACAGATTTCAGATGGTTTCGGCAGGTT 945
QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGlyGluLysValAlaVal 260
DB 946 GGTAAAGGCCGGTATGGAGAAAGATGGATGGGTAATGGCGTGGTGAAGAAAGTGGCTGTG 1005
QY 261 LysValPhePheThrThrGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
DB 1006 AAAGTATTTTACCACCTGAAGAGCTAGCTGGTTTAGAGAAACAGAAATCTACACAGACG 1065
QY 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
DB 1066 GTGTTAATGCGTCATGAAATATATCTGGTTTATAGCTGCAGACATTAAGGCCACCGGT 1125
QY 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
DB 1126 TCCTGGACTCAGCTGATTTGATTACTTACCATTAGAAATGGGTCTCTCTATGACTTTC 1185
QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaLys 340
DB 1186 CTGAAATGTGCCACCTCGACACACAGAGCCCTACTCAAGTTAGCTTATTTCTGCTGCTGT 1245
QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
DB 1246 GGTCTGTGCCACCTCCACACAGAAATTTATGGCAGCAAGGCAAGCCTGCAATTTGCTCAT 1305
QY 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
DB 1306 CGAGACCTGGAAGAGCAAAACATCCTTATTAGAAAAATGGTAGTTGCTGTATTGCTGAC 1365
QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
DB 1366 CTGGGCTTAGCTGTTAAATTCACACAGTCACACAAATGAAGTTGACATACCTTTGAACACC 1425
QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
DB 1426 AGGTGGGCGCACCGCGGTACATGCTCCAGAAAGTCTGGAGAGAGCCTGAGTAAAAAC 1485
QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
DB 1486 CATTTCCAGCCCTACATCATGCTGACATCTACAGCTTTGGTTTGTATCATTTGGGAGATG 1545
QY 441 AlaArgArgCysIleThrGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
DB 1546 GCCCGTCCGCTGTTTACAGGAGGAATCGTGGAGGAATATCAATTACCATATTACAACATG 1605
QY 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
DB 1606 GTGCCCTAGTACCCATCTTATGAAGACATGCGTAGAGTCTGTGTGTGTAACCGTTGCGG 1665
QY 481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
DB 1666 CCAATCGTCTCTAACCGCTGGAAACAGTGAATGATGCTCTTCGAGCGCTTTTGAAGCTGATG 1725
QY 501 SerGluCysTyrAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
DB 1726 TCAGAAATGCTGGGCCCATTAATCCAGCATCCAGACTCACAGCTTTTCAGAAATCAAGAAGACG 1785
QY 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
DB 1786 CTCGCAAGAGTGGTTGAATCCAGGATGTAAGATT 1821

RESULT 8
US-10-868-497-89
; Sequence 89: Application US/10868497
; Publication No. US20050106683A1
; GENERAL INFORMATION:
; APPLICANT: Winkler, David G.
; APPLICANT: Shi, Jiye
```

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; APPLICANT: Latham, John
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR SCLEROSTIN AND
; TITLE OF INVENTION: METHODS FOR INCREASING BONE MINERALIZATION
; FILE REFERENCE: 60117-128
; CURRENT APPLICATION NUMBER: US/10/868,497
; CURRENT FILING DATE: 2004-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 3167
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-868-497-89

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Alignment Scores:	
Pred. No.:	0
Score:	2838.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	9
Length:	3167
Matches:	532
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-10-600-645-2 (1-532) x US-10-868-497-89 (1-3167)

1	MetThrGlnLeuTyThrTyrlleargLeuLeuGlyAlaCysLeuPheIlelleSerHis	20
226	ATGACTCAGCTATACACTTACATCAGATTCTGGGAGCCTGTCTGTTCATCATTTCTCAT	285
21	ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetIysSerAspValAsp	40
286	GTTCAAGGGCGAATCTAGATAGTAGTGTCTCATCGTACTGGTATGAAATCAGACGTGGAC	345
41	GlnIlysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys	60
346	CAGAAGAAGCCGGAATAATGGAGTCACGTTAGCACCCAGAGACACCTTACCTTCTTTAAAA	405
61	CysTyrCysSerGlyHisCysProAspAlaIleAsnAsnThrCysIleThrAsnGly	80
406	TGCTATTTCCTCAGGACACTGCCACAGATCAGCTATTATAACACATGCATAACTAATGCG	465
81	HisCysPheAlaIlelleGluGluAspGlnGlyGluThrThrLeuthrSerGlyCys	100
466	CATTGCTTTGGCATTTATAGAAGAAGATGATCAGGGAGAAACCCACGTTAACTTCCTGGGTGT	525
101	MetIysTyrGluGlySerAspPheGlnCysIysAspSerProIysAlaGlnLeuAspArg	120
526	ATGAAGTATGAAGGCTCTGATTTTCAATGCAGAGATTACACAAAGCCAGCTACGCAGG	585
121	ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro	140
586	ACAAATAGAATGTTGTCGACCAATTTGTGCAACCAATATTTGCAGCCTACACTGCCCCCT	645
141	ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaVallelleSerMet	160
646	GTCGTATPAGCCCAATCTTTGATGGCAGCGTCCGATGGCTGTGCTCATCTCTATG	705
161	AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrIysHisTyrCys	180
706	GCTGTCTGTATTGTCGCAATGATCGTCTTCTCAGCTGCTTCTGTTACAAACATTA	765
181	LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGlnAspGluAlaPheIle	200
766	AAGAGTATCTCAAGCAGAGGTCTGTACAAACCGTGACTTGGAAACAGGATGAAGCATTTATT	825
201	ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer	220
826	CCAGTAGGAGAATCACTGAAGAGACCTGATTGACAGCTCAAAAGCTCTCGTAGTGGATCT	885
221	GlyLeuProLeuValGlnArgThrIleAlaIysGlnIleGlnMetValargGlnVal	240
886	GGATTACCTTTATTGGTTTCAGCGAACTATTATGGCAAAACAGATTACAGATGTTGTCGGCAGGTT	945
241	GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal	260

RESULT 9

RESOL 9
US-09-903-068-13

03-03-203-008-13
; Sequence 13. Application US/09903068

; Patent No. US20020123139A1

; GENERAL INFORMATION:

APPLICANT: Miyazono, Kohei; Di'jke, Peter Ten;

Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik

TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins

Having Serine Threonine Kinase Domains And Their Use
NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felife & Lynch

STREET: 805 Third Avenue

; CITY: New York City

STATE: New York
ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/903,068
FILING DATE: 11-Jul-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/679,187
FILING DATE: <Unknown>
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. US20020123139A1ember-1993
APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. US20020123139A1ember-1992
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
APPLICATION NUMBER: 9304680.3
FILING DATE: 8-March-1993
APPLICATION NUMBER: 9311047.6
FILING DATE: 28-May-1993
APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
APPLICATION NUMBER: 9316099.2
FILING DATE: 3-August-1993
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-October-1993

ATTORNEY/AGENT INFORMATION:

NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 698-9200
TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
LENGTH: 2070 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Mouse

FEATURE:

NAME/KEY: CDS
LOCATION: 217..1812
SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-903-068-13

Alignment Scores:

Pred. No.:	0	Length:	2070
Score:	2823.00	Matches:	526
Percent Similarity:	99.81%	Conservative:	5
Best Local Similarity:	98.87%	Mismatches:	1
Query Match:	99.47%	Indels:	0
DB:	3	Gaps:	0

US-10-600-645-2 (1-532) x US-09-903-068-13 (1-2070)

QY	1	MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleSerHis	20
DB	217	ATGACTCAGCTATACACTTACATCAGATTACTGGGAGCCTGCTGTTCATCATTTCTCAT	276
QY	21	ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp	40
DB	277	GTTCAAGGGCAGAACTAGATAGTATGCTCCATGGCAGCTGGTATGAAATCAGACTTGGAC	336
QY	41	GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuPheLeuLys	60

DB	337	CAGAAAGCCAGAAAATGGAGTGACTTTAGCCACGAGGATACCTTGTCTTTCTTAAG	396
QY	61	CysTyrCysSerGlyHisCysProAspAlaIleAsnAsnThrCysIleThrAsnGly	80
DB	397	TGCTATTGCTCAGGACACTGCCACAGATGCTATTATAACACATGCATACTAATGCC	456
QY	81	HisCysPheAlaIleGluGluAspGlnGlyGluThrThrLeuThrSerGlyCys	100
DB	457	CATTGCTTTGCCATTATAGAAAGATGATCAGGGAGAAACACATTAACTTCTGTGGTGT	516
QY	101	MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgAsp	120
DB	517	ATGAAGATGAAGGCTCTGATTTTCAATGCAAGGATTCACCGAAAGCCAGCTACGAG	576
QY	121	ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro	140
DB	577	ACAATAGAATGTTGTCGGACCAATTTGTCAACCAAGTATTTGCAGCCTACACTGCCCT	636
QY	141	ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet	160
DB	637	GTTGTTATAGGTCCTGTTTCATGGCAGCATCCGATGGCTGGTGTGTCTCATTTCCATG	696
QY	161	AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys	180
DB	697	GCTGTCTGTATAGTTGCTATGATCATCTTCTCAGCTGCTTTTGCTATTAAGCATATTGT	756
QY	181	LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle	200
DB	757	AAGAGTATCTCAAGCAGGGGTCTGTACAAACCGTGATTTGGAACAGGATCAAGCATTTAT	816
QY	201	ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer	220
DB	817	CCAGTAGGAGAAATCAATTGAAAGACCTGATTCAGCAGTCCCAAGCTCTGGGAGTGATCT	876
QY	221	GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal	240
DB	877	GGATTGCCCTTTATTGGTTCAGCGAACTATTGCCAAACAGATTTCAGATGGTTCCGGAGGTT	936
QY	241	GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal	260
DB	937	GGTAAAGGCCGCTATGGAGAGTATGGATGGGTAATGGCGTGGTGAAAGAGTGGCTGC	996
QY	261	LysValPhePheThrThrGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr	280
DB	997	AAAGTGTTTTTACCACCTGAGAGAGCTAGCTGGTTTAGAGAAACAGAAATCTACCAGCG	1056
QY	281	ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly	300
DB	1057	GTGTTAATGCCGTCATGAAATATATCTGTTTTATAGCTGCAGACATTAAAGCACTGGT	1116
QY	301	SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe	320
DB	1117	TCCTGGACTCAGCTGATTGATTACTGATTACCATGAAATGGATCTCTCTATGACTTC	1176
QY	321	LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys	340
DB	1177	CTGAAATGTGCCACACTAGACACAGAGCCCTACTCAAGTTAGCTTATTTCTGCTGTTGT	1236
QY	341	GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis	360
DB	1237	GGTCTGTGCCACCTCCACAGAAATTTATGGTATCCCAAGGGAAGCCTGCAATTTGCTCAT	1296
QY	361	ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp	380
DB	1297	CGAGACCTGAAGAGCAAAACATCCTTATTAGAAAAATGGAAGTTGCTGTATTCGTGAC	1356
QY	381	LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr	400
DB	1357	CTGGGCCCTAGCTGTTAAATTTCAACAGTATACAAATGAAGTTGACATACCTTGAATACC	1416
QY	401	ArgValGlyThrArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn	420

Db 1417 AGGTGGGACCAACGGGTACATGGCTCCAGAACTGCTGGATGAAAGCCTGAATAAAAAAC 1476
Qy 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTyrGluMet 440
Db 1477 CATTTCCAGGCCCTACATCATGGCTGACATCTATAGCTTTGGTTTGATCAATTTGGGAAATG 1536
Qy 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1537 GCTCGTGTGTATTACAGGAGGANTCGTGGAGGAATATCAATACCATATTACAACTG 1596
Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValIleAspArgLeuArg 480
Db 1597 GTGCCAGTGACCCATCTCTATAGGACATGCGTGAGGTGTGTGTGTGTAAGACGCTTCCGG 1656
Qy 481 ProfileValSerAsnArgTyrAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1657 CCAATCGTGTCTAACCCCTGGAACAGCGATGAATGTCTTCGAGCAGTTTTTGAAGCTAATG 1716
Qy 501 SerGluCysTyrAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db 1717 TCAGAAATGTTGGGCCCATATCCAGCTCCAGACTCACAGCTTTGAGAAATCAAGAGACA 1776

RESULT 10

US-10-739-413-13
; Sequence 13, Application US/10739413
; Publication No. US20050048607A1
; GENERAL INFORMATION:
; APPLICANT: MIYAZONO, Kohei
; APPLICANT: INAMURA, Takeshe
; APPLICANT: DEN DIJKE, Peter
; TITLE OF INVENTION: PROTEINS HAVING SERINE/THREONINE KINASE DOMAINS, CORRESPONDING
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND THEIR USE
; FILE REFERENCE: LUD 5539.1 CIP
; CURRENT APPLICATION NUMBER: US/10/739,413
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US/09/267,963
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/GB93/02367
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: US 09/039,177
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-739-413-13

Alignment Scores:

Pred. No.:	0	Length:	2070
Score:	2823.00	Matches:	526
Best Similarity:	99.81%	Conservative:	5
Best Local Similarity:	98.87%	Mismatches:	0
Query Match:	99.47%	Indels:	0
DB:	9	Gaps:	0

US-10-600-645-2 (1-532) x US-10-739-413-13 (1-2070)

Qy 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
Db 217 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCCTGTCTGTTCATCACTTCTCAT 276
Qy 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db 277 GTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGGCACTGGTATGAATCAGACTTGGAC 336
Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60

Db 337 CAGAAGAAGCCAGAAATGGAGTGACTTTTAGCACCAGAGGATACCTTTGCTCTTTCTTAAG 396
Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
Db 397 TGTATTTGGCTCAGGACATGCCCCAGATGATGCTATTAAATAACACATGCATCAATAATG 456
Qy 81 HisCysPheAlaIleIleGluGluAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 457 CATTTGCTTTGCCATTATAGAAAGAGATGATCAGGGAGAAACCAATTAATCTTGGGTGT 516
Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 517 ATCAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCGAAAGCCAGCTACGCAGG 576
Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrIleGlnProThrLeuProPro 140
Db 577 ACAATAGAATGTTGTTCGGACCAATTTTGTGCAACAGTATTTGCGAGCCTACATGCCCC 636
Qy 141 ValValIleGlyProPhePheAspGlySerValArgTyrLeuAlaValLeuIleSerMet 160
Db 637 GTTGTATAGTCCGTTCTTTGATGGCAGCATCCGATGGCTGGTGTGCTCATTTCCATG 696
Qy 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
Db 697 GCTGTCTGTATAGTGTCTATGATCATCTTCTCAGCTGCTTTTGTCTATAAGCATTTATGT 756
Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGlnGlnAspGluAlaPheIle 200
Db 757 AAGAGTATCTCAAGCAGGGTCTGTACACCGTATTTGGAAACAGGATGAAGCATTTATTT 816
Qy 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
Db 817 CCAGTAGGAGATCATTTGAAAGACCTGATTGACCATGCCAAGCTCTGGAGTGATCT 876
Qy 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 877 GGATTCCTTTATTTGGTTTCAGCGAACTATTTCGCAACAGATTCAGATGGTTCCGAGTT 936
Qy 241 GlyLysGlyArgTyrGlyGluValTyrMetGlyLysTyrArgGlyGluLysValAlaVal 260
Db 937 GGTAAGGCGCTATCGAGAAGTATGGATGGGTAAATGGCTGTTGAAAAAGTGGCTGTC 996
Qy 261 LysValPhePheThrThrGluGluAlaSerTyrPheArgGluThrGluIleTyrGlnThr 280
Db 997 AAGTGTGTTTTTACCACCTGAAGAGCTAGCTGGTTAGAGAAACAGAAATCTACCAGAC 1056
Qy 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db 1057 GTGTTAATGCGTCATGAAATATATCTTGGTTTTTATAGCTGCAGACATTAAGGCACCTGT 1116
Qy 301 SerTyrThrGlnLeuTyrIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 1117 TCCTGGACTCAGCTGTATTTGATTTACTGATTACCATGAAATGGATCTCTCTATGACTTC 1176
Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 1177 CTGAAATGTCCACACTAGACAGCCCTACTCAAGTTAGCTTATTCTGCTGCTGTGT 1236
Qy 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1237 GGTCTGTGCCACCTCCACACAGAAATTTATGGTACCAAGGAAAGCTGCAATTTGCTCAI 1296
Qy 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
Db 1297 CGAGACTCTGAAGAGCAAAACATCTCTTATTAAGAAAAATGGAAAGTTGCTGTATTGTG 1356
Qy 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1357 CTGGGCTAGCTGTGTTAAATTTCAACAGTGATACAAATGAAGTTGACATACCTTGAATACC 1416
Qy 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db 1417 AGGTGGGACCAACGCGGTACATGGCTCCAGAAAGTCTCGATGAAAGCCTGAATAAAAAAC 1476

QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
DB 1477 CATTTCCAGCCCTACATCATGCTGACATCTATAGCTTTGGTTGGTATCATTTGGGAAATG 1536
QY 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
DB 1537 GCTCGTCTGTATTACAGAGAGAAATCGTGGAGGAATATCAATTTACCATATTACAAATG 1596
QY 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValIysArgLeuArg 480
DB 1597 GTGCCAGTGACCCATCTATCAGGACATGCGTGAGGTTGTGTGTGAACGCTTGGCG 1656
QY 481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuIysLeuMet 500
DB 1657 CCAATCGTCTCAACCGCTGGGAACAGCGATGAATGTCTTCGAGCAGTTTTGAAGCTAATG 1716
QY 501 SerGluCysTrpAlaHisAsnProIleSerArgLeuThrAlaLeuArgIleIysIysThr 520
DB 1717 TCAGAAATGTGGCCCATTAATCCAGCCTCCAGACTCACAGCTTTGAGAAATCAAGAAGACA 1776
QY 521 LeuAlaLysMetValGluSerGlnAspValIysIle 532
DB 1777 CTTGCAAAAATGGTTGAATCCCGAGGATGTAAGATT 1812

RESULT 11

US-09-742-153-11
; Sequence 11, Application US/09742153
; Publication No. US20030096296A1
; GENERAL INFORMATION:
; APPLICANT: Rosenbaum, Jan S
; TITLE OF INVENTION: The Use of a BMP Protein Receptor
; Complex for Screening Bone Metabolism Actives and Cells
; Co-Transfected With a Type II BMP Receptor and a Type I
; BMP Receptor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Procter & Gamble Company
; STREET: 11810 East Miami River Road
; CITY: Ross
; STATE: OH
; COUNTRY: USA
; ZIP: 45061
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/742,153
; FILING DATE: 20-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,467
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hersko, Bart S.
; REGISTRATION NUMBER: 32,572
; REFERENCE/DOCKET NUMBER: 5474R
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 627-0633
; TELEFAX: (513) 627-0260
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2402 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-742-153-11
Alignment Scores:

Pred. No.: 0 Length: 2402
Score: 2823.00 Matches: 526
Percent Similarity: 99.81% Conservative: 5
Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 3 Gaps: 0
US-10-600-645-2 (1-532) x US-09-742-153-11 (1-2402)
QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
DB 11 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCGTCTCTGTTTCATCATTTCTCAT 70
QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
DB 71 GTTCAAGGGCAGAAATCTAGATAGTAGTCTCCATGGCACTGGTATGAAATCAGACTTGGAC 130
QY 41 GlnIysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
DB 131 CAGAAGAAAGCCAGAAAATGGAGTGACTTTAGCACAGAGGATACCTTGGCTTTCTTTAAAG 190
QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
DB 191 TGCTATTGCTCAGGACACTGCCAGATCATGCTATTATAACACATGCATAAATAATGGC 250
QY 81 HisCysPheAlaIleIleGluGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
DB 251 CATTTGCTTTGCCATTATAGAAGAAATGATCAGGGAGAAACACATTAACATTTCTGGGTGT 310
QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
DB 311 ATGAAGATGATGAAGGCTCTGATTTTCAATGCAAGGATTCAACGAAAGCCAGCTACGAGG 370
QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
DB 371 ACAATAGAAATGTTGTCGGACCAATTTGTGCAACAGTATTTGCAGCCTACACTGCCCT 430
QY 141 ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
DB 431 GTTGTATAGGTCCGTTCTTTGATGGCAGCATCCGATGGCTGGTTGTGCTCATTTCCATG 490
QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrIleHisTyrCys 180
DB 491 GCTGTCTGTATAGTTGCTATCATCTCTCCAGCTGCTTTTGTGCTATAAGCATTAATTGT 550
QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
DB 551 AAGAGTATCTCAAGCAGGGGTCTGTACAACTGATTTTGAACAGGATGAAGCATTTATT 610
QY 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
DB 611 CCAGTAGGAGAAATCATTTGAAAGACCTGATTGACAGTCCCAAATCTTTGGAGTATAT 240
QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 260
DB 671 GGATTGCCCTTTATTGGTTTCAGGAACTATTGCCAAACAGATTTCAGATGGTTCGGCAGGT 730
QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGlyLysValAlaVal 260
DB 731 GGTAAGGCCCGCTATGGAGAAGTAGGATGGTAAATGCGCTGGTGAAGAAAGTGGCTGTC 790
QY 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
DB 791 AAAGTGTTTTTTACCACCTGAAGAGCTAGCTGGTTTGTAGAGAAACAGAAATCTTACCAGAG 850
QY 281 ValLeuMetArgHisGluAsnIleGlyPheIleAlaAlaAspIleIysGlyThrGly 300
DB 851 GTGTTAATGCGCTCATGAAAATATATCTTGGTTTTATAGCTGCAGACATTAAAGGCACTGGT 910
QY 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
DB 911 TCCTGGACTCAGCTGATTTTCTGATTACTGATTACCATGAAATGGATCTCTCTATGACTTC 970

Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 971 CTGAAATGTGCGCACCTAGACACAGAGCCCTACTCAAGTTAGCTTATTCTGCTGCTGT 1030
Qy 341 GlyLeuCyHisLeuHisThrGluLeuTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1031 GGTCTGTGTCACCTCCACAGAAATTTATGGTACCCAGGGAAGCCCTGCAATTTGCTCAT 1090
Qy 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
Db 1091 CGAGACCTGAAGAGCAAAACATCTTATTAGAAAATGGAAGTTGCTGTATTGCTGAC 1150
Qy 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1151 CTGGCCCTAGCTGTAAATTTCAACAGTGATACAAATGAAGTTGACATACCTTTGAATACC 1210
Qy 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLysAsn 420
Db 1211 AGGTGGGCACCAAGCGGTACATGGCTCCAGAAAGTGTGGATGAAAGCCCTGAATAAAAC 1270
Qy 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTyrGluMet 440
Db 1271 CATTTCCAGCCCTACATCATGGCTGACATCTATAGCTTTGTTGATCATTTGGGAATG 1330
Qy 441 AlaArgCysIleThrGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1331 GCTCGTGTGTTATTACAGGAGGAATCGTGGAGGAATATCAATTACCATTATCAACATG 1390
Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1391 GTGCCAGTGACCCATCCTATGAGGACATCGTGAGGTTGTGTGTGTGAACCGTTGCGG 1450
Qy 481 ProIleValSerAsnArgTyrAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1451 CCAATGTGTCTAACCGCTGGAACAGCATGAATGCTTTCGAGCAGTTTTTGAAGCTAATG 1510
Qy 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db 1511 TCAGATGTTTGGGCCCATATCCAGCTCCAGACTCCAGACTTTTGAGATCAAGAGACA 1570
Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1571 CTTTGCAAAATGTTGAATCCAGGATGTAAGATT 1606

RESULT 12

US-10-641-319-3
; Sequence 3, Application US/10641319
; Publication No. US20040143863A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jwang
; APPLICANT: Li, Linheng
; TITLE OF INVENTION: Hematopoietic Stem Cell Niche Cells
; FILE REFERENCE: 64928
; CURRENT APPLICATION NUMBER: US/10/641,319
; CURRENT FILING DATE: 2003-08-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 2056
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-641-319-3

Alignment Scores:
Pred. No.: 0 Length: 2056
Score: 2798.00 Matches: 526
Percent Similarity: 94.48% Conservative: 5
Best Local Similarity: 93.59% Mismatches: 1
Query Match: 98.59% Indels: 30
DB: 7 Gaps: 1

US-10-600-645-2 (1-532) x US-10-641-319-3 (1-2056)

Qy 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
Db 291 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCCCTGTCTGTTTCATCTTCTCAT 350
Qy 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db 351 GTTCAAGGCGAGAATCTAGATAGTATGCTCCATGGCACTGGTATGAAATCAGACTTTGGAC 410
Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
Db 411 CAGAAGACCGCAAAATGAGTGACTTTAGCACAGAGGATACCTTGCCTTCTTCTTAAAG 470
Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
Db 471 TGCTATTGCTCAGGACACTGCCCCAGATGATGCTATTATAACACACATGACATAATGGC 530
Qy 81 HisCysPheAlaIleIleGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 531 CATTTGCTTTGCCATTATAGAAGAAGATGATCAGGGAGAAACCCACATTAACTTCTGGTGT 590
Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArg 120
Db 591 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCGAAGCCAGCTACCCAGG 650
Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 651 ACAATAGATGTTTGTGCGACCAATTTTGTCAACACAGTATTTCAGCGCTACACTGCCCCCT 710
Qy 141 ValValIleGlyProPheAspGlySerValArgTyrLeuAlaValLeuIleSerMet 160
Db 711 GTTGTATTAGTCCGTTCTTTGATGGCAGCATCCGATGGCTGGTGTGCTCATTTCCATG 770
Qy 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
Db 771 GCTGTCTGTATAGTGTCTATGATCATCTTCTCCAGCTGCTTTTGTCTATTAAGCATTTATT 830
Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
Db 831 AAGAGTATCTCAAGCAGGGGTGCTTACAAACCGTGATTTCGAACAGGATGAAGCATTTATT 890
Qy 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
Db 891 CCAGTAGGAGAAATCATTTAAAGACCTGATTGACCACTCCCAAGCTCTGGGAGTGATCT 950
Qy 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 951 GGATTTGCCCTTATTGTTTTCAGCGAATATTTCGCAACACAGATTTCAGATGGTTCCGGCAG 1010
Qy 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
Db 1011 GGTAAAGCCGCTATGGAGAGTATGGATGGGTAAATGGCTGGTGAAGGAGTGGCTGTC 1070
Qy 261 LysValPhePheThrThrGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db 1071 AAAGTGTGTTTTTACCACCTGAAGAGCTAGCTGCTTTAGAGAAACAGAAAATCTACCAGAC 1130
Qy 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db 1131 GTGTTAATGCGTCATGAAATATATCTGTTTATAGCTGCAGACATTAAGAGCATGTTGT 1190
Qy 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 1191 TCCTGGACTCAGCTGATTGTTGATTACTGATTACCATGAAATGGATCTCTCTATGACTTC 1250
Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 1251 CTGAAATGTGCCACACTAGACACAGAGCCCTACTCAAGTTAGCTTATTCTGCTGCTTGT 1310
Qy 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1311 GGTCTGTGCCCTCCACACAGAAATTTATGTGTACCCAGGGAAGCCCTCAATTTGCTCAT 1370
Qy 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysIleAlaAsp 380

Db 961 CTGAAATGTGCTACACTGGACACAGAGCCCTGCTTAAATGGCTTATTAGCTGCCTGT 1020
Qy GlyLeuCyHisLeuHisThrGluLeuTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1021 GGTCTGTGCCACCTGCACACAGAAATTTATGGCCACCAAGAAAGCCGCAATGTCTCAT 1080
Qy 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
Db 1081 CGAGACCTAAAGAGCAAAACATCTCATCAAGAAAAATGGAGTTGCTGCATTGCTGAC 1140
Qy 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1141 CTGGGCTTGTGTTAAATTAACAGTCACACAAATGAAGTTGATGGCCCTTGAATACC 1200
Qy 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db 1201 AGGGTGGGACCAACGCTACATGGCTCCCGAGTGTGGACGAAGCCCTGAACAAAAAC 1260
Qy 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTyrGluMet 440
Db 1261 CACTTCCAGCCCTACATCATGGCTGACATCTACAGCTTCGGCCTTAATCATTTGGGAGATG 1320
Qy 441 AlaArgGlnCysIleThrGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1321 GCTCGTGTGTATCACAGAGGATCGTGGAAAGAAATACCAATTGGCATAATTACAACATG 1380
Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1381 GTACCGAGTGATCGTCATACGAAGATATCGTGAGGTGTGTGTGTCAAACGTTTGGCG 1440
Qy 481 ProIleValSerAsnArgTyrAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1441 CCAATTGTGCTAATCGGTGGAACAGTGAATGATCTACAGACAGTTTGAAGCTAATG 1500
Qy 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db 1501 TCAGAATGTGTGGGCCCAACATCCAGCTCCAGACTCACAGCATTGAGAAATTAAGAAGACG 1560
Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1561 CTTGCCAAGATGTTGAATCCCAAGATGTAAATAATC 1596

RESULT 14

US-10-153-217-1
; Sequence 1, Application US/10153217
; Publication No. US20030072758A1
; GENERAL INFORMATION:
; APPLICANT: HOWE, JAMES R.
; TITLE OF INVENTION: BMPRIA INVOLVEMENT IN JUVENILE POLYPOSI
; FILE REFERENCE: IOWA:037US
; CURRENT APPLICATION NUMBER: US/10/153,217
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: 60/292,691
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1596)
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-153-217-1
Alignment Scores:
Pred. No.: 0 Length: 2623
Score: 2769.00 Matches: 517
Percent Similarity: 98.50% Conservative: 7
Best Local Similarity: 97.18% Mismatches: 8

Query Match: 97.57% Indels: 0
DB: 5 Gaps: 0
US-10-600-645-2 (1-532) x US-10-153-217-1 (1-2623)
Qy 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
Db 1 ATGACTCAGCTATACATTTACATCAGATTATTGGGAGCCTATTGTTCATCATCTTCGT 60
Qy 21 ValGlnGlyGluAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db 61 GTTCAAGAGCAGAACTCTGGATAGTAGTCTCATGGCAGCTGGGATGAAATCAGACTCCGAC 120
Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
Db 121 CAGAAAAAGTCAGAAAAATCGAGTAACTTAGCACCAGAGAGATACCTTGGCTTTTAAAG 180
Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
Db 181 TGTATTGTCTCAGGGCAGCTGTCAGATGATGCTATTATAACACATGCATTAACATAATGA 240
Qy 81 HisCysPheAlaIleIleGluAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 241 CATTTGCTTTGCCATCATAGAAAGATGACCAGGGAGAAACACACATTAGCTTCAGGGTGT 300
Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 301 ATGAAATATGAAGGATCTGATTTTTCAGTGCNAAGATTCTCCAAAGAGCCAGCTACGCCG 360
Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 361 ACAATAGAATGTGTGCGACCAATTTATGTAAACAGTATTTGCAACCCACACTGCCCCCT 420
Qy 141 ValValIleGlyProPheAspGlySerValArgTyrLeuAlaValLeuLeuSerMet 160
Db 421 GTTGTATAGTGCCTTTTTCATGGCAGCATTCGATGGCTGCTTTTGTCTCATTTCTATG 480
Qy 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
Db 481 GCTGTCTGCATAAATTTGCTATGATCATCTTCCAGCTGCTTTTGTACAAACATTATTCG 540
Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
Db 541 AAGAGCATCTCAAGCAGACGTCGTTACAATCGTATTTGGAACAGGATCAAGCATTTATT 600
Qy 201 ProValGlyGluSerLeuLysAspLeuLeuAspGlnSerGlnSerSerGlySerGlySer 220
Db 601 CCAGTTGGAGAAATCACTAAAGACCTTATTGACCAAGTTCACAAAGTTCTGGTAGTGGTCT 660
Qy 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 661 GGACTACCTTTATTTGTTTTCAGGAACTATTGCCAAACAGATTTCAGATGGTCCGGCAAGTT 720
Qy 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGlyLysValAlaVal 260
Db 721 GGTAAAGCCCGATATGGAGAAAGTATGGATGGCAAAATGGCGTGGCGAAAAAGTGGCGGTG 780
Qy 261 LysValPhePheThrThrGluGluAspSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db 781 AAAGTATTCTTTTACCACCTGAAGAACCCAGCTGGTTTCGAGAAACAGAAATCTACCAAACT 840
Qy 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db 841 GTGCTAATGGCCCATGAAACATATCTGTTTTCATAGCGGCAGACATTAAAGGTACAGGT 900
Qy 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 901 TCCTGGACTCAGCTCTATTGATTACTGATTACCATGAAATGGATCTCTCTATGACTTC 960
Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 961 CTGAAATGTGCTACACTGGACACAGAGCCCTGCTTAAATTTGGCTTATTACGTGCTGCTGT 1020

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QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1021 GGTCTGTGCACCTGTCACACAGAAATTTATGGACCCCAAGGAAAGCCCAATATGCTCAT 1080
QY 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
Db 1081 CGAGACCTAAAGACGAAACATCCTCATCAAGAAATATGGAGTTGCTGCATTCCTGAC 1140
QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1141 CTGGGCTTGTCTGTTAAATTTCAACAGTGCACACAAATGAAGTTGATGTGCTTGAATACC 1200
QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLysAsn 420
Db 1201 AGGGTGGGCAACCAAGCTTACATGGCTCCGAAGTGTGGAGAAAGCCGTGAACAAAAC 1260
QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTyrGluMet 440
Db 1261 CACTTCCAGCCCTACATCATGCTGACATCTACAGCTTCGGCTAATCATTTGGAGATG 1320
QY 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTrpAsnMet 460
Db 1321 GCTCGTGTGTATCACAGGAGGATCGTGAAGAAATACCAATTGCATATTACAACATG 1380
QY 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1381 GTACCGAGTGATCCGTCACCAAGATATGCGTGAGGTTGTGTGTCAACGTTTGGCGG 1440
QY 481 ProIleValSerAsnArgTyrAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1441 CCAATTGTCTTAATCGTGGAACTGATGATGATCTACGACGAGTTTGAAGCTAATG 1500
QY 501 SerGluCysTyrAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db 1501 TCAGAATGCTGGGCGCCACAAATCCAGCTCCAGACTCACAGCATTCAGAAATTAAGAAGACG 1560
QY 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1561 CITGCCAAGATGGTTGAATCCCAAGATGTAAATAATC 1596

RESULT 15
US-09-903-068-5
; Sequence 5, Application US/09903068
; Patent No. US20020123139A1
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
; Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Felife & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/903,068
; FILING DATE: 11-Jul-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/679,187
; FILING DATE: <Unknown>
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: 17-No. US20020123139A1ember-1993
; APPLICATION NUMBER: 9224057.1
; FILING DATE: 17-No. US20020123139A1ember-1992
; APPLICATION NUMBER: 9304677.9
; FILING DATE: 8-March-1993
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; APPLICATION NUMBER: 9304680.3
; FILING DATE: 8-March-1993
; APPLICATION NUMBER: 9311047.6
; FILING DATE: 28-May-1993
; APPLICATION NUMBER: 9313763.6
; FILING DATE: 2-July-1993
; APPLICATION NUMBER: 9136099.2
; FILING DATE: 3-August-1993
; APPLICATION NUMBER: 9321344.5
; FILING DATE: 15-October-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohlei, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2932 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 310..1905
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-903-068-5

Alignment Scores:
Pred. No.: 0 Length: 2932
Score: 2769.00 Matches: 517
Percent Similarity: 98.50% Conservative: 7
Best Local Similarity: 97.18% Mismatches: 8
Query Match: 97.57% Indels: 0
DB: 3 Gaps: 0

US-10-600-645-2 (1-532) x US-09-903-068-5 (1-2932)
QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
Db 310 ATGACTCAGCTATACATTTACATCAGATTATTGGAGCCTATTTCCTCATCATTTCTCGT 369
QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db 370 GTTCAAGGACAGAATCTGGATAGTAGTCTTTCATGGCACTGGGATGAAATCAGACTCCGAC 429
QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
Db 430 CAGAAAAAGTCAGAAAAATGGAGTAGAACCTTAGCACCAGAGGATACCTTGCCCTTTTAAAG 489
QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
Db 490 TGCTATTGCTCAGGGCACTGTCCAGATGATGCTATTATAACACATGATCAATAATGGA 549
QY 81 HisCysPheAlaIleIleGluGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 550 CATTGCTTTGCCATCATAGAAGAGATGACCAGGGAGAAACACATATTAGCTTTCAGGGTGT 609
QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 610 ATGAAATATGAAGGATCTGATTTTCAGTGCAGAAAGATCTCCAAAAGCCAGCTACGCCGG 669
QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 670 ACAATAGAATGTTGTCCGACCAATTTATGTAAACAGTATTATTGCAACACCACTGCCCCCT 729
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Qy	141	ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet	160
Db	730	GTTGTCTATAGTCGCGTTTTTTGATGGCAGCATTCGATGGCTGGTTTTTGTCTCATTTCTATG	789
Qy	161	AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys	180
Db	790	GCTGCTGTGCATAATTGCTATGATCATCTTCTCCAGCTGTCTTTTGTTTACAACATTATTG	849
Qy	181	LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle	200
Db	850	AAGAGCATCTCAAGCAGACGTCGTTACAATCGTCATTGGAAACAGGATGAAGCATTTATT	909
Qy	201	ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer	220
Db	910	CCAGTTGGAGAAATCACTAAAAAGACCTTATTACACAGTCACAAAGTTCTCTGGTAGTGGGTCT	969
Qy	221	GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal	240
Db	970	GGACTACCTTTATTGGTTTCAGCAACTATTGCCAAACAGATTTCAGATGGTTCGGCAAGTT	1029
Qy	241	GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal	260
Db	1030	GGTAAAGGCCGATATGGAGAAGTATGGATGGCAATGGCGTGGCGAAAGTGGCGGTG	1089
Qy	261	LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr	280
Db	1090	AAAGTATTCTTTAGCACTGAAGAAGCAGCTGGTTTCGAGAAAACAGAAAATCTACCAACT	1149
Qy	281	ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAspIleLysGlyThrGly	300
Db	1150	GTGCTAATGGCCCATGAAGAAACATACTTGGTTTTCATAGCGGACACATTAAGAGTACAGGT	1209
Qy	301	SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe	320
Db	1210	TCCTGGACTCAGCTCTATTGATTACTGATTACCATGAAATGGATCTCTCTATGACTTC	1269
Qy	321	LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys	340
Db	1270	CTGAAATGCTGTACACTGGACACACAGAGCCCTGCTTAAATTTGGCTTATTTCAGTGCCTGT	1329
Qy	341	GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis	360
Db	1330	GGTCTGTGGCCACCTGCACACAGAAATTTATGGCACCCCAAGAAAGCCCGAAATGGTCTAT	1389
Qy	361	ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp	380
Db	1390	CGAGACCTTAAGACGACAAACATCTCTCATCAAGNAAAATGGAGTTGCTGCATTTGCTGAC	1449
Qy	381	LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr	400
Db	1450	CTGGCCCTTGTGTTAAATTCAACAGTGCACAAATCAAGTTGATGTGCCCTTTGAATACC	1509
Qy	401	ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn	420
Db	1510	AGGGTGGGCACCAAAACGCTACATGGCTCCGCAAGTGTGGACGAAAGCCCTGGAACAAAAC	1569
Qy	421	HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleIleTrpGluMet	440
Db	1570	CACCTCCAGCCCTACATCATGGCTGACATCTACAGCTTCGGCCTTAATCATTTGGGAGATG	1629
Qy	441	AlaArgArgCysIleThrGlyGlyIleValIleGluTyrGlnLeuProTyrTyrAsnMet	460
Db	1630	GCTCGTCTGTTGATCACAGGAGGGATCGTGGAGAATACCAATTTGCCATATTACAACATG	1689
Qy	461	ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg	480
Db	1690	GTACCGAGTGATCCGTCATACGAAGAATATGCGTGAGGTTGTGTGTGTCAAAACGTTTGGCGG	1749
Qy	481	ProfileValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet	500
Db	1750	CCAAATGTGTCTAATTCGGTGAACAGTGATGAATGCTACGAGCAGTTTTTGAAGAGCTAATG	1809
Qy	501	SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr	520

Search completed: December 10, 2005, 00:09:40
Job time : 852 secs

Db	1810	TCAGAATGCTGGGGCCCAACTCCAGCCTCCAGACTCAGCATTGAGAAATTAAGAAGACGC	1869
Qy	521	LeuAlaIysMetValGluSerGlnAspValIysIle	532
Db	1870	CTTCCCAAGATGGTTGAATCCCAAGATGTAAAAATC	1905

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